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(54) Title: NOVEL MEANS AND METHODS FOR CEREAL PATHOGEN RESISTANCE

(57) Abstract: The present disclosure provides means and methods for conferring pathogen resistance to, or increasing pathogen resistance of, a cereal plant cell, or a cereal plant or part thereof, comprising inhibiting the expression or activity of the at least one WRKY protein in a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or control plant or part thereof, lacking the inhibition of the expression or activity of the at least one WRKY protein, wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid, and/or at least one modification enhancing the expression or activity of a jasmonate receptor protein as compared to a corresponding control plant cell lacking the at least one modification. The present invention also provides cereal plant cells, or cereal plants or parts thereof, carrying the inhibition of the expression or activity of the at least one WRKY protein. In particular, the pathogen is *Zymoseptoria tritici*.



NOVEL MEANS AND METHODS FOR CEREAL PATHOGEN RESISTANCE

TECHNICAL FIELD

The present disclosure relates generally to the field of plant biotechnology, and more specifically to the field of cereal pathogen resistance. In particular, the present disclosure relates to novel means and methods for providing pathogen resistance to cereals based on the identification of key WRKYs whose expression or activity is fertilizer-responsive and/or which are characterized by the amino acid sequence motif D-G/E-X₁-X₂-W-R-K-Y-G-K/E/Q-K/E, wherein X₁ is a hydrophobic amino acid and X₂ is a polar, non-hydrophobic amino acid, and on the identification of a key jasmonate receptor protein.

BACKGROUND

The foundation of global food security is built on the three cereals wheat, rice and maize, where wheat is the leading source of vegetable protein in human food. In the UK for example this cereal is the most important crop grown with an annual value of about £1.2 billion. The average yield of wheat in the field in the UK is currently 8.4 tonnes/ha, but this yield is dependent on high levels of mineral fertilizer (especially Nitrogen, Phosphorus and Potassium) and pesticide usage.

Nitrogen (N) fertilizer use is of concern because it is associated both with high levels of energy use and greenhouse gas emissions (e.g. CO₂, N₂O) that cause climate change, in addition to eutrophication of fresh water and marine ecosystems. However, nitrogen fertilization is required for achieving high yield in wheat and other cereals, and increasing sustainability through decrease in nitrogen input is not commercially feasible due to the resulting fall in yield. Given that high-nitrogen nutrient regimes are reality in the field, decreasing pesticide usage is a target for enhancing sustainability of production of cereals, in particular wheat.

Zymoseptoria tritici is the fungal pathogen that causes Septoria leaf blotch disease (STB) in wheat. STB disease is the most economically important foliar disease of winter wheat in most western European countries. The disease is characterized by necrotic blotches on the foliage which significantly reduces the plants ability to efficiently grow and produce grain. There is increasing evidence that high soil nitrogen and other mineral fertilizers have the undesirable side-effect of enhancing the development of fungal diseases including Septoria (Simón M. R., et al. Influence of nitrogen supply on the susceptibility of wheat to *Septoria tritici*. *Journal of Phytopathology* 151.5 (2003): 283-289.; Loyce Chantal, et al. Interaction between cultivar and crop management effects on winter wheat diseases, lodging, and yield. *Crop protection* 27.7

(2008): 1131-1142). The mechanisms leading to the above mentioned nutrient induced changes in disease development are largely unknown.

Zymoseptoria tritici are Ascomycete pycnidia-producing fungi which unlike most other plant pathogens, infects through stomata rather than by direct penetration. The principle method of spread from leaf to leaf in the field is via rain splash. The disease is characterized by a long latent period of approximately two weeks during which the fungus manages to evade the host defences. Following the latent phase, there is a rapid switch to necrotrophy immediately prior to symptom expression.

Despite its importance as a disease, there is very little information available on the defense mechanisms or immune responses that allow cereals such as wheat to counter *Septoria* infection. Fungicides provide the only control measure for this devastating disease, but in addition to the high cost, the currently available fungicides are becoming less effective against new resistant strains of *Septoria*.

Susceptible varieties of wheat will be susceptible to the disease throughout the life cycle whenever there are healthy green leaves available for the pathogen to colonise. Examples where virulence is restricted to a particular development stage (i.e. adult or seedling stage) do exist but these are limited to isolate specific major gene relationships which are of limited interest to breeding for quantitative, durable disease resistance (Kema, Gert HJ, and Cor H. van Silfhout. Genetic variation for virulence and resistance in the wheat-*Mycosphaerella graminicola* pathosystem III. Comparative seedling and adult plant experiments. *Phytopathology* 87.3 (1997): 266-272). Growth stage 39 (GS39) on the Zadok scale, when the flag leaf is fully emerged is agronomically the most important stage since the flag leaf is the principle driver of yield; necrosis on the flag leaf reduces its photosynthetic capacity and consequently overall yield potential is reduced.

A defense mechanisms or immune responses against fungal pathogens like *Septoria* might be triggered by Jasmonic acid (JA) based signaling pathway. JA and its derivatives are fatty acid-derived hormones ubiquitously present in the plant kingdom. JA acts as a regulatory molecule in many developmental processes including fertility, sex determination, root elongation and fruit ripening and is also a potent signal activating plant defences against pathogens, herbivory, wounding and abiotic stress. JA also plays a critical role when plants have to decide whether 'to defend' rather than 'grow', with transcriptional reprogramming activating the cells defence mechanisms and arresting cell cycle and growth (Pauwels, Laurens, et al. "Mapping methyl jasmonate-mediated transcriptional reprogramming of metabolism and cell cycle progression in cultured *Arabidopsis* cells." *Proceedings of the National Academy of Sciences* 105.4 (2008): 1380-1385).

According to the accepted model of jasmonate regulated defense genes, in the absence of stimuli, JA is not synthesized. The absence of JA allows the Jasmonate ZIM-domain (JAZ) proteins to bind to transcription factors, such as MYC2, and prevent expression of the JA-responsive genes. MYC2 is a bHLH-type transcription factor that can bind the G-box or T/G-box in promoters of JA-regulated genes. Therefore, in absence of JA, JAZ perform its repression via binding and sequestering MYC2, preventing MYC2 associating with the promoters of its targets.

The core of the JA perception and signaling is currently defined by the SCF^{COI1}/JAZ/MYC2 complex. COI1 (coronatine insensitive 1-like protein) is a JA receptor and forms the F-box component of a multiprotein SKIP–CULLIN–F-box complex. These complexes are E3 ubiquitin ligases which function to catalyze the ubiquitination of proteins. The F-box is the component that confers specificity for the substrate.

Following pathogen attack, JA biosynthesis is stimulated, resulting in accumulation of its bioactive form (JA-Ile). In the presence of JA-Ile, the COI1 complex is able to recognize the JAZ proteins, and target them for degradation via the 26S proteasome. JA triggers this by binding to and stabilize the F-box subunit of the complex. Following JAZ degradation, the MYC2 transcription factor is free to recruit the RNA polymerase II transcriptional machinery to the promoter of the JA-responsive genes, assisted the Mediator complex. JA responsive genes include a series of specific defence gene including Pathogen Response (PR) genes.

In comparison to Arabidopsis, knowledge on JA signaling and biosynthesis in wheat and other cereals is very limited and fragmented. However, JA-dependent responses to diseases, biotic and abiotic stresses have been increasingly investigated in wheat during the last few years with recent studies providing strong evidence for the involvement of JA in wheat defense against pathogens.

There is no other nutrient as important as nitrogen (N) to drive cereal yields, in particular wheat yields. Nitrogen and along with phosphorus (P) and potassium (K), make up the three macronutrients required for growth. A typical nitrogen fertilization regime for UK winter wheat may mean an application of ~200kg/ha of nitrogen, typically applied in a single or split application when the plants reach their most active growth in the spring (GS31, around mid April in Eastern UK), when the plants make the physiological switch between vegetative and reproductive development. Additional, smaller applications are often made for bread wheat crops later in development in order to boost protein yield.

A number of reports have linked increased nitrogen availability with higher susceptibility to *S. tritici* (Shipton, W. A., et al. The common Septoria diseases of wheat. *The Botanical Review* 37.2 (1971): 231-262; Prew, R. D., et al. Effects of eight factors on the growth and nutrient

uptake of winter wheat and on the incidence of pests and diseases. *The Journal of Agricultural Science* 100.02 (1983): 363-382). The mechanisms leading to these nutrient induced changes in disease development are currently not known, although additional studies have suggested that this could be due to the increased nutritional status of the host tissue studies (Leitch, M. H., and P. D. Jenkins. Influence of nitrogen on the development of Septoria epidemics in winter wheat. *The Journal of Agricultural Science* 124.03 (1995): 361-368; Simón et al., 2003). In contrast, several studies have found that high nitrogen actually reduces disease severity (Gooding, M. J., and W. P. Davies. Foliar urea fertilization of cereals: a review. *Fertilizer Research* 32.2 (1992): 209-222; Johnston, H. W., J. A. MacLeod, and K. S. Clough. Effects of cycocel (CCC) and fungicide sprays on spring wheat grown at three nitrogen levels. *Canadian Journal of Plant Science* 59.4 (1979): 917-929; Broschius, S. C., J. A. Frank, and J. R. Frederick. Influence of winter wheat management practices on the severity of powdery mildew and Septoria blotch in Pennsylvania. *Phytopathology* 75.5 (1985): 538-542), although these studies were limited in scope or were only showing a partial effect. A more recent study investigated the effects of different fungicides in combination to different N rates on the severity of foliar diseases, senescence and yield (Ishikawa S. M. C. Hare and P. S. Kettlewell (2012). Effects of strobilurin fungicide programmes and fertilizer nitrogen rates on winter wheat: severity of Septoria tritici, leaf senescence and yield. *The Journal of Agricultural Science*, 150, pp 411-426. doi:10.1017/S0021859611000670). However, the authors were unable to draw any robust conclusions due to the limited data set available.

A single study has suggested that potassium fertilization was positively correlated with disease resistance (Arabi, M. I. E., N. MirAli, and M. Jawhar. Effect of foliar and soil potassium fertilisation on wheat yield and severity of Septoria tritici blotch. *Australasian plant pathology* 31.4 (2002): 359-362), with the effects being genotype dependent. A study by Paraschivu et al, (Influence of nitrogen and phosphorus on the risk of epidemics by septoria tritici in winter wheat. *Annals of the University of Craiova-Agriculture, Montanology, Cadastre Series* 41.2 (2011): 215-219), suggested that the increase in disease severity seen under high nitrogen can be limited by increasing phosphorus fertilization.

In short, there is less known about the mechanisms leading to the above mentioned nutrient induced changes in disease development. Therefore the objective of the present disclosure is to provide means and methods for providing or boosting pathogen resistance to cereals, in particular resistance against fungal pathogens such as *Septoria*, under fertilizer input growth conditions necessary for maintaining yield.

SUMMARY OF THE DISCLOSURE

The present disclosure provides means and methods for conferring pathogen resistance to, or increasing pathogen resistance of, a cereal plant cell, or a cereal plant or part thereof, comprising inhibiting the expression or activity of the at least one WRKY protein in a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or control plant or part thereof, lacking the inhibition of the expression or activity of the at least one WRKY protein, and/or enhancing the expression or activity of a jasmonate receptor protein in a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or control plant or part thereof, lacking the enhancement of the expression or activity of the jasmonate receptor protein, wherein the jasmonate receptor protein a) having the amino acid sequence of SEQ ID NO: 76, b) having an amino acid sequence exhibiting an identity of at least 80% to the amino acid sequence of SEQ ID NO: 76, c) is encoded by the nucleic acid sequence of SEQ ID NO: 75, d) is encoded by a nucleic acid sequence exhibiting an identity of at least 80% to the nucleic acid sequence of SEQ ID NO: 75, or e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c), and wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In particular, the present disclosure provides a cereal plant cell having introduced into its genome at least one modification inhibiting the expression or activity of at least one WRKY protein as compared to a corresponding control plant cell lacking the at least one modification, wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid, and/or at least one modification enhancing the expression or activity of a jasmonate receptor protein as compared to a corresponding control plant cell lacking the at least one modification, wherein the jasmonate receptor protein a) having the amino acid sequence of SEQ ID NO: 76, b) having an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, c) is encoded by the nucleic acid sequence of SEQ ID NO: 75, d) is encoded by a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c). Preferably, the at least one modification(s) are introduced into the at least one endogenous WRKY gene encoding the at least one WRKY protein and/or into an endogenous jasmonate receptor gene encoding the jasmonate receptor protein.

Aspects and embodiments encompassed by the present invention include the following, without being limited thereto:

[1] A cereal plant cell having introduced into its genome at least one modification inhibiting the expression or activity of at least one WRKY protein as compared to a corresponding control plant cell lacking the at least one modification, wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid, and/or at least one modification enhancing the expression or activity of a jasmonate receptor protein as compared to a corresponding control plant cell lacking the at least one modification, wherein the jasmonate receptor protein a) having the amino acid sequence of SEQ ID NO: 76, b) having an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, c) is encoded by the nucleic acid sequence of SEQ ID NO: 75, d) is encoded by a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c), preferably wherein the at least one modification(s) are introduced into the at least one endogenous WRKY gene encoding the at least one WRKY protein and/or into an endogenous jasmonate receptor gene encoding the jasmonate receptor protein, preferably wherein the at least one modification(s) are introduced into the at least one endogenous WRKY gene encoding the at least one WRKY protein and/or a jasmonate receptor gene encoding the jasmonate receptor protein.

[2] The cereal plant cell of item [1], wherein the at least one WRKY protein is a negative and/or the jasmonate receptor protein is a positive regulator of the plant cell defense mechanism against a pathogen, preferably against a fungal pathogen, more preferably against *Septoria*.

[3] The cereal plant cell of item [1] or [2], wherein the amino acid sequence motif is D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E-X-X-X3-X-X2 shown in SEQ ID NO: 2, wherein X is any amino acid, X1 is a hydrophobic amino acid, X2 is a polar, non-hydrophobic amino acid, and X3 is a polar, non-aromatic amino acid.

[4] The cereal plant cell of any one of items [1]-[3], wherein the inhibition of the expression or activity of the at least one WRKY protein leads to an enhanced expression or activity of the jasmonate receptor protein as defined in item [1].

[5] The plant cell of any one of items [1]-[4], wherein the cereal plant cell is the cell of a wheat plant (*Triticum aestivum*), the cell of a rye plant (*Secale cereale*), the cell of a barley plant (*Hordeum vulgare*), or the cell of a maize plant (*Zea mays*).

[6] The cereal plant cell of any one of items [1]-[5], wherein the at least one WRKY gene comprises a nucleic acid sequence selected from the group consisting of TaWRKY10 (SEQ ID NO: 3), TaWRKY13 (SEQ ID NO: 5), TaWRKY19 (SEQ ID NO: 7), TaWRKY29 (SEQ ID NO: 9), TaWRKY39 (SEQ ID NO: 11), TaWRKY53B (SEQ ID NO: 13), and TaWRKY68A (SEQ ID NO: 15), or homologs thereof, and wherein the jasmonate receptor gene comprises (a) the nucleic acid sequence of TaCOI1 (SEQ ID NO: 75), (b) a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, (c) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (a), (d) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (e) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76.

[7] The cereal plant cell of any one of items [1]-[6], wherein the at least one WRKY protein comprises an amino acid sequence selected from the group consisting of TaWRKY10 (SEQ ID NO: 4), TaWRKY13 (SEQ ID NO: 6), TaWRKY19 (SEQ ID NO: 8), TaWRKY29 (SEQ ID NO: 10), TaWRKY39 (SEQ ID NO: 12), TaWRKY53B (SEQ ID NO: 14), and TaWRKY68A (SEQ ID NO: 16), or homologs thereof.

[8] The cereal plant cell of any one of items [1]-[7], wherein the at least one modification(s) result in increased pathogen resistance of a cereal plant comprising said cereal plant cell as compared to a control plant, preferably wherein the at least one modification results in an increased resistance against a fungal pathogen, in particular against Septoria.

[9] The cereal plant cell of any one of items [1]-[8], wherein the at least one modification inhibiting the expression or activity of at least one WRKY protein is caused by RNA interference, sense suppression, allele swap, insertional mutagenesis, mutagenesis or genome editing of the endogenous WRKY gene, and/or the at least one modification enhancing the expression or activity of the jasmonate receptor protein is caused by transgenic overexpression, allele swap, mutagenesis or genome editing of the endogenous jasmonate receptor gene.

[10] The cereal plant cell of any one of items [1]-[9], wherein the at least one modification comprises one or more transposons, one or more insertions, one or more additions, one or

more deletions or one or more point mutations in the at least one endogenous WRKY gene and/or in the jasmonate receptor gene.

[11] The cereal plant cell of any one of items [1]-[10], wherein the at least one modification is introduced into the cereal plant cell by

(a) introducing at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising (i) at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), or (ii) at least 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 400, 500, 700, 800, 900 or 1000 contiguous nucleotides of the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A), and a homolog thereof, preferably in sense and/or in antisense, into the plant cell such that the at least one polynucleotide sequence is operatively linked to a promoter in a sense or antisense orientation; or

(b) introducing at least one polynucleotide sequence comprising one or more subsequences of a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), into the plant cell, wherein the at least one polynucleotide sequence is configured for RNA interference, preferably wherein the at least one polynucleotide sequence is configured for endogenous (post transcriptional) gene silencing or virus-induced gene silencing; or

(c) introducing at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising the nucleic acid sequence of TaCOI1 (SEQ ID NO: 75), (b) a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or (c) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (a), preferably the at least one polynucleotide sequence is operatively linked to a heterologous promoter.

[12] The cereal plant cell of any one of items [1]-[11], which is in a plant comprising a phenotype of increased pathogen resistance, preferably a phenotype of increased resistance against a fungal pathogen, in particular against *Septoria*.

[13] The cereal plant cell of any one of items [2], [8] or [12], wherein the fungal pathogen is *Zymoseptoria tritici*.

[14] A cereal plant comprising or containing the cereal plant cell of any one of items [1]-[13].

[15] A cereal plant having an increased pathogen resistance, preferably having an increased resistance against a fungal pathogen, wherein the increased pathogen resistance results from at least one modification introduced into the genome of the plant inhibiting the expression or activity of at least one WRKY protein as compared to a corresponding control plant lacking the at least one modification, wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid, and/or from at least one modification introduced into the genome of the cereal plant enhancing the expression or activity of a jasmonate receptor protein as compared to a corresponding control plant cell lacking the at least one modification wherein the jasmonate receptor protein a) having the amino acid sequence of SEQ ID NO: 76, b) having an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, c) is encoded by the nucleic acid sequence of SEQ ID NO: 75, d) is encoded by a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c), preferably wherein the at least one modification(s) are introduced into the at least one endogenous WRKY gene encoding the at least one WRKY protein, and/or into an endogenous jasmonate receptor gene encoding the jasmonate receptor protein.

[16] The cereal plant of item [15], wherein the increased pathogen resistance results from: (a) a modification in at least one endogenous WRKY gene comprising a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), wherein the modification comprises

one or more transposons, one or more insertions, one or more additions, one or more deletions or one or more point mutations in the at least one endogenous WRKY gene; or (b) at least one introduced transgene comprising a nucleic acid sequence, or a complement thereof, comprising (i) at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), or (ii) at least 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 400, 500, 700, 800, 900 or 1000 contiguous nucleotides of the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A), and a homolog thereof, preferably in sense and/or in antisense, wherein the transgene is operatively linked to a promoter in a sense or antisense orientation; or (c) at least one introduced polynucleotide sequence comprising one or more subsequences of a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), wherein the at least one polynucleotide sequence is in RNA interference configuration, preferably wherein the at least one polynucleotide sequence is configured for endogenous (post transcriptional) gene silencing or virus-induced gene silencing; or (d) a modification in the endogenous jasmonate receptor gene comprising (i) the nucleotide sequence of TaCOI1 (SEQ ID NO: 75), (ii) a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, (iii) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (i), (iv) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (v) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, wherein the modification comprises one or more transposons, one or more insertions, one or more additions, one or more deletions, or one or more point mutations in the endogenous jasmonate receptor gene; or (e) an introduced transgene comprising a nucleic acid sequence, or a complement thereof, comprising (i) the nucleic acid sequence of SEQ ID NO: 75, (ii) a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, (iii) a nucleic

acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (i), (iv) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (v) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, wherein the transgene is operatively linked to a heterologous promoter.

[17] The cereal plant of any one of item or [15] or [16], wherein the inhibition of the expression or activity of the at least one WRKY protein leads to an enhanced expression or activity of the jasmonate receptor protein as defined in item [15].

[18] The cereal plant of any of one of items [15]-[17], wherein the plant is a hybrid cereal plant.

[19] The cereal plant of any one of items [15b] or [15d], wherein the promoter is a tissue-specific promoter, a temporally regulated promoter, or an inducible promoter (e.g. pathogen responsive promoter).

[20] A method for conferring pathogen resistance to, or increasing pathogen resistance of, a cereal plant cell, or a cereal plant or part thereof, the method comprising the step of inhibiting the expression or activity of at least one WRKY protein in a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or plant or part thereof, lacking the inhibition, wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid, and/or the step of enhancing the expression or activity of a jasmonate receptor protein of a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or plant or part thereof, lacking the enhancement, wherein the jasmonate receptor protein a) having the amino acid sequence of SEQ ID NO: 76, b) having an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, c) is encoded by the nucleic acid sequence of SEQ ID NO: 75, d) is encoded by a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c).

[21] A method of producing a cereal plant cell, or a cereal plant or part thereof, having an increased pathogen resistance as compared to a corresponding control plant cell, or plant or part thereof, the method comprising the step of inhibiting the expression or activity of at least

one WRKY protein in a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or plant or part thereof, lacking the inhibition, wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid, and/or the step of enhancing the expression or activity of a jasmonate receptor protein of a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or plant or part thereof, lacking the enhancement, wherein the jasmonate receptor protein a) having the amino acid sequence of SEQ ID NO: 76, b) having an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, c) is encoded by the nucleic acid sequence of SEQ ID NO: 75, d) is encoded by a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c).

[22] The method of item 20 or 21, wherein the step of inhibiting the expression or activity of at least one WRKY protein comprises introducing into the genome of the cereal plant cell, or a cereal plant or part thereof, at least one modification inhibiting the expression and/or activity of the at least one WRKY protein as compared to a corresponding control plant cell, or a cereal plant or part thereof, lacking the at least one modification, and/or introducing into the genome of the cereal plant cell, or a cereal plant or part thereof, at least one modification enhancing the expression and/or activity of the jasmonate receptor protein as compared to a corresponding control plant cell, or a cereal plant or part thereof, lacking the at least one modification, preferably wherein the at least one modification(s) are introduced into the at least one endogenous WRKY gene encoding the at least one WRKY protein and/or into a jasmonate receptor gene encoding the jasmonate receptor protein.

[23] The method of any one of items [20]-[22], wherein the amino acid sequence motif is D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E-X-X-X3-X-X2 shown in SEQ ID NO: 2, wherein X is any amino acid, X1 is a hydrophobic amino acid, X2 is a polar, non-hydrophobic amino acid, and X3 is a polar, non-aromatic amino acid.

[24] The method of any one of items [20]-[23], wherein the inhibition of the expression or activity of the at least one WRKY protein leads to an enhanced expression or activity of the jasmonate receptor protein as defined in item [20] or item [21].

[25] The method of any one of items [20]-[24], wherein the at least one WRKY gene comprises a nucleic acid sequence selected from the group consisting of TaWRKY10 (SEQ ID NO: 3), TaWRKY13 (SEQ ID NO: 5), TaWRKY19 (SEQ ID NO: 7), TaWRKY29 (SEQ ID NO: 9), TaWRKY39 (SEQ ID NO: 11), TaWRKY53B (SEQ ID NO: 13), and TaWRKY68A (SEQ ID NO: 15), or homologs thereof, and wherein the jasmonate receptor gene comprises (a) the nucleic acid sequence of TaCOI1 (SEQ ID NO: 75), (b) a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, (c) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (a), (d) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (e) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76.

[26] The method of any one of items [20]-[25], wherein the at least one WRKY protein comprises an amino acid sequence selected from the group consisting of TaWRKY10 (SEQ ID NO: 4), TaWRKY13 (SEQ ID NO: 6), TaWRKY19 (SEQ ID NO: 8), TaWRKY29 (SEQ ID NO: 10), TaWRKY39 (SEQ ID NO: 12), TaWRKY53B (SEQ ID NO: 14), and TaWRKY68A (SEQ ID NO: 16), or homologs thereof, or is encoded by a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A).

[27] The method of any one of items [22]-[26], wherein the at least one modification comprises one or more transposons, one or more insertions, one or more additions, one or more deletions or one or more point mutations in the at least one endogenous WRKY gene and/or the jasmonate receptor protein.

[28] The method of any one of items [22]-[27], wherein the at least one modification is introduced into the cereal plant cell, or cereal plant or part thereof, by (a) introducing at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising (i) at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A) or (ii) at least 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 400, 500, 700, 800, 900 or 1000 contiguous nucleotides of the nucleic acid sequence

of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A), and a homolog thereof, preferably in sense and/or in antisense, into the cereal plant cell, or cereal plant or part thereof, such that the at least one polynucleotide sequence is operatively linked to a promoter in a sense or antisense orientation; or (b) introducing at least one polynucleotide sequence comprising one or more subsequences of a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), into the plant cell, or plant or part thereof, wherein the at least one polynucleotide sequence is configured for RNA interference, preferably wherein the at least one polynucleotide sequence is configured for endogenous (post transcriptional) gene silencing or virus-induced gene silencing; or (c) introducing at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising (i) the nucleic acid sequence of SEQ ID NO: 75 (TaCOI1), (ii) a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or (iii) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (a).

[29] A method of identifying a cereal plant cell, or a cereal plant or part thereof, having an increased pathogen resistance as compared to a corresponding control plant cell, or plant or part thereof, the method comprising the step of identifying a cereal plant cell, or a cereal plant or part thereof, in which the expression or activity of at least one WRKY protein, is inhibited as compared to a corresponding control plant cell, or plant or part thereof, lacking the inhibition, wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid, and/or in which the expression or activity of a jasmonate receptor protein is enhanced as compared to a corresponding control plant cell, or plant or part thereof, lacking the enhancement, wherein the jasmonate receptor protein a) having the amino acid sequence of SEQ ID NO: 76, b) having an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, c) is encoded by the nucleic acid sequence of SEQ ID NO: 75, d) is encoded by a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least

97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c), preferably wherein the at least one modification(s) are introduced into the at least one endogenous WRKY gene encoding the at least one WRKY protein and/or into an endogenous jasmonate receptor gene encoding the jasmonate receptor protein.

[30] The method of item [29], wherein the amino acid sequence motif is D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E-X-X-X3-X-X2 shown in SEQ ID NO: 2, wherein X is any amino acid, X1 is a hydrophobic amino acid, X2 is a polar, non-hydrophobic amino acid, and X3 is a polar, non-aromatic amino acid.

[31] The method of items [29] or [30], wherein the inhibition of the expression or activity of the at least one WRKY protein leads to an enhanced expression or activity of the jasmonate receptor protein as defined in item [29].

[32] The method of any one of items [29]-[31], wherein the at least one WRKY gene comprises a nucleic acid sequence selected from the group consisting of TaWRKY10 (SEQ ID NO: 3), TaWRKY13 (SEQ ID NO: 5), TaWRKY19 (SEQ ID NO: 7), TaWRKY29 (SEQ ID NO: 9), TaWRKY39 (SEQ ID NO: 11), TaWRKY53B (SEQ ID NO: 13), and TaWRKY68A (SEQ ID NO: 15), or homologs thereof, and wherein the jasmonate receptor gene comprises (a) the nucleic acid sequence of TaCOI1 (SEQ ID NO: 75), (b) a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, (c) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (a), (d) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (e) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76.

[33] The method of any one of items [29]-[32], wherein the at least one WRKY protein comprises an amino acid sequence selected from the group consisting of TaWRKY10 (SEQ ID NO: 4), TaWRKY13 (SEQ ID NO: 6), TaWRKY19 (SEQ ID NO: 8), TaWRKY29 (SEQ ID NO: 10), TaWRKY39 (SEQ ID NO: 12), TaWRKY53B (SEQ ID NO: 14), and TaWRKY68A (SEQ ID NO: 16), or homologs thereof, or is encoded by a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7

(TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A).

[34] The method of any one of items [22]-[29], wherein the cereal plant cell, or cereal plant or part thereof, comprises a heterozygous or homozygous mutation in the at least one WRKY gene encoding the at least one WRKY protein and/or a heterozygous or homozygous mutation in the jasmonate receptor gene encoding the jasmonate receptor protein.

[35] The method of item [34], wherein the mutant form of the at least one WRKY gene and/or the mutant form of the jasmonate receptor gene is/are introduced by *Agrobacterium*-mediated transfer, electroporation, micro-projectile bombardment, or sexual cross.

[36] The method of any one of items [20]-[35], wherein the cereal plant cell, or cereal plant or part thereof, has an increased resistance against a fungal pathogen, preferably an increased resistance against *Septoria* leaf blotch disease (or *Septoria tritici blotch*, *STB*), *Fusarium* disease (*Fusarium* sp.) or rust diseases (*Puccinia* sp.).

[37] A cereal plant cell, or a cereal plant or part thereof, produced or identified by the method of any one of items [20]-[36].

[38] A recombinant DNA construct comprising a polynucleotide sequence, or a fragment thereof, operatively linked to a heterologous promoter, wherein the polynucleotide sequence, or a fragment thereof, produces upon expression in a cereal plant cell, or cereal a plant or part thereof: (a) a protein that interferes with the expression or activity of at least one endogenous WRKY protein, which preferably comprises an amino acid sequence selected from the group consisting of TaWRKY10 (SEQ ID NO: 4), TaWRKY13 (SEQ ID NO: 6), TaWRKY19 (SEQ ID NO: 8), TaWRKY29 (SEQ ID NO: 10), TaWRKY39 (SEQ ID NO: 12), TaWRKY53B (SEQ ID NO: 14), and TaWRKY68A (SEQ ID NO: 16), or homologs thereof, or is encoded by a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A); (b) an RNA molecule that suppresses the expression of at least one endogenous WRKY protein, which preferably comprises an amino acid sequence selected from the group consisting of TaWRKY10 (SEQ ID NO: 4), TaWRKY13 (SEQ ID NO: 6), TaWRKY19 (SEQ ID NO: 8), TaWRKY29 (SEQ ID NO: 10), TaWRKY39 (SEQ ID NO: 12), TaWRKY53B (SEQ ID NO: 14), and TaWRKY68A (SEQ ID NO: 16), or homologs thereof, or is encoded by a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence

of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A); or (c) a loss-of-function mutation in at least one endogenous WRKY gene or the protein encoded thereby, which comprises a nucleic acid sequence selected from the group consisting of TaWRKY10 (SEQ ID NO: 3), TaWRKY13 (SEQ ID NO: 5), TaWRKY19 (SEQ ID NO: 7), TaWRKY29 (SEQ ID NO: 9), TaWRKY39 (SEQ ID NO: 11), TaWRKY53B (SEQ ID NO: 13), and TaWRKY68A (SEQ ID NO: 15), or homologs thereof, wherein the polynucleotide sequence comprises a nucleic acid sequence, or a complement thereof, comprising (i) at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A); or (ii) at least 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 400, 500, 700, 800, 900 or 1000 contiguous nucleotides of the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A) or a homolog thereof. An RNA molecule of (b) is for example a double-stranded RNA (dsRNA) molecule described in item [47].

[39] A recombinant DNA construct comprising a polynucleotide sequence, or a fragment thereof, operatively linked to a heterologous promoter, wherein the polynucleotide sequence comprises the nucleic acid sequence of SEQ ID NO: 75, a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c).

[40] A method of producing a (transgenic) cereal plant cell, or a cereal plant or part thereof, having an increased pathogen resistance as compared to a corresponding control plant cell, or plant or part thereof, the method comprising the steps of (a) incorporating or introducing into a cereal plant cell, or a cereal plant or part thereof, the recombinant DNA construct of item [38] or [39]; and (b) selecting a cereal plant cell, or a cereal plant or part thereof, comprising the said recombinant DNA construct and having an increased pathogen resistance as compared to a corresponding control plant cell, or plant or part thereof, that does not comprise the said recombinant DNA construct.

[41] The method of item [40], wherein the cereal plant cell, or cereal plant or part thereof, has an increased resistance against a fungal pathogen, preferably an increased resistance against

Septoria leaf blotch disease (*Septoria tritici blotch*, *STB*), Fusarium disease (*Fusarium sp.*) or rust diseases (*Puccinia sp.*).

[42] A cereal plant cell, or a cereal plant or part thereof, produced by the method of item [40] or [41].

[43] A cereal plant cell, or a cereal plant or part thereof, comprising the recombinant DNA construct of item [38] or [39] and having an increased pathogen resistance as compared to a corresponding control plant cell, or plant or part thereof, that does not comprise the said recombinant DNA construct.

[44] A method of producing a (transgenic) cereal plant having an increased pathogen resistance as compared to a corresponding control plant, the method comprising obtaining and planting seeds produced by the cereal plant of item [42] or [43], wherein the seed comprises the recombinant DNA construct of item [38] or [39], and wherein the plant grown from the planted seed is a progeny plant having an increased pathogen resistance as compared to a corresponding control plant that does not comprise the said recombinant DNA construct.

[45] The method of item [44], wherein the plant has an increased resistance against a fungal pathogen, preferably an increased resistance against Septoria leaf blotch disease (*Septoria tritici blotch*, *STB*), Fusarium disease (*Fusarium sp.*) or rust diseases (*Puccinia sp.*).

[46] A cereal plant produced by the method of item [44] or [45].

[47] A double-stranded RNA (dsRNA) molecule comprising: (a) a first strand comprising a nucleotide sequence having a length of at least 19, 20, 21, 22, 23, 24, 25, 30, 40 or 50 nucleotides, preferably at least 60, 70, 80, 90 or 100 nucleotides, more preferably at least 150, 200, 250, 300, 400, 500, 750 or 1000 nucleotides and having at least 90%, 91%, 92%, 93% or 94%, more preferably 95%, 96%, 97%, 98%, 99% or even 100% sequence identity to consecutive nucleotides of a target nucleic acid sequence; and (b) a second strand comprising in the 5' to 3' direction a nucleic acid sequence which is at least 90%, 91%, 92%, 93% or 94%, more preferably 95%, 96%, 97%, 98%, 99% or even 100% complementary to the first strand and/or is able to hybridize with the first strand, preferably under stringent conditions, wherein the target nucleic acid sequence is a coding region of an mRNA deduced from a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleotide sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A).

[48] A composition comprising the dsRNA molecule of item [47].

[49] A method of regulating the expression of at least one WRKY gene in a cereal plant cell, or cereal plant or part thereof, the method comprising applying the composition of item [48] to a cereal plant cell, or cereal plant or part thereof, preferably wherein the composition is applied onto the surface of the plant cell, or plant or part thereof.

[50] A cereal plant cell, or a cereal plant or part thereof, produced by the method of item [49].

[51] A cereal plant cell, or a cereal plant or part thereof, comprising the dsRNA molecule of item [47] and having an increased pathogen resistance as compared to a corresponding control plant cell, or plant or part thereof, that does not comprise the said dsRNA molecule.

[52] Use of at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising at least 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45 or 50 contiguous nucleotides of (a) the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A) and SEQ ID NO: 75 (TaCOI1), (b) a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of any one of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15 and SEQ ID NO: 75, or (c) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (a), (d) a nucleic acid encoding the amino acid sequence of any one of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16 and SEQ ID NO: 76, or (e) a nucleic acid encoding the amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of any one of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16 and SEQ ID NO: 76, as molecular marker for identifying a cereal plant cell, or a cereal plant or part thereof, having an increased pathogen resistance as compared to a corresponding control plant cell. Such molecular markers may be used for instance in the method of any one of items [29]-[36].

[53] A composition for topical application to a cereal plant cell, or a cereal plant or part thereof, comprising at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising (i) at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A); or (ii) at least 20, 21, 22, 23, 24, 25,

30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 400, 500, 700, 800, 900 or 1000 contiguous nucleotides of the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A), and a homolog thereof, preferably in sense and/or in antisense, wherein the at least one polynucleotide sequence is configured for RNA interference, preferably wherein the at least one polynucleotide sequence is configured for endogenous (post transcriptional) gene silencing or virus-induced gene silencing.

[54] Use of the recombinant DNA construct of item [38] or [39], the dsRNA molecule of item [47], or the composition of item [53], for conferring pathogen resistance to, or increasing pathogen resistance of, a cereal plant cell, or a cereal plant or part thereof.

[55] The cereal plant cell of any one of items [1]-[13], [37], [42]-[43], and [50]-[51], or the cereal plant or part thereof of any one of items [14]-[19], [37], [42]-[43], [46], and [50]-[51], or the method of any one of items [20]-[36], [40]-[41], [44]-[45], [47] and [49], or the composition of item [48], or the use of item [52] or [54], wherein the cereal plant cell, or cereal plant or part thereof, is a dicotyledonous or a monocotyledonous cereal plant cell, or cereal plant or part thereof, preferably wherein the cereal plant cell, or cereal plant or part thereof, is a wheat plant cell, or wheat plant or part thereof.

[56] The cereal plant cell of any one of items [1]-[13], [37], [42]-[43], and [50]-[51], or the cereal plant or part thereof of any one of items [14]-[19], [37], [42]-[43], [46], and [50]-[51], or the method of any one of items [20]-[36], [40]-[41], [44]-[45], [47] and [49], or the composition of item [48], or the use of item [52] or [54], wherein the WRKY gene or WRKY protein is a *Triticum aestivum* L. WRKY gene or *Triticum aestivum* L. WRKY protein, respectively.

The details of one or more embodiments of the disclosure are set forth in the accompanying drawings and the description below. Other features, objects, and advantages will be apparent from the description and drawings, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGURE 1 shows sequence motifs (SEQ ID NOs: 1 and 2) common to WRKY proteins whose expression or activity is to be inhibited in accordance with the present disclosure.

FIGURE 2 shows the nucleic acid and amino acid sequence of WRKY10 from *Triticum aestivum* (SEQ ID NO: 3 and SEQ ID NO: 4, respectively).

FIGURE 3 shows the nucleic acid and amino acid sequence of WRKY13 from *Triticum aestivum* (SEQ ID NO: 5 and SEQ ID NO: 6, respectively).

FIGURE 4 shows the nucleic acid and amino acid sequence of WRKY19 from *Triticum aestivum* (SEQ ID NO: 7 and SEQ ID NO: 8, respectively).

FIGURE 5 shows the nucleic acid and amino acid sequence of WRKY29 from *Triticum aestivum* (SEQ ID NO: 9 and SEQ ID NO: 10, respectively).

FIGURE 6 shows the nucleic acid and amino acid sequence of WRKY39 from *Triticum aestivum* (SEQ ID NO: 11 and SEQ ID NO: 12, respectively).

FIGURE 7 shows the nucleic acid and amino acid sequence of WRKY53B from *Triticum aestivum* (SEQ ID NO: 13 and SEQ ID NO: 14, respectively).

FIGURE 8 shows the nucleic acid and amino acid sequence of WRKY68A from *Triticum aestivum* (SEQ ID NO: 15 and SEQ ID NO: 16, respectively).

FIGURE 9 shows nucleic acid and amino acid sequences of homologs of WRKY10 from *Triticum aestivum* (TaWRKY10) found in wheat (*Triticum aestivum*), rye (*Secale cereale*), and barley (*Hordeum vulgare*). SEQ ID NO: 17 shows the nucleic acid sequence of WRKY6 from *Triticum aestivum* having 91.1% sequence identity to the nucleic acid sequence of TaWRKY10 shown in SEQ ID NO: 3. SEQ ID NO: 18 shows the amino acid sequence of WRKY6 from *Triticum aestivum* having 83.7% sequence identity to the amino acid sequence of TaWRKY10 shown in SEQ ID NO: 4. SEQ ID NO: 19 shows the nucleic acid sequence of WRKY10A from *Triticum aestivum* having 90.9% sequence identity to the nucleic acid sequence of TaWRKY10 shown in SEQ ID NO: 3. SEQ ID NO: 20 shows the amino acid sequence of WRKY10A from *Triticum aestivum* having 86.8% sequence identity to the amino acid sequence of TaWRKY10 shown in SEQ ID NO: 4. SEQ ID NO: 21 shows the nucleic acid sequence of a TaWRKY10-homolog from *Secale cereale* having 91.4% sequence identity to the nucleic acid sequence of TaWRKY10 shown in SEQ ID NO: 3. SEQ ID NO: 22 shows the amino acid sequence of a TaWRKY10-homolog from *Secale cereale* having 88.5% sequence identity to the amino acid sequence of TaWRKY10 shown in SEQ ID NO: 4. SEQ ID NO: 23 shows the nucleic acid sequence of a TaWRKY10-homolog from *Hordeum vulgare* having 91.2% sequence identity to the nucleic acid sequence of TaWRKY10 shown in SEQ ID NO: 3. SEQ ID NO: 24 shows the amino acid sequence of a TaWRKY10-homolog from *Hordeum vulgare* having 87.3% sequence identity to the amino acid sequence of TaWRKY10 shown in SEQ ID NO: 4.

FIGURE 10 shows nucleic acid and amino acid sequences of homologs of WRKY13 from *Triticum aestivum* (TaWRKY13) found in wheat (*Triticum aestivum*), rye (*Secale cereale*), and barley (*Hordeum vulgare*). SEQ ID NO: 25 shows the nucleic acid sequence of WRKY46 from *Triticum aestivum* having 100% sequence identity to the nucleic acid sequence of TaWRKY13 shown in SEQ ID NO: 5. SEQ ID NO: 26 shows the amino acid sequence of WRKY46 from *Triticum aestivum* having 100% sequence identity to the amino acid sequence of TaWRKY13 shown in SEQ ID NO: 6. SEQ ID NO: 27 shows the nucleic acid sequence of a TaWRKY13-homolog from *Secale cereale* having 86.4% sequence identity to the amino acid sequence of

TaWRKY13 shown in SEQ ID NO: 5. SEQ ID NO: 28 shows the amino acid sequence of a TaWRKY13-homolog from *Secale cereale* having 86.9% sequence identity to the amino acid sequence of TaWRKY13 shown in SEQ ID NO: 6. SEQ ID NO: 29 shows the nucleic acid sequence of a TaWRKY13-homolog from *Hordeum vulgare* having 95.7% sequence identity to the nucleic acid sequence of TaWRKY13 shown in SEQ ID NO: 5. SEQ ID NO: 30 shows the amino acid sequence of a TaWRKY13-homolog from *Hordeum vulgare* having 96.0% sequence identity to the amino acid sequence of TaWRKY13 shown in SEQ ID NO: 6.

FIGURE 11 shows nucleic acid and amino acid sequences of homologs of WRKY19 from *Triticum aestivum* (TaWRKY19) found in wheat (*Triticum aestivum*), rye (*Secale cereale*), and barley (*Hordeum vulgare*). SEQ ID NO: 31 shows the nucleic acid sequence of WRKY19C from *Triticum aestivum* having 90.0% sequence identity to the nucleic acid sequence of TaWRKY19 shown in SEQ ID NO: 7. SEQ ID NO: 32 shows the amino acid sequence of WRKY19C from *Triticum aestivum* having 83.6% sequence identity to the amino acid sequence of TaWRKY19 shown in SEQ ID NO: 8. SEQ ID NO: 33 shows the nucleic acid sequence of a TaWRKY19-homolog from *Secale cereale* having 84.3% sequence identity to the nucleic acid sequence of TaWRKY19 shown in SEQ ID NO: 7. SEQ ID NO: 34 shows the amino acid sequence of a TaWRKY19-homolog from *Secale cereale* having 82.7% sequence identity to the amino acid sequence of TaWRKY19 shown in SEQ ID NO: 8. SEQ ID NO: 35 shows the nucleic acid sequence of a TaWRKY19-homolog from *Hordeum vulgare* having 84.5% sequence identity to the nucleic acid sequence of TaWRKY19 shown in SEQ ID NO: 7. SEQ ID NO: 36 shows the amino acid sequence of a TaWRKY19-homolog from *Hordeum vulgare* having 77.6% sequence identity to the amino acid sequence of TaWRKY19 shown in SEQ ID NO: 8.

FIGURE 12 shows nucleic acid and amino acid sequences of homologs of WRKY29 from *Triticum aestivum* (TaWRKY29) found in rye (*Secale cereale*) and barley (*Hordeum vulgare*). SEQ ID NO: 37 shows the nucleic acid sequence of a TaWRKY29-homolog from *Secale cereale* having 89.9% sequence identity to the nucleic acid sequence of TaWRKY29 shown in SEQ ID NO: 9. SEQ ID NO: 38 shows the amino acid sequence of a TaWRKY29-homolog from *Secale cereale* having 90.6% sequence identity to the amino acid sequence of TaWRKY29 shown in SEQ ID NO: 10. SEQ ID NO: 39 shows the nucleic acid sequence of a TaWRKY29-homolog from *Hordeum vulgare* having 90.0% sequence identity to the nucleic acid sequence of TaWRKY29 shown in SEQ ID NO: 9. SEQ ID NO: 40 shows the amino acid sequence of a TaWRKY29-homolog from *Hordeum vulgare* having 89.1% sequence identity to the amino acid sequence of TaWRKY29 shown in SEQ ID NO: 10.

FIGURE 13 shows nucleic acid and amino acid sequences of homologs of WRKY39 from *Triticum aestivum* (TaWRKY39) found in wheat (*Triticum aestivum*), rye (*Secale cereale*), and barley (*Hordeum vulgare*). SEQ ID NO: 41 shows the nucleic acid sequence of WRKY43 from

Triticum aestivum having 90.4% sequence identity to the nucleic acid sequence of TaWRKY39 shown in SEQ ID NO: 11. SEQ ID NO: 42 shows the amino acid sequence of WRKY43 from *Triticum aestivum* having 87.2% sequence identity to the amino acid sequence of TaWRKY39 shown in SEQ ID NO: 12. SEQ ID NO: 43 shows the nucleic acid sequence of WRKY79 from *Triticum aestivum* having 90.7% sequence identity to the nucleic acid sequence of TaWRKY39 shown in SEQ ID NO: 11. SEQ ID NO: 44 shows the amino acid sequence of WRKY79 from *Triticum aestivum* having 79.4% sequence identity to the amino acid sequence of TaWRKY39 shown in SEQ ID NO: 12. SEQ ID NO: 45 shows the nucleic acid sequence of WRKY79A from *Triticum aestivum* having 99.7% sequence identity to the nucleic acid sequence of TaWRKY39 shown in SEQ ID NO: 11. SEQ ID NO: 46 shows the amino acid sequence of WRKY79A from *Triticum aestivum* having 90.0% sequence identity to the amino acid sequence of TaWRKY39 shown in SEQ ID NO: 12. SEQ ID NO: 47 shows the nucleic acid sequence of a TaWRKY39-homolog from *Secale cereale* having 88.6% sequence identity to the nucleic acid sequence of TaWRKY39 shown in SEQ ID NO: 11. SEQ ID NO: 48 shows the amino acid sequence of a TaWRKY39-homolog from *Secale cereale* having 79.2% sequence identity to the amino acid sequence of TaWRKY39 shown in SEQ ID NO: 12. SEQ ID NO: 49 shows the nucleic acid sequence of a TaWRKY39-homolog from *Hordeum vulgare* having 88.0% sequence identity to the nucleic acid sequence of TaWRKY39 shown in SEQ ID NO: 11. SEQ ID NO: 50 shows the amino acid sequence of a TaWRKY39-homolog from *Hordeum vulgare* having 77.5% sequence identity to the amino acid sequence of TaWRKY39 shown in SEQ ID NO: 12.

FIGURE 14 shows nucleic acid and amino acid sequences of homologs of WRKY53B from *Triticum aestivum* (TaWRKY53B) found in wheat (*Triticum aestivum*) and rye (*Secale cereale*). SEQ ID NO: 51 shows the nucleic acid sequence of WRKY53 from *Triticum aestivum* having 92.1% sequence identity to the nucleic acid sequence of TaWRKY53B shown in SEQ ID NO: 13. SEQ ID NO: 52 shows the amino acid sequence of WRKY53 from *Triticum aestivum* having 86.1% sequence identity to the amino acid sequence of TaWRKY53B shown in SEQ ID NO: 14. SEQ ID NO: 53 shows the nucleic acid sequence of WRKY53A from *Triticum aestivum* having 87.7% sequence identity to the nucleic acid sequence of TaWRKY53B shown in SEQ ID NO: 13. SEQ ID NO: 54 shows the amino acid sequence of WRKY53A from *Triticum aestivum* having 85.2% sequence identity to the amino acid sequence of TaWRKY53B shown in SEQ ID NO: 14. SEQ ID NO: 55 shows the nucleic acid sequence of a TaWRKY53B-homolog from *Secale cereale* having 83.9% sequence identity to the nucleic acid sequence of TaWRKY53B shown in SEQ ID NO: 13. SEQ ID NO: 56 shows the amino acid sequence of a TaWRKY39-homolog from *Secale cereale* having 82.8% sequence identity to the amino acid sequence of TaWRKY53B shown in SEQ ID NO: 14.

FIGURE 15 shows nucleic acid and amino acid sequences of homologs of WRKY68A from *Triticum aestivum* (TaWRKY68A) found in wheat (*Triticum aestivum*) and rye (*Secale cereale*).

SEQ ID NO: 57 shows the nucleic acid sequence of WRKY9 from *Triticum aestivum* having 94.1% sequence identity to the nucleic acid sequence of TaWRKY68A shown in SEQ ID NO: 15. SEQ ID NO: 58 shows the amino acid sequence of WRKY9 from *Triticum aestivum* having 80.4% sequence identity to the amino acid sequence of TaWRKY68A shown in SEQ ID NO: 16. SEQ ID NO: 59 shows the nucleic acid sequence of WRKY68 from *Triticum aestivum* having 99.0% sequence identity to the nucleic acid sequence of TaWRKY68A shown in SEQ ID NO: 15. SEQ ID NO: 60 shows the amino acid sequence of WRKY68 from *Triticum aestivum* having 97.6% sequence identity to the amino acid sequence of TaWRKY68A shown in SEQ ID NO: 16. SEQ ID NO: 61 shows the nucleic acid sequence of WRKY68C from *Triticum aestivum* having 88.8% sequence identity to the nucleic acid sequence of TaWRKY68A shown in SEQ ID NO: 15. SEQ ID NO: 62 shows the amino acid sequence of WRKY68C from *Triticum aestivum* having 85.5% sequence identity to the amino acid sequence of TaWRKY68A shown in SEQ ID NO: 16. SEQ ID NO: 63 shows the nucleic acid sequence of a TaWRKY68A-homolog from *Secale cereale* having 94.1% sequence identity to the nucleic acid sequence of TaWRKY68A shown in SEQ ID NO: 15. SEQ ID NO: 64 shows the amino acid sequence of a TaWRKY68A-homolog from *Secale cereale* having 93.9% sequence identity to the amino acid sequence of TaWRKY68A shown in SEQ ID NO: 16.

FIGURE 16 shows nucleic acid sequences of WRKY fragments used for VIGS gene silencing. SEQ ID NO: 65 shows the nucleic acid sequence of fragment A from TaWRKY10 for WRKY gene silencing (97 nucleotides). SEQ ID NO: 66 shows the nucleic acid sequence of fragment A from TaWRKY13/46 for WRKY gene silencing (164 nucleotides). SEQ ID NO: 67 shows the nucleic acid sequence of fragment B from TaWRKY13/46 for WRKY gene silencing (174 nucleotides). SEQ ID NO: 68 shows the nucleic acid sequence of fragment A from TaWRKY19 for WRKY gene silencing (99 nucleotides). SEQ ID NO: 69 shows the nucleic acid sequence of fragment B from TaWRKY19 for WRKY gene silencing (83 nucleotides). SEQ ID NO: 70 shows the nucleic acid sequence of fragment A from TaWRKY29 for WRKY gene silencing (105 nucleotides). SEQ ID NO: 71 shows the nucleic acid sequence of fragment A from TaWRKY53B for WRKY gene silencing (70 nucleotides). SEQ ID NO: 72 shows the nucleic acid sequence of fragment A from TaWRKY68A for WRKY gene silencing (80 nucleotides).

FIGURE 17 shows phytoene desaturase gene (PDS) silenced cv. *Avalon* (Av) vs. cv. *Cordiale* (Crd). The 18S subunit ribosomal protein was used for normalization. BSMV:00 means empty BSMV vector (=control; Ev). BSMV:PDS means BSMV vector carrying fragment for PDS silencing (Pds).

FIGURE 18 shows the effect of WRKY10 silencing on picnidia and spores count in cv. *Cordiale* after *Septoria* infection. BSMV:00 means empty BSMV vector (=control). BSMV:WRKY10 means BSMV vector carrying gene silencing sequence for silencing WRKY10.

FIGURE 19 shows the effect of WRKY silencing to *Septoria* infection on cv. *Avalon*. BSMV:00 means empty BSMV vector (=control). BSMV:WRKY10 means BSMV vector carrying gene silencing sequence for silencing WRKY10.

FIGURE 20 shows the effect of WRKY10 silencing on picnidia and spores count in cv. *Cordiale* after *Septoria* infection. BSMV:00 means empty BSMV vector (=control). BSMV:WRKY10 means BSMV vector carrying gene silencing sequence for silencing WRKY10.

FIGURE 21 shows the effect of WRKY10 silencing on picnidia and spores count in cv. *KWS Santiago* after *Septoria* infection. EV means empty vector (=control). BSMV:WRKY10 means BSMV vector carrying gene silencing sequence for silencing WRKY10.

FIGURE 22 shows the effect of WRKY10 silencing on picnidia and spores count in cv. *KWS Lili* after *Septoria* infection. EV means empty vector (=control). BSMV:WRKY10 means BSMV vector carrying gene silencing sequence for silencing WRKY10.

FIGURE 23 shows the susceptibility of cv. *KWS Santiago* vs. cv. *KWS Lili* towards *Septoria* infection.

FIGURE 24 shows a comparison of *Septoria* sporulation in WRKY10 silenced cv. *KWS Santiago* vs. cv. *KWS Lili* with full WRKY10 expression. EV *KWS Lili* means cv. *KWS Lili* transformed with an empty BSMV vector. BSMV:WRKY10 *KWS Santiago* means WRKY10 silenced cv. *KWS Santiago* using BSMV vector carrying gene silencing sequence for silencing WRKY10.

FIGURE 25 is an excerpt from Figure 1 of Yuan et al. 2011, PLoS ONE, Vol. 6(10), e26468, and shows in particular a schematic representation of pCaBS- α , pCaBS- β and pCaBS- γ used for VIGS as depicted in Figure 1A of Yuan et al., 2011.

FIGURE 26 shows a list of possible positions in the sequences of TaWRKY10, TaWRKY13, TaWRKY19, TaWRKY29, TaWRKY39, TaWRKY53B, and TaWRKY68A for mutations which effect an early stop-codon and which can be used in TILLING or genome editing approaches for inhibiting WRKYs according to the disclosure.

FIGURE 27 shows the comparison of the response of root growth to JA treatment in wheat cv. *KWS Lili* and cv. *KWS Santiago*. A-C: photographs of germinating wheat seedlings of cv. *KWS Lili* (above) and cv. *KWS Santiago* (below) on day 1 (A), day 2 (B) and day 3 (C) grown in MS medium (left) and MS medium supplemented with 10 μ M of JA (right). D: Plot shows the measured root length of germinating wheat seedlings of cv. *KWS Lili* (above) and cv. *KWS Santiago* (below) on three consecutive days grown in MS medium (left) and MS medium supplemented with 10 μ M of JA. The day of measurement is indicated by number in the column. The experiment has been carried out 3 times, error bars represent standard error.

FIGURE 28 shows the comparison of relative transcript abundance of *TaCOI1* in cvs. *KWS Lili* and *KWS Santiago*, in both shoots and roots under control condition (MS medium) of 4 days old seedlings. The experiment has been carried out twice, each sample has been made by

pooling 5 seedlings. Relative expression is calculated by the $\Delta\Delta C_T$ method, comparing against the reference gene *Ta18S*. Error bars show the standard error across two biological and three technical replicates.

FIGURE 29 presents relative *TaWRKY10* expression in seedlings following VIGs in cv. Lili and Santiago. BSMV:00 represents the empty vector control for the VIGs experiment, while *BSMV:TaWRKY10A* and *BSMV:TAWRKY10B* represent the two silencing fragments used. Relative expression is calculated by the $\Delta\Delta C_T$ method, comparing against the reference gene *TaEF1*. Error bars show the standard error across three biological and three technical replicates.

FIGURE 30 presents relative expression of *TaCoi1* in *TaWRKY10*-knocked down wheat seedlings from cvs *KWS Lili* and *KWS Santiago*. BSMV:00 represents the empty vector control for the VIGs experiment, while *BSMV:TaWRKY10A* and *BSMV:TAWRKY10B* represent the two silencing fragments used. Relative expression is calculated by the $\Delta\Delta C_T$ method, comparing against the reference gene *Ta18S*. Error bars show the standard error across three biological and three technical replicates.

DETAILED DESCRIPTION OF THE DISCLOSURE

As used herein and in the appended claims, the singular forms “a”, “and”, and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to “a cell” or “the cell” includes reference to one or more cells and equivalents thereof (e.g., plurality of cells) known to those skilled in the art. Similarly, reference to “a composition” includes a plurality of such compositions, and refers to one or more compositions, respectively, unless the context clearly dictates otherwise. The term “about” when referring to a number or a numerical range means that the number or numerical range referred to is an approximation within experimental variability (or within statistical experimental error), and thus the number or numerical range may vary between 1% and 15% of the stated number or numerical range. The term “comprising” (and related terms such as “comprise” or “comprises” or “having” or “including”) is not intended to exclude that in other certain embodiments, for example, an embodiment of any plant cell, plant or part thereof, composition, method, or process, or the like, described herein, may “consist of” or “consist essentially of” the described features. The term “at least one” comprises the integers larger than or equal to 1, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 and so forth.

As used herein “operatively linked” or “operably linked” includes reference to a functional linkage between a first sequence, such as a promoter, and a second sequence, wherein the promoter sequence initiates and mediates transcription of the second sequence, *i.e.*, the promoter is in a correct functional location and/or orientation in relation to the second nucleic

acid sequence to control transcriptional initiation and/or expression of that sequence. Generally, operatively linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame.

The term “promoter region” or “promoter” is used herein in its ordinary sense to refer to a nucleotide region comprising a DNA regulatory sequence, wherein the regulatory sequence is derived from a gene which is capable of binding RNA polymerase and initiating transcription of a downstream (3'-direction) coding sequence. The regulatory sequence may be homologous or heterologous to the desired gene sequence. The promoter is oriented relative to a DNA sequence such that it is capable of initiating transcription of the said DNA sequence, i.e., the term “promoter” includes reference to a region of DNA upstream from the start of transcription and involved in recognition and binding of RNA polymerase and/or other proteins to initiate transcription. A “plant promoter” is a promoter capable of initiating transcription in plant cells. Exemplary plant promoters include, but are not limited to, those that are obtained from plants, plant viruses and bacteria, which comprise genes expressed in plant cells such as *Agrobacterium* or *Rhizobium*.

The term “regulatory nucleic acid sequence” refers collectively to promoter sequences, polyadenylation signals, transcription termination sequences, upstream regulatory domains, origins of replication, enhancers and the like, which collectively provide for the replication, transcription and translation of a coding sequence in a recipient cell. Not all of these control sequences need always be present so long as the selected coding sequence is capable of being replicated, transcribed and translated in an appropriate cell. One skilled in the art can readily identify regulatory nucleic acid sequence from public databases and materials. Furthermore, one skilled in the art can identify a regulatory sequence that is applicable for the intended use.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this disclosure belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice of the disclosed methods and compositions, the exemplary methods, devices and materials are described herein.

The observation that cereals grown under low-input nutrient regimes are less susceptible to disease has been a “given” in agronomy for many years, although direct data showing such a link has been difficult to generate due to a range of compounding factors. Preliminary data analysis carried out by the present inventors from transcriptomic data suggested that the WRKYs may be responsible for relating nitrogen input to expression of genes involved in

disease resistance. In the course of research projects, the present inventors identified specific WRKY transcription factors and jasmonate receptors and their roles in the interaction between wheat and *Septoria* disease and nitrogen input. Part of that project was the use of Virus induced gene silencing (VIGS) as a tool to knockdown the activity of key WRKYs in wheat seedlings cultivated under varying nitrogen levels and study the effect under *Septoria* infection.

The present disclosure provides means and methods for conferring or boosting pathogen resistance to cereals, in particular resistance against fungal pathogens such as *Septoria*, under fertilizer input growth conditions necessary for maintaining yield. The present disclosure is based *inter alia* on the identification of key WRKYs whose expression or activity is fertilizer-responsive and/or which are characterized by the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. WRKYs are one of the largest families of transcriptional regulators in plants, with 72 representatives in *Arabidopsis*, 100 in rice and to date 111 in wheat (PLANT TFDB, Centre for Bioinformatics, Peking University). WRKY transcription factors are so called because of the presence of a highly conserved 60 amino acid domain, which contain the WRKYGQK motif or variants thereof. WRKYs transcription factors are important components of plant signaling webs, which are often found to regulate plant response to biotic and abiotic stresses. In addition, the present disclosure is based on the identification of a jasmonate receptor whose expression or activity have a direct impact on the *Septoria* resistance and is potentially influenced by the appearance of at least one of the identified key WRKYs.

The present inventors performed knockdown of certain WRKYs using Virus induced gene silencing (VIGS), and the effect on *Septoria* disease progression under varying nitrogen levels was ascertained. The appearance of disease symptoms varied, suggesting that these WRKYs play a major role in resistance.

In this WRKY gene expression screen in wheat leaf tissue upon *Septoria* infection, TaWRKY10, TaWRKY13, TaWRKY19, TaWRKY29, TaWRKY39, TaWRKY53B and TaWRKY68A were identified to show altered gene expression and considered as possible key WRKYs. Furthermore, the *Coi1* gene expression screen shows that the jasmonate receptor COI1 plays a key role in the pathogen defense and can be linked to the WRKY activity.

In all identified WRKYs the spore and pycnidia count is reduced in the knockdown data generated so far, which has the potential to be highly important for disease spread in a whole-plant/crop situation.

Data linking the key WRKYs of the present disclosure to both nitrogen regime and disease resistance has been generated in experiments carried out both in the field and in growth room trials (cf. Examples 1-3). In two winter wheat varieties studied, low Nitrogen levels resulted in

lower levels of susceptibility to STB disease. Subsequent QPCR data showed that the nitrogen sensitive TaWRKYs had similar differential expression pattern during Septoria infection.

For example, by knocking down TaWRKY10 in the cv. Avalon, spore and pycnidia counts were significantly reduced (Example 7, Figure 18). This indicates that the infection of the wheat plants with Septoria is efficiently inhibited and the plant defense is improved. Consequently the resistance/tolerance of wheat against Septoria disease is enhanced. In addition, in TaWRKY10 silenced cv *Avalon* plants the visible symptoms of Septoria infection were delayed by around 4 days (Example 7, Figure 19).

The reduced spore and pycnidia counts could be shown also in other cultivars like *Cordiale* (Figure 20), *KWS Santiago* (Figure 21) and *KWS Lili* (Figure 22). The enhanced resistance has also been demonstrated in the following experiment. Naturally the cv. *KWS Santiago* is more susceptible to Septoria compared to cv. *KWS Lili*. That can be shown by spore counts (Example 7, Figure 23) as well as in field trials. The resistant cv. *KWS Lili* has been transformed with an empty VIGS vector (EV) and the susceptible cv. *KWS Santiago* with BSMV:WRKY10. The result is that both the non-silenced cv. *KWS Lili* and the silenced cv. *KWS Santiago* show a comparable Septoria sporulation (Example 7, Figure 24).

Comparable results as seen for WRKY10 have been achieved for WRKY13, WRKY19, WRKY29, WRKY39, WRKY53B and WRKY68A. For all of these WRKYs, it is suggested that their expression or activity is fertilizer-responsive and/or are characterized by the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid.

The results obtained in the present examples are based on the VIGS-induced silencing of the specific key WRKY genes. However, it is possible to achieve the same or comparable results through other methods: For example, one can build up TILLING populations of a plant and screen for mutations leading to amino acid exchanges or splicing errors. Such mutation can result in a knock-down or a knock-out of the WRKY gene (e.g., if the mutation creates an early stop codon), in an altered (reduced) activity of the WRKY protein, or in a shift of the reading frame if splicing errors occur. On the other hand, in TILLING populations it can be screen for mutations leading to a single nucleotide exchange, small deletions or insertions in the promoter or in coding regions whereby an altered expression level or activity of the jasmonate receptor COI1 could be achieved. Besides of TILLING, such mutations can be introduced/targeted by the known genome editing tools like Zinc Finger Nucleases, TAL Effector Nucleases, CRISPR systems based e.g. on Cas9 or Cpf1, etc. Another example is the introduction of a DNA construct encoding a double stranded RNA construct suitable for silencing the above WRKY genes (RNAi approach, Example 8) or the introduction of a DNA construct encoding the coding

regions of above jasmonate receptor gene, preferably operatively linked to a promoter, for overexpression. Figure 26 shows a list of possible positions in the sequences of TaWRKY10, TaWRKY13, TaWRKY19, TaWRKY29, TaWRKY39, TaWRKY53B, and TaWRKY68A for mutations (point mutations) which effect an early stop-codon and which can be used in TILLING or genome editing approaches for inhibiting WRKYs according to the disclosure.

In line with the above findings, the present disclosure provides a cereal plant cell having introduced into its genome at least one modification inhibiting the expression or activity of at least one WRKY protein as compared to a corresponding control plant cell lacking the at least one modification, wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In various embodiments of the present disclosure, the hydrophobic amino acid of residue X1 of the amino acid sequence motif shown in SEQ ID NO: 1 or 2 (Figure 1) means any one of Alanine (A), Isoleucine (I), Leucine (L), Methionine (M), Phenylalanine (F), Tryptophan (W), Tyrosine (Y), Valine (V), Histidine (H), Lysine (K), Threonine (T), Cysteine (C), and Glycine (G). Preferably, the hydrophobic amino acid of residue X1 of the amino acid sequence motif shown in SEQ ID NO: 1 or 2 (Figure 1) is Phenylalanine (F), Tyrosine (Y), Histidine (H), or Cysteine (C). In various embodiments of the present disclosure, the polar, non-hydrophobic amino acid of residue X2 of the amino acid sequence motif shown in SEQ ID NO: 1 or 2 (Figure 1) means any one of Arginine (R), Asparagine (N), Aspartic Acid (D), Glutamic Acid (E), Glutamine (Q), and Serine (S). Preferably, the polar, non-hydrophobic amino acid of residue X2 of the amino acid sequence motif shown in SEQ ID NO: 1 or 2 (Figure 1) is Arginine (R), Asparagine (N), Glutamine (Q), or Serine (S).

Accordingly, in the present disclosure, the at least one WRKY protein whose expression or activity is to be inhibited is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the amino acid sequence motif is D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E-X-X-X3-X-X2 shown in SEQ ID NO: 2, wherein X is any amino acid, X1 is a hydrophobic amino acid, X2 is a polar, non-hydrophobic amino acid, and X3 is a polar, non-aromatic amino acid. In various embodiments of the present disclosure, the polar, non-aromatic amino acid of residue X3 of the amino acid sequence motif shown in SEQ ID NO: 2 (Figure 1) means any one of Arginine (R), Asparagine (N), Aspartic Acid (D), Glutamic Acid (E), Glutamine (Q), Lysine (K), Threonine (T), Cysteine (C), and Serine (S). Preferably, the polar, non-aromatic

amino acid of residue X3 of the amino acid sequence motif shown in SEQ ID NO: 2 (Figure 1) is Arginine (R), Glutamine (Q), Lysine (K), or Serine (S).

As described herein, the terms “amino acid” and “amino acid residue” may be used herein interchangeably.

In the literature, different WRKY transcription factors are described acting as negative or positive regulators. In various embodiments of the present disclosure, the least one WRKY protein whose expression or activity is to be inhibited is a negative regulator of the cereal plant cell or plant defense mechanism/response against a pathogen, *i.e.*, is a negative regulator of the pathogen defense mechanism of the wild-type plant cell lacking the modification inhibiting the expression or activity of the at least one WRKY protein. Here, negative regulation means that the pathogen defense mechanism/response of the cereal plant cell, or cereal plant or part thereof, is reduced, inhibited or blocked.

The identified jasmonate receptor COI1 acts as positive regulator; the expression or activity of COI1 to be enhanced is a positive regulator of the cereal plant cell or plant defense mechanism/response against a pathogen, *i.e.*, is a positive regulator of the pathogen defense mechanism of the wild-type plant cell lacking the modification enhancing the expression or activity of the COI1 protein. Here, positive regulation means that the pathogen defense mechanism/response of the cereal plant cell, or cereal plant or part thereof, is established, increased or improved. COI1 might interact with WRKY transcription factors since TaCoil1 transcription is suppressed by the appearance of at least one WRKY, like TaWRKY10.

In various embodiments of the present disclosure, the at least one WRKY gene is selected from the group consisting of TaWRKY10 (SEQ ID NO: 3), TaWRKY13 (SEQ ID NO: 5), TaWRKY19 (SEQ ID NO: 7), TaWRKY29 (SEQ ID NO: 9), TaWRKY39 (SEQ ID NO: 11), TaWRKY53B (SEQ ID NO: 13), and TaWRKY68A (SEQ ID NO: 15), or homologs thereof, and the jasmonate receptor gene comprises (a) the nucleic acid sequence of TaCOI1 (SEQ ID NO: 75), (b) a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, (c) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (a), (d) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (e) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76. In various embodiments of the disclosure, a WRKY10 gene or protein or a variant or homolog thereof according the present disclosure is a WRKY10 from cereals. Preferably, a WRKY10 gene or protein or a variant or homolog thereof according the present

disclosure is a WRKY10 gene or protein from any of wheat (*Triticum aestivum*, TaWRKY10), rye (*Secale cereale*, ScWRKY10), or barley (*Hordeum vulgare*, HvWRKY10). In certain preferred embodiments, a WRKY10 gene or protein or a variant or homolog thereof according to the present disclosure is a TaWRKY10 gene or protein (*i.e.*, WRKY10 from *Triticum aestivum*).

In various embodiments of the disclosure, a WRKY13 gene or protein or a variant or homolog thereof according to the present disclosure is a WRKY13 from cereals. Preferably, a WRKY13 gene or protein or a variant or homolog thereof according to the present disclosure is a WRKY13 gene or protein from any of wheat (*Triticum aestivum*, TaWRKY13), rye (*Secale cereale*, ScWRKY13), or barley (*Hordeum vulgare*, HvWRKY13). In certain preferred embodiments, a WRKY13 gene or protein or a variant or homolog thereof according to the present disclosure is a TaWRKY13 gene or protein (*i.e.*, WRKY13 from *Triticum aestivum*).

In various embodiments of the disclosure, a WRKY19 gene or protein or a variant or homolog thereof according to the present disclosure is a WRKY19 from cereals. Preferably, a WRKY19 gene or protein or a variant or homolog thereof according to the present disclosure is a WRKY19 gene or protein from any of wheat (*Triticum aestivum*, TaWRKY19), rye (*Secale cereale*, ScWRKY19), or barley (*Hordeum vulgare*, HvWRKY19). In certain preferred embodiments, a WRKY19 gene or protein or a variant or homolog thereof according to the present disclosure is a TaWRKY19 gene or protein (*i.e.*, WRKY19 from *Triticum aestivum*).

In various embodiments of the disclosure, a WRKY29 gene or protein or a variant or homolog thereof according to the present disclosure is a WRKY29 from cereals. Preferably, a WRKY29 gene or protein or a variant or homolog thereof according to the present disclosure is a WRKY29 gene or protein from any of wheat (*Triticum aestivum*, TaWRKY29), rye (*Secale cereale*, ScWRKY29), or barley (*Hordeum vulgare*, HvWRKY29). In certain preferred embodiments, a WRKY29 gene or protein or a variant or homolog thereof according to the present disclosure is a TaWRKY29 gene or protein (*i.e.*, WRKY29 from *Triticum aestivum*).

In various embodiments of the disclosure, a WRKY39 gene or protein or a variant or homolog thereof according to the present disclosure is a WRKY39 from cereals. Preferably, a WRKY39 gene or protein or a variant or homolog thereof according to the present disclosure is a WRKY39 gene or protein from any of wheat (*Triticum aestivum*, TaWRKY39), rye (*Secale cereale*, ScWRKY39), or barley (*Hordeum vulgare*, HvWRKY39). In certain preferred embodiments, a WRKY39 gene or protein or a variant or homolog thereof according to the present disclosure is a TaWRKY39 gene or protein (*i.e.*, WRKY39 from *Triticum aestivum*).

In various embodiments of the disclosure, a WRKY53B gene or protein or a variant or homolog thereof according to the present disclosure is a WRKY53B from cereals. Preferably, a WRKY53B gene or protein or a variant or homolog thereof according to the present disclosure is a WRKY53B

gene or protein from any of wheat (*Triticum aestivum*, TaWRKY53B), rye (*Secale cereale*, ScWRKY53B), or barley (*Hordeum vulgare*, HvWRKY53B). In certain preferred embodiments, a WRKY53B gene or protein or a variant or homolog thereof according the present disclosure is a TaWRKY53B gene or protein (*i.e.*, WRKY53B from *Triticum aestivum*).

In various embodiments of the disclosure, a WRKY68A gene or protein or a variant or homolog thereof according the present disclosure is a WRKY68A from cereals. Preferably, a WRKY68A gene or protein or a variant or homolog thereof according the present disclosure is a WRKY68A gene or protein from any of wheat (*Triticum aestivum*, TaWRKY68A), rye (*Secale cereale*, ScWRKY68A), or barley (*Hordeum vulgare*, HvWRKY68A). In certain preferred embodiments, a WRKY68A gene or protein or a variant or homolog thereof according the present disclosure is a TaWRKY68A gene or protein (*i.e.*, WRKY68A from *Triticum aestivum*).

In various embodiments of the disclosure, a jasmonate receptor gene (e.g. COI1 gene) or protein or a homologous sequence thereof according the present disclosure, *i.e.* exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99%, is a COI1 from cereals. Preferably, a jasmonate receptor gene (e.g. COI1 gene) or protein (e.g. COI1 protein) or a homologous sequence thereof according the present disclosure is a COI1 gene or protein from any of wheat (*Triticum aestivum*, TaCOI1), rye (*Secale cereale*, ScCOI1), or barley (*Hordeum vulgare*, HvCOI1). In certain preferred embodiments, a COI1 gene or protein or a homologous sequence thereof according the present disclosure is a COI1 gene or protein (*i.e.*, COI1 from *Triticum aestivum*). In various embodiments of the disclosure, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 80% homology or sequence identity to the nucleic acid sequence of TaWRKY10 (SEQ ID NO: 3, Figure 2), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY10 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 85% or at least 90% homology or sequence identity to the nucleic acid sequence of TaWRKY10 (SEQ ID NO: 3, Figure 2), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY10 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the nucleic acid sequence of TaWRKY10 (SEQ ID NO: 3,

Figure 2), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY10 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY10 as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY10 encoded by the sequence of SEQ ID NO: 3 (Figure 2). In a particularly preferred embodiment, the nucleic acid sequence of the at least one WRKY gene comprises (or consists of) the sequence of SEQ ID NO: 3 (Figure 2), or the sequence of any one SEQ ID NOs: 17, 19, 21, and 23 (Figure 9).

In various embodiments of the disclosure, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 80% homology or sequence identity to the nucleic acid sequence of TaWRKY13 (SEQ ID NO: 5, Figure 3), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY13 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 85% or at least 90% homology or sequence identity to the nucleic acid sequence of TaWRKY13 (SEQ ID NO: 5, Figure 3), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY13 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the nucleic acid sequence of TaWRKY13 (SEQ ID NO: 5, Figure 3), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY13 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY13 as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY13 encoded by the sequence of SEQ ID NO: 5 (Figure 3). In a particularly preferred embodiment, the nucleic acid sequence of the at least one WRKY gene comprises (or consists of) the sequence of SEQ ID NO: 5 (Figure 3), or the sequence of any one SEQ ID NOs: 25, 27, and 29 (Figure 10).

In various embodiments of the disclosure, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 80% homology or sequence identity to the nucleic acid sequence of TaWRKY19 (SEQ ID NO: 7, Figure 4), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY19 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 85% or at least 90% homology or sequence identity to the nucleic acid sequence of TaWRKY19 (SEQ ID NO: 7, Figure 4), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY19 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the nucleic acid sequence of TaWRKY19 (SEQ ID NO: 7, Figure 4), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY19 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY19 as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY19 encoded by the sequence of SEQ ID NO: 7 (Figure 4). In a particularly preferred embodiment, the nucleic acid sequence of the at least one WRKY gene comprises (or consists of) the sequence of SEQ ID NO: 7 (Figure 4), or the sequence of any one SEQ ID NOs: 31, 33, and 35 (Figure 11).

In various embodiments of the disclosure, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 80% homology or sequence identity to the nucleic acid sequence of TaWRKY29 (SEQ ID NO: 9, Figure 5), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY29 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 85% or at least 90% homology or sequence identity to the nucleic acid sequence of TaWRKY29 (SEQ ID NO: 9, Figure 5), wherein the variant or homologous nucleic acid

sequence encodes a WRKY protein, preferably a WRKY29 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the nucleic acid sequence of TaWRKY29 (SEQ ID NO: 9, Figure 5), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY29 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY29 as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY29 encoded by the sequence of SEQ ID NO: 9 (Figure 5). In a particularly preferred embodiment, the nucleic acid sequence of the at least one WRKY gene comprises (or consists of) the sequence of SEQ ID NO: 9 (Figure 5), or the sequence of SEQ ID NO: 37 or 39 (Figure 12).

In various embodiments of the disclosure, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 80% homology or sequence identity to the nucleic acid sequence of TaWRKY39 (SEQ ID NO: 11, Figure 6), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY39 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 85% or at least 90% homology or sequence identity to the nucleic acid sequence of TaWRKY39 (SEQ ID NO: 11, Figure 6), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY39 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the nucleic acid sequence of TaWRKY39 (SEQ ID NO: 11, Figure 6), wherein the variant nucleic acid sequence encodes a WRKY protein, preferably a WRKY39 protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2

is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY39 as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY39 encoded by the sequence of SEQ ID NO: 11 (Figure 6). In a particularly preferred embodiment, the nucleic acid sequence of the at least one WRKY gene comprises (or consists of) the sequence of SEQ ID NO: 11 (Figure 6), or the sequence of any one SEQ ID NOs: 41, 43, 45, 47, and 49 (Figure 13).

In various embodiments of the disclosure, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 80% homology or sequence identity to the nucleic acid sequence of TaWRKY53B (SEQ ID NO: 13, Figure 7), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY53B protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 85% or at least 90% homology or sequence identity to the nucleic acid sequence of TaWRKY53B (SEQ ID NO: 13, Figure 7), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY53B protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the nucleic acid sequence of TaWRKY53B (SEQ ID NO: 13, Figure 7), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY53B protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY53B as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY53B encoded by the sequence of SEQ ID NO: 13 (Figure 7). In a particularly preferred embodiment, the nucleic acid sequence of the at least one WRKY gene comprises (or consists of) the sequence of SEQ ID NO: 13 (Figure 7), or the sequence of any one SEQ ID NOs: 51, 53, and 55 (Figure 14).

In various embodiments of the disclosure, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 80% homology or sequence identity to the nucleic acid sequence of TaWRKY68A (SEQ ID NO: 15, Figure 8), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY68A protein,

which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 85% or at least 90% homology or sequence identity to the nucleic acid sequence of TaWRKY68A (SEQ ID NO: 15, Figure 8), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY68A protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homolog of the nucleic acid sequence of the at least one WRKY gene shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the nucleic acid sequence of TaWRKY68A (SEQ ID NO: 15, Figure 8), wherein the variant or homologous nucleic acid sequence encodes a WRKY protein, preferably a WRKY68A protein, which is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY68A as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY68A encoded by the sequence of SEQ ID NO: 15 (Figure 8). In a particularly preferred embodiment, the nucleic acid sequence of the at least one WRKY gene comprises (or consists of) the sequence of SEQ ID NO: 15 (Figure 8), or the sequence of any one SEQ ID NOs: 57, 59, 61, and 63 (Figure 15).

In various embodiments of the disclosure, the variant or homolog of the nucleic acid sequence of the jasmonate receptor gene (e.g. COI1 gene) shows at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% homology or sequence identity to the nucleic acid sequence of TaCOI1 (SEQ ID NO: 75), wherein the variant or homologous nucleic acid sequence encodes a jasmonate receptor protein (e.g. COI1 protein). In certain embodiments, variants or homologs of TaCOI1 as described above exhibit the same expression or activity as the native TaCOI1 encoded by the sequence of SEQ ID NO: 75. In a particularly preferred embodiment, the nucleic acid sequence of the COI1 gene comprises (or consists of) the sequence of SEQ ID NO: 75, or the sequence of any one SEQ ID NOs: 77 (HvCOI1), and 79 (ScCOI1).

In various embodiments of the present disclosure, the at least one WRKY protein is selected from the group consisting of TaWRKY10 (SEQ ID NO: 4), TaWRKY13 (SEQ ID NO: 6), TaWRKY19 (SEQ ID NO: 8), TaWRKY29 (SEQ ID NO: 10), TaWRKY39 (SEQ ID NO: 12),

TaWRKY53B (SEQ ID NO: 14), and TaWRKY68A (SEQ ID NO: 16), or homologs thereof, and the COI1 protein (SEQ ID NO: 76) or homologs thereof.

In various embodiments of the disclosure, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 80% homology or sequence identity to the amino acid sequence of TaWRKY10 (SEQ ID NO: 4, Figure 2), wherein the variant or homologous WRKY10 protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 85% or at least 90% homology or sequence identity to the amino acid sequence of TaWRKY10 (SEQ ID NO: 4, Figure 2), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY10 protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the amino acid sequence of TaWRKY10 (SEQ ID NO: 4, Figure 2), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY10 protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY10 as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY10 having the sequence of SEQ ID NO: 4 (Figure 2). In a particularly preferred embodiment, the amino acid sequence of the at least one WRKY protein comprises (or consists of) the sequence of SEQ ID NO: 4 (Figure 2), or the sequence of any one SEQ ID NOs: 18, 20, 22, and 24 (Figure 9).

In various embodiments of the disclosure, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 80% homology or sequence identity to the amino acid sequence of TaWRKY13 (SEQ ID NO: 6, Figure 3), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY13 protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 85% or at least 90% homology or sequence identity to the amino acid sequence of TaWRKY13 (SEQ ID NO: 6, Figure 3), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY13 protein,

characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the amino acid sequence of TaWRKY13 (SEQ ID NO: 6, Figure 3), wherein the variant or homologous WRKY13 protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY13 as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY13 having the sequence of SEQ ID NO: 6 (Figure 3). In a particularly preferred embodiment, the amino acid sequence of the at least one WRKY protein comprises (or consists of) the sequence of SEQ ID NO: 6 (Figure 3), or the sequence of any one SEQ ID NOs: 26, 28, and 30 (Figure 10).

In various embodiments of the disclosure, the variant or homologous amino acid sequence of the at least one WRKY gene shows at least 80% homology or sequence identity to the amino acid sequence of TaWRKY19 (SEQ ID NO: 8, Figure 4), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY19 protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 85% or at least 90% homology or sequence identity to the amino acid sequence of TaWRKY19 (SEQ ID NO: 8, Figure 4), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY19 protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the amino acid sequence of TaWRKY19 (SEQ ID NO: 8, Figure 4), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY19 protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY19 as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY19 having the sequence of SEQ ID NO: 8 (Figure 4). In a particularly preferred

embodiment, the amino acid sequence of the at least one WRKY gene comprises (or consists of) the sequence of SEQ ID NO: 8 (Figure 4), or the sequence of any one SEQ ID NOs: 32, 34, and 36 (Figure 11).

In various embodiments of the disclosure, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 80% homology or sequence identity to the amino acid sequence of TaWRKY29 (SEQ ID NO: 10, Figure 5), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY29 protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 85% or at least 90% homology or sequence identity to the amino acid sequence of TaWRKY29 (SEQ ID NO: 10, Figure 5), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY29 protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the amino acid sequence of TaWRKY29 (SEQ ID NO: 10, Figure 5), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY29 protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY29 as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY29 having the sequence of SEQ ID NO: 10 (Figure 5). In a particularly preferred embodiment, the amino acid sequence of the at least one WRKY protein comprises (or consists of) the sequence of SEQ ID NO: 10 (Figure 5), or the sequence of SEQ ID NO: 38 or 40 (Figure 12).

In various embodiments of the disclosure, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 80% homology or sequence identity to the amino acid sequence of TaWRKY39 (SEQ ID NO: 12, Figure 6), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY39 protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 85% or at least 90% homology or

sequence identity to the amino acid sequence of TaWRKY39 (SEQ ID NO: 12, Figure 6), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY39 protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the amino acid sequence of TaWRKY39 (SEQ ID NO: 12, Figure 6), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY39 protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY39 as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY39 having the sequence of SEQ ID NO: 12 (Figure 6). In a particularly preferred embodiment, the amino acid sequence of the at least one WRKY protein comprises (or consists of) the sequence of SEQ ID NO: 12 (Figure 6), or the sequence of any one SEQ ID NOs: 42, 44, 46, 48, and 50 (Figure 13).

In various embodiments of the disclosure, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 80% homology or sequence identity to the amino acid sequence of TaWRKY53B (SEQ ID NO: 14, Figure 7), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY53B protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 85% or at least 90% homology or sequence identity to the amino acid sequence of TaWRKY53B (SEQ ID NO: 14, Figure 7), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY53B protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the amino acid sequence of TaWRKY53B (SEQ ID NO: 14, Figure 7), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY53B protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar,

non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY53B as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY53B having the sequence of SEQ ID NO: 14 (Figure 7). In a particularly preferred embodiment, the amino acid sequence of the at least one WRKY protein comprises (or consists of) the sequence of SEQ ID NO: 14 (Figure 7), or the sequence of any one SEQ ID NOs: 52, 54, and 56 (Figure 14).

In various embodiments of the disclosure, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 80% homology or sequence identity to the amino acid sequence of TaWRKY68A (SEQ ID NO: 16, Figure 8), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY68A protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. Preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 85% or at least 90% homology or sequence identity to the amino acid sequence of TaWRKY68A (SEQ ID NO: 16, Figure 8), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY68A protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. More preferably, the variant or homologous amino acid sequence of the at least one WRKY protein shows at least 95%, 96%, 97%, 98%, or 99% homology or sequence identity to the amino acid sequence of TaWRKY68A (SEQ ID NO: 16, Figure 8), wherein the variant or homologous protein is a WRKY protein, preferably a WRKY68A protein, characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid. In certain embodiments, variants or homologs of TaWRKY68A as described above exhibit the same fertilizer-responsive expression or activity as the native TaWRKY68A having the sequence of SEQ ID NO: 16 (Figure 8). In a particularly preferred embodiment, the amino acid sequence of the at least one WRKY protein comprises (or consists of) the sequence of SEQ ID NO: 16 (Figure 8), or the sequence of any one SEQ ID NOs: 58, 60, 62, and 64 (Figure 15).

In various embodiments of the disclosure, the variant or homologous amino acid sequence of the jasmonate receptor protein shows at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% homology or sequence identity to the amino acid sequence of TaCOI1 (SEQ ID NO: 76), wherein the variant or homologous protein is a COI1 protein. In certain embodiments, variants or homologs of TaCOI1 as described above

exhibit the same expression or activity as the native TaCOI1 having the sequence of SEQ ID NO: 76. In a particularly preferred embodiment, the amino acid sequence of the COI1 protein comprises (or consists of) the sequence of SEQ ID NO: 76, or the sequence of any one SEQ ID NOs: 78 (HvCOI1), and 80 (ScCOI1).

In the present disclosure, the at least one modification in the at least one WRKY gene inhibiting the expression or activity of the at least one WRKY protein (as compared to a corresponding control plant cell lacking the at least one modification) results in an increased pathogen resistance of a cereal plant comprising the cereal plant cell having introduced into its genome the said at least one modification inhibiting the expression or activity of the at least one WRKY protein as compared to a control plant lacking the said cereal plant cell. In other words, the at least one modification in the at least one WRKY gene inhibiting the expression or activity of the at least one WRKY protein provides for an activation or upregulation of plant immunity against pathogens. The at least one modification in the jasmonate receptor gene enhancing the expression or activity of the jasmonate receptor protein (as compared to a corresponding control plant cell lacking the at least one modification) results in an increased pathogen resistance of a cereal plant comprising the cereal plant cell having introduced into its genome the said at least one modification enhancing the expression or activity of the jasmonate receptor protein as compared to a control plant lacking the said cereal plant cell. In other words, the at least one modification in the jasmonate receptor gene enhancing the expression or activity of the jasmonate receptor protein provides for an activation or upregulation of plant immunity against pathogens. Both of the above at least one modification(s) may provide for a further improved or increased activation or upregulation of plant immunity against pathogens due to a synergistic effect.

In accordance with the present disclosure, a pathogen as described herein generally is a plant pathogen (phytopathogen). In various preferred embodiments of the present disclosure, the at least one modification results in an increased resistance against fungal pathogens. More preferably, the fungal pathogens are pathogenic filamentous fungi. In various other preferred embodiments, the fungal pathogen is a pathogenic ascomycete, *i.e.*, a fungal pathogen belonging to the Phylum *Ascomycota*. More preferably, the pathogenic ascomycetes are filamentous ascomycete fungi. In various embodiments of the present disclosure, the pathogenic ascomycete fungi belong to the family *Mycosphaerellaceae*. Preferably, the fungal pathogen or pathogenic ascomycete is a member of the genus *Zymoseptoria*. In particular preferred embodiments, the fungal pathogen or pathogenic ascomycete is *Zymoseptoria tritici*. As described herein, the terms *Zymoseptoria tritici* and *Septoria tritici* may be used herein interchangeably. More preferably, Thus, in particularly preferred embodiments of the present disclosure, the at least one modification inhibiting the expression or activity of the at least one

WRKY protein and/or the at least one modification enhancing the expression or activity of the jasmonate receptor protein result in an increased resistance against Septoria leaf blotch disease, which is caused by fungal pathogens belonging to the genus *Zymoseptoria*, in particular *Zymoseptoria tritici*, preferably even under high fertilizer conditions (e.g. nitrogen), i.e. not negatively influenced by the applied fertilizer regimes (e.g. nitrogen regime). In other particular preferred embodiments, the fungal pathogen or pathogenic ascomycete is *Fusarium graminearum*, *Fusarium culmorum*, *Fusarium avenaceum*, *Fusarium poae*, *Fusarium equiseti*, *Puccinia triticina*, *Puccinia striiformis* f. sp. *tritici*, or *Puccinia graminis*.

As described herein, the terms “Septoria disease”, “Septoria leaf blotch disease”, or “*Septoria tritici* blotch” may be used herein interchangeably.

In various embodiments of the present disclosure, the least one modification in the at least one WRKY gene inhibiting the expression or activity of the at least one WRKY protein and/or the least one modification in the jasmonate receptor gene enhancing the expression or activity of the jasmonate receptor protein is caused or effected by mutagenesis. In various embodiments of the present disclosure, the least one modification in the at least one WRKY gene inhibiting the expression or activity of the at least one WRKY protein and/or the least one modification in the jasmonate receptor gene enhancing the expression or activity of the jasmonate receptor protein is caused or effected by random mutagenesis. In various other embodiments of the present disclosure, the least one modification in the at least one WRKY gene inhibiting the expression or activity of the at least one WRKY protein and/or the least one modification in the jasmonate receptor gene enhancing the expression or activity of the jasmonate receptor protein is caused or effected by targeted mutagenesis. Preferably, mutagenesis according to the present disclosure means a mutagenesis of the endogenous WRKY gene and/or a mutagenesis of the endogenous jasmonate receptor gene.

In various embodiments of the present disclosure, the at least one modification inhibiting the expression or activity of the at least one WRKY protein is caused by RNA interference, sense suppression, insertional mutagenesis, chemically induced mutagenesis or genome editing of the at least one endogenous WRKY gene and/or the at least one modification enhancing the expression or activity of the jasmonate receptor protein is caused insertional mutagenesis, chemically induced mutagenesis or genome editing of the endogenous jasmonate receptor gene. In various embodiments of the present disclosure, the least one modification inhibiting the expression or activity of the at least one WRKY protein or enhancing the expression or activity of the jasmonate receptor protein is caused or effected by targeting induced local lesions in genomes (TILLING), which is a technique that was introduced at the beginning of this century using the model plant *Arabidopsis thaliana*. In various embodiments of the present disclosure, the least one modification is caused or effected by the known genome editing tools

like Zinc Finger Nucleases, TAL Effector Nucleases, CRISPR systems based e.g. on Cas9, Cpf1, CasX or CasY etc. In various preferred embodiments, the least one modification inhibiting the expression or activity of the at least one WRKY protein is caused by virus-induced gene silencing (VIGS). In various other embodiments of the present disclosure, the at least one modification inhibiting the expression or activity of the at least one WRKY protein or enhancing the expression or activity of the jasmonate receptor protein comprises one or more transposons, one or more insertions, one or more additions, one or more deletions or one or more point mutations in the at least one endogenous WRKY gene or in the endogenous jasmonate receptor gene. In various embodiments of the present disclosure, the least one modification inhibiting the expression or activity of the at least one WRKY protein is a disruption of the at least one endogenous WRKY gene.

In various embodiments of the present disclosure, the at least one modification is introduced into the cereal plant cell, or cereal plant or part thereof, by (a) introducing at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising (i) at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), or (ii) at least 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 400, 500, 700, 800, 900 or 1000 contiguous nucleotides of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A), and a homolog thereof, preferably in sense and/or in antisense, into the plant cell such that the at least one polynucleotide sequence is operatively linked to a promoter in a sense or antisense orientation; or (b) introducing at least one polynucleotide sequence comprising one or more subsequences of a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), and a homolog thereof into the plant cell, wherein the at least one polynucleotide sequence is configured for RNA interference, preferably wherein the at least one polynucleotide sequence is configured for endogenous (post transcriptional) gene silencing or virus-induced gene silencing, and/or (c) introducing at least one polynucleotide sequence (preferably as transgene) comprising a nucleic acid sequence, or a complement thereof, comprising (i) the nucleic acid sequence of SEQ ID NO: 75, (ii) a nucleic acid sequence

showing an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or (iii) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (i), (iv) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (v) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, wherein the transgene is operatively linked to a promoter, wherein the at least one polynucleotide sequence is configured for overexpression of the jasmonate receptor gene.

In various embodiments of the present disclosure, the fertilizer is a mineral fertilizer, preferably nitrogen, phosphorus, or potassium. Thus, in various embodiments of the present disclosure the fertilizer-responsive expression or activation of the at least one WRKY protein means mineral fertilizer-responsive expression or activation of the at least one WRKY protein.

In various embodiments of the present disclosure, fertilizer-responsive expression or activation of the at least one WRKY protein means nitrogen-responsive expression or activation of the at least one WRKY protein. In various other embodiments of the present disclosure, fertilizer-responsive expression or activation of the at least one WRKY protein means potassium-responsive expression or activation of the at least one WRKY protein. In still other embodiments of the present disclosure, fertilizer-responsive expression or activation of the at least one WRKY protein means phosphorus-responsive expression or activation of the at least one WRKY protein. Preferably, fertilizer-responsive expression or activation of the at least one WRKY protein means nitrogen-responsive expression or activation of the at least one WRKY protein.

The term “nitrogen fertilization”, “potassium fertilization”, or “phosphorus fertilization” respectively as used herein shall be interpreted to mean any man-made or artificial environmental condition in which plant-available nitrogen, potassium, or phosphorus respectively in the soil is more than would be available under natural environmental conditions, wherein the more of plant-available nitrogen in the soil causes a significant increase in yield or allows to tend to or to exploit the maximum yield potential of a specific crop or cultivar grown on the soil.

As used herein the term “inhibition of the expression or activity of a WRKY protein” or “inhibiting the expression or activity of a WRKY protein” shall be interpreted to mean any change in a level of synthesis of the functional WRKY protein or a WRKY biological activity, which can include a reduced level of functional WRKY protein present in a plant cell, reduced efficacy of the WRKY protein, reduced ability to recognize or bind the DNA at the corresponding cis-

regulatory elements like the W box ((T)TGAC(C/T)) or variants thereof, or any other means which affects one or more of the biological properties of a WRKY protein of the present disclosure in relation to its role as transcriptional regulator, in particular its role as negative regulator of genes involved in plant pathogen defense. Accordingly, "inhibition of the expression or activity of a WRKY protein" encompasses a reduction in the efficacy of the protein or a reduction in the level of WRKY protein present in a plant cell, for example, due to a reduction in the expression of a WRKY gene.

In various embodiments of the present disclosure, inhibiting the expression or activity of at least one WRKY protein means inhibiting the level of expression or level of activity of the at least one WRKY gene or the at least one WRKY protein. Furthermore, in various embodiments of the present disclosure, inhibiting the expression of at least one WRKY protein is effected or targeting at the level of expression of the WRKY gene encoding the at least one WRKY protein. Inhibition of gene expression may be performed or can occur, but is not limited to, at the level of mRNA transcription or at the post-transcriptional level.

In the present disclosure, inhibiting the expression or activity of at least one WRKY protein does not necessarily mean, *i.e.*, is not limited to, a total inhibition of the expression or activity of the at least one WRKY protein. Rather, inhibiting the expression of at least one WRKY protein means that the expression of the at least one WRKY gene encoding the at least one WRKY protein is reduced or decreased to an extent that no or no significant mRNA or protein expression transcribed or encoded, respectively, by the at least one WRKY gene occurs. Techniques for measuring and determining gene expression by measuring and determining mRNA or protein expression are well known to the one of ordinary skill in the art. Thus, in various embodiments of the present disclosure, inhibiting the expression of at least one WRKY protein means inhibiting the expression of the mRNA (or mRNA transcript) derived from the at least one WRKY gene encoding the at least one WRKY protein. Additionally or alternatively, inhibiting the expression of at least one WRKY protein may mean that the expression of the at least one WRKY gene encoding the at least one WRKY protein is reduced or decreased to an extent that no or no significant activity of the at least one WRKY protein is measurable. Techniques for measuring and determining the activity of WRKYs are well known to the one of ordinary skill in the art.

As used herein the term "enhancement of the expression or activity of a jasmonate receptor protein" or "enhancing the expression or activity of a jasmonate receptor protein" shall be interpreted to mean any change in a level of synthesis of the functional WRKY protein or a WRKY biological activity, which can include a increased level of functional jasmonate receptor protein present in a plant cell, increased efficacy of the jasmonate receptor protein, or any other means which affects one or more of the biological properties of a jasmonate receptor

protein of the present disclosure in relation to its role as receptor of jasmonate, in particular its role as positive regulator involved in plant pathogen defense. Accordingly, "enhancement of the expression or activity of a jasmonate receptor protein" encompasses an increase in the efficacy of the protein or an increase in the level of jasmonate receptor protein present in a plant cell, for example, due to an increase in the expression or overexpression of a jasmonate receptor gene.

In various embodiments of the present disclosure, enhancing the expression or activity of the jasmonate receptor protein means enhancing the level of expression or level of activity of the jasmonate receptor gene or the jasmonate receptor protein. Furthermore, in various embodiments of the present disclosure, enhancing the expression of the jasmonate receptor protein is effected or targeting at the level of expression of the jasmonate receptor gene encoding the jasmonate receptor protein. Enhancement of gene expression may be performed or can occur, but is not limited to, at the level of DNA, epigenetics, or mRNA transcription. Techniques for measuring and determining gene expression by measuring and determining mRNA or protein expression are well known to the one of ordinary skill in the art.

In various embodiments of the present disclosure, expression of the at least one WRKY protein may mean over-expression of the at least one WRKY protein.

In various preferred embodiments of the present disclosure, "activity of at least one WRKY protein" describes the (transcriptional) activation of at least one gene regulated by the at least one WRKY protein. More preferably, the at least one gene regulated by the at least one WRKY protein is involved in the cereal plant cell or cereal plant defense mechanism/response against a pathogen. Still more preferably, activation of the at least one gene, which is regulated by the at least one WRKY protein and which is involved in the cereal plant cell defense mechanism/response against a pathogen, results in, or forms part of, a negative regulation of the defense mechanism/response of the cereal plant cell or cereal plant against a pathogen.

As described herein, the terms "WRKY" and "WRKY transcription factor" or "WRKY-type transcription factor" may be used herein interchangeably. WRKYs are transcription factors specifically found in plants. Thus, a "WRKY" according to the present disclosure may inherently be considered a "plant WRKY" or "plant cell WRKY".

In various preferred embodiments of the present disclosure, "activity of a jasmonate receptor protein" describes the involvement of COI1 in JA perception and signaling by the SCF^{COI1}/JAZ/MYC2 complex, preferably the function of the complex to catalyze the ubiquitination of proteins. The F-box (COI1) is the component that confers specificity for the substrate. More preferably, the jasmonate receptor gene or the SCF^{COI1}/JAZ/MYC2 complex ,

respectively, is involved in the cereal plant cell or cereal plant defense mechanism/response against a pathogen.

Furthermore, in various embodiments of the disclosure, corresponding control plant cell, or control plant or part thereof, means that the control plant cell, or control plant or part thereof, is of the same species, preferably of the same variety or cultivar, as the cereal plant cell, or cereal plant or part thereof, having introduced into its genome the at least one modification inhibiting the expression and/or activity of the at least one WRKY protein of the present disclosure or the at least one modification enhancing the expression and/or activity of the jasmonate receptor protein of the present disclosure. For example, if the cereal plant cell of the disclosure is a cell of a wheat plant (e.g., cv. Avalon), the corresponding control plant cell is a cell of the same wheat plant cultivar (e.g., cv. Avalon), but is actually lacking the at least one modification.

In various embodiments of the present disclosure, the cereal plant cell, or cereal plant or part thereof, is a monocotyledonous cereal plant cell, or cereal plant or part thereof. In various embodiments of the present disclosure, the cereal plant cell is the cell of a wheat plant (*Triticum aestivum*), the cell of a rye plant (*Secale cereale*), the cell of a barley plant (*Hordeum vulgare*), the cell of a maize plant (*Zea mays*), the cell of a rice plant (*Oryza sativa*), the cell of an oat plant (*Avena sativa*), or the cell of a millet plant (*Panicum miliaceum*). In preferred embodiments, the cereal plant cell is the cell of a wheat plant (*Triticum aestivum*). In other preferred embodiments, the cereal plant cell is the cell of a rye plant (*Secale cereale*). In still other preferred embodiments, the cereal plant cell is the cell of a barley plant (*Hordeum vulgare*).

In various embodiments of the present disclosure, the cereal plant or part thereof is a wheat plant (*Triticum aestivum*) or part thereof, a rye plant (*Secale cereale*) or part thereof, a barley plant (*Hordeum vulgare*) or part thereof, a maize plant (*Zea mays*) or part thereof, a rice plant (*Oryza sativa*) or part thereof, an oat plant (*Avena sativa*) or part thereof, or a millet plant (*Panicum miliaceum*) or part thereof. In preferred embodiments, the cereal plant or part thereof is a wheat plant (*Triticum aestivum*). In other preferred embodiments, the cereal plant or part thereof is a rye plant (*Secale cereale*) or part thereof. In still other preferred embodiments, the cereal plant or part thereof is a barley plant (*Hordeum vulgare*) or part thereof.

The present disclosure provides a cereal plant comprising or containing a cereal plant cell of the disclosure and having a phenotype of increased pathogen resistance, preferably a phenotype of increased resistance against a fungal pathogen, more preferably a phenotype of increased resistance against Septoria leaf blotch disease (or *Septoria tritici blotch*, STB), Fusarium disease (*Fusarium sp.*) or rust diseases (*Puccinia sp.*).

The present disclosure provides a cereal plant having an increased pathogen resistance, preferably having an increased resistance against a fungal pathogen, more preferably having an increased resistance against Septoria leaf blotch disease (or *Septoria tritici blotch*, *STB*), Fusarium disease (*Fusarium sp.*) or rust diseases (*Puccinia sp.*), wherein the increased pathogen resistance results from at least one modification introduced into the genome of the plant inhibiting the expression or activity of at least one WRKY protein as compared to a corresponding control plant lacking the at least one modification, wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid, and/or from at least one modification introduced into the genome of the cereal plant enhancing the expression or activity of a jasmonate receptor protein as compared to a corresponding control plant cell lacking the at least one modification wherein the jasmonate receptor protein a) having the amino acid sequence of SEQ ID NO: 76, b) having an amino acid sequence showing an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, c) is encoded by the nucleic acid sequence of SEQ ID NO: 75, d) is encoded by a nucleic acid sequence showing an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c). Preferably, the increased pathogen resistance results from: (a) a modification in at least one endogenous WRKY gene comprising a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), wherein the modification comprises one or more transposons, one or more insertions, one or more additions, one or more deletions or one or more point mutations in the at least one endogenous WRKY gene; (b) at least one introduced transgene comprising a nucleic acid sequence, or a complement thereof, comprising (i) at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), or (ii) at least 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 400, 500, 700, 800, 900 or 1000 contiguous nucleotides of the nucleotide sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13),

SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A), and a homolog thereof, preferably in sense and/or in antisense, wherein the transgene is operatively linked to a promoter in a sense and/or antisense orientation; or (c) at least one introduced polynucleotide sequence comprising one or more subsequences of a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), wherein the at least one polynucleotide sequence is in RNA interference configuration, preferably wherein the at least one polynucleotide sequence is configured for endogenous (post transcriptional) gene silencing or virus-induced gene silencing, and/or (d) a modification in the endogenous jasmonate receptor gene comprising (i) the nucleotide sequence of TaCOI1 (SEQ ID NO: 75), (ii) a nucleic acid sequence showing an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, (iii) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (i), (iv) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (v) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, wherein the modification comprises one or more transposons, one or more insertions, one or more additions, one or more deletions, or one or more point mutations in the endogenous jasmonate receptor gene; or (e) an introduced transgene comprising a nucleic acid sequence, or a complement thereof, comprising (i) the nucleic acid sequence of SEQ ID NO: 75, (ii) a nucleic acid sequence showing an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or (iii) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (i), (iv) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (v) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, wherein the transgene is operatively linked to a promoter.

In various embodiments of the present disclosure, the cereal plant is a hybrid cereal plant.

In various embodiments of the disclosure, the promoter is a tissue-specific promoter, a temporally regulated promoter, or an inducible promoter, preferably a pathogen inducible promoter.

The present disclosure provides a method for conferring pathogen resistance to, or increasing pathogen resistance of, a cereal plant cell, or a cereal plant or part thereof, the method comprising the step of inhibiting the expression or activity of at least one WRKY protein of the present disclosure in a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or control plant or part thereof, lacking the inhibition, and/or the step of enhancing the expression or activity of a jasmonate receptor protein of a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or plant or part thereof, lacking the enhancement.

The present disclosure also provides a method of producing a cereal plant cell, or a cereal plant or part thereof, having an increased pathogen resistance as compared to a corresponding control plant cell, or control plant or part thereof, the method comprising the step of inhibiting the expression or activity of at least one WRKY protein of the present disclosure in a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or plant or part thereof, lacking the inhibition, and/or the step of enhancing the expression or activity of a jasmonate receptor protein of a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or plant or part thereof, lacking the enhancement.

In various embodiments of the methods of the present disclosure, the step of inhibiting the expression or activity of at least one WRKY protein comprises introducing into the genome of the cereal plant cell, or a cereal plant or part thereof, at least one modification inhibiting the expression or activity of the at least one WRKY protein as compared to a corresponding control plant cell, or control plant or part thereof, lacking the at least one modification, and the step of enhancing the expression or activity of a jasmonate receptor protein comprises introducing into the genome of the cereal plant cell, or a cereal plant or part thereof, at least one modification enhancing the expression or activity of the jasmonate receptor protein as compared to a corresponding control plant cell, or control plant or part thereof, lacking the at least one modification.

In various embodiments of the methods of the present disclosure, the at least one modification comprises one or more transposons, one or more insertions, one or more additions, one or more deletions or one or more point mutations in the at least one endogenous WRKY gene and/or at least one modification comprises one or more transposons, one or more insertions,

one or more additions, one or more deletions or one or more point mutations in the endogenous jasmonate receptor gene.

In various embodiments of the methods of the present disclosure, the at least one modification is introduced into the cereal plant cell, or cereal plant or part thereof, by (a) introducing at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising (i) at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A) or (ii) at least 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 400, 500, 700, 800, 900 or 1000 contiguous nucleotides of the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A), and a homolog thereof, preferably in sense and/or in antisense, into the cereal plant cell, or cereal plant or part thereof, such that the at least one polynucleotide sequence is operatively linked to a promoter in a sense and/or antisense orientation; or (b) introducing at least one polynucleotide sequence comprising one or more subsequences of a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), into the plant cell, or plant or part thereof, wherein the at least one polynucleotide sequence is configured for RNA interference, preferably wherein the at least one polynucleotide sequence is configured for endogenous (post transcriptional) gene silencing or virus-induced gene silencing, and/or introducing at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising (i) the nucleic acid sequence of SEQ ID NO: 75, (ii) a nucleic acid sequence showing an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or (iii) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (i), (iv) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (v) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, preferably wherein the at least

one polynucleotide sequence is operatively linked to a promoter, more preferably the at least one polynucleotide sequence is configured for overexpression.

The present disclosure provides a method of identifying a cereal plant cell, or a cereal plant or part thereof, having an increased pathogen resistance as compared to a corresponding control plant cell, or control plant or part thereof, the method comprising the step of identifying a cereal plant cell, or a cereal plant or part thereof, in which the expression or activity of at least one WRKY protein of the present disclosure is inhibited as compared to a corresponding control plant cell, or plant or part thereof, lacking the inhibition, and/or in which the expression or activity of a jasmonate receptor protein is enhanced as compared to a corresponding control plant cell, or plant or part thereof, lacking the enhancement, wherein the jasmonate receptor protein a) having the amino acid sequence of SEQ ID NO: 76, b) having an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76, c) is encoded by the nucleic acid sequence of SEQ ID NO: 75, d) is encoded by a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, or e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c), preferably wherein the at least one modification(s) are introduced into the at least one endogenous WRKY gene encoding the at least one WRKY protein and/or into an endogenous jasmonate receptor gene encoding the jasmonate receptor protein.

In various embodiments of the present disclosure, the cereal plant cell, or cereal plant or part thereof, comprises a heterozygous or homozygous mutation in the at least one WRKY gene encoding the at least one WRKY protein or the jasmonate receptor gene encoding the jasmonate receptor protein, wherein the mutation causes the inhibition of the expression or activity of the at least one WRKY protein encoded by the at least one WRKY gene or the mutation causes the enhancement of the expression or activity of the jasmonate receptor protein encoded by the jasmonate receptor gene.

In various embodiments of the present disclosure, the above mutant form is introduced into the cereal plant cell, or cereal plant or part thereof, by *Agrobacterium*-mediated transfer, electroporation, micro-projectile bombardment, or sexual cross. The techniques of *Agrobacterium*-mediated transfer, electroporation, micro-projectile bombardment, and sexual cross are well-known to the skilled person and methods are described in the literature. For example, transformation of cereals via particle bombardment may be performed as described in Sparks and Jones, 2014, Genetic transformation of wheat via particle bombardment, *Methods Mol. Biol.* 1099, 201-218.

In various embodiments of the present disclosure, the cereal plant cell, or cereal plant or part thereof, has an increased resistance against a fungal pathogen, preferably an increased resistance against *Septoria* leaf blotch disease (or *Septoria tritici blotch*, *STB*), *Fusarium* disease (*Fusarium sp.*) or rust diseases (*Puccinia sp.*).

The present disclosure provides a cereal plant cell, or a cereal plant or part thereof, produced by any of the methods of the present disclosure.

The present invention provides a recombinant DNA construct comprising a polynucleotide sequence, or a fragment thereof, operatively linked to a heterologous promoter, wherein the polynucleotide sequence, or a fragment thereof, produces upon expression in a cereal plant cell, or cereal a plant or part thereof: (a) a protein that interferes with the expression or activity of at least one endogenous WRKY protein of the present disclosure; (b) an RNA molecule that suppresses the expression of at least one endogenous WRKY protein of the present disclosure; or (c) a loss-of-function mutation in at least one endogenous WRKY gene or the protein encoded thereby of the present disclosure, wherein the polynucleotide sequence comprises a nucleic acid sequence, or a complement thereof, comprising (i) at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A); or (ii) at least 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 400, 500, 700, 800, 900 or 1000 contiguous nucleotides of the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A), and homologs thereof, preferably in sense and/or in antisense.

The present invention provides a recombinant DNA construct comprising a polynucleotide sequence, or a fragment thereof, operatively linked to a heterologous promoter, wherein the polynucleotide sequence comprises (a) the nucleic acid sequence of SEQ ID NO: 75, (b) a nucleic acid sequence showing an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of SEQ ID NO: 75, (c) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (a), (d) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (e) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the amino acid sequence of SEQ ID NO: 76.

The present disclosure provides a method of producing a cereal plant cell, or a cereal plant or part thereof, having an increased pathogen resistance as compared to a corresponding control plant cell, or control plant or part thereof, the method comprising the steps of (a) incorporating into a cereal plant cell, or a cereal plant or part thereof, one or more recombinant DNA construct(s) of the present disclosure; and (b) selecting a cereal plant cell, or a cereal plant or part thereof, comprising the said one or more recombinant DNA construct(s) and having an increased pathogen resistance as compared to a corresponding control plant cell, or control plant or part thereof, that does not comprise the said one or more recombinant DNA construct.

The present disclosure provides a cereal plant cell, or a cereal plant or part thereof, comprising one or more recombinant DNA construct(s) of the present disclosure and having an increased pathogen resistance as compared to a corresponding control plant cell, or plant or part thereof, that does not comprise the said one or more recombinant DNA construct(s).

The present disclosure provides a method of producing a cereal plant having an increased pathogen resistance as compared to a corresponding control plant, the method comprising obtaining and planting seeds produced by a cereal plant of the present disclosure, wherein the seed comprises one or more recombinant DNA construct(s) of the present disclosure, and wherein the plant grown from the planted seed is a progeny plant having an increased pathogen resistance as compared to a corresponding control plant that does not comprise the said one or more recombinant DNA construct(s).

The present disclosure provides a double-stranded RNA (dsRNA) molecule comprising: (a) a first strand comprising a nucleotide sequence having a length of at least 19, 20, 21, 22, 23, 24, 25, 30, 40 or 50 nucleotides, preferably at least 60, 70, 80, 90 or 100 nucleotides, more preferably at least 150, 200, 250, 300, 400, 500, 750 or 1000 nucleotides and having at least 90%, 91%, 92%, 93% or 94%, more preferably 95%, 96%, 97%, 98%, 99% or even 100% sequence identity to consecutive nucleotides of a target nucleic acid sequence; and (b) a second strand comprising in the 5' to 3' direction a nucleotide sequence which is at least 90%, 91%, 92%, 93% or 94%, more preferably 95%, 96%, 97%, 98%, 99% or even 100% complementary to the first strand and/or is able to hybridize with the first strand, preferably under stringent conditions, wherein the target nucleic acid sequence is a coding region of an mRNA deduced from a nucleic acid sequence, or a complement thereof, comprising at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98%, 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A).

The present disclosure provides a composition comprising a dsRNA molecule of the present disclosure.

The present disclosure provides a method of regulating the expression of at least one WRKY gene of the present disclosure in a cereal plant cell, or cereal plant or part thereof, the method comprising applying a composition comprising a dsRNA molecule of the present disclosure to a cereal plant cell, or cereal plant or part thereof, preferably wherein the composition is applied onto the surface of the plant cell, or plant or part thereof.

The present disclosure provides a cereal plant cell, or a cereal plant or part thereof, comprising a dsRNA molecule of the present disclosure and having an increased pathogen resistance as compared to a corresponding control plant cell, or control plant or part thereof, that does not comprise the said dsRNA molecule.

The present disclosure provides the use of at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising (i) at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A); or (ii) at least 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 400, 500, 700, 800, 900 or 1000 contiguous nucleotides of the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A), and a homolog thereof, as molecular marker for identifying a cereal plant cell, or a cereal plant or part thereof, having an increased pathogen resistance as compared to a corresponding control plant cell.

The present disclosure provides a method of identifying a cereal plant cell, or a cereal plant or part thereof, having an increased pathogen resistance as compared to a corresponding control plant cell, the method comprising the use of at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising at least at least 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45 or 50 contiguous nucleotides of (a) the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A) and SEQ ID NO: 75 (TaCOI1), (b) a nucleic acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of any one of SEQ ID NO: 3, SEQ ID NO: 5, SEQ

ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15 and SEQ ID NO: 75, or (c) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (a), (d) a nucleic acid encoding the amino acid sequence of any one of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16 and SEQ ID NO: 76, or (e) a nucleic acid encoding the amino acid sequence exhibiting an identity of at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% to the nucleic acid sequence of any one of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16 and SEQ ID NO: 76, as molecular marker for identifying a cereal plant cell, or a cereal plant or part thereof, having an increased pathogen resistance as compared to a corresponding control plant cell. A “molecular marker” is a nucleic acid that is polymorphous in a plant population. Such a marker is thus able to detect and differentiate different allelic states (alleles). Known analytical methods used for this purpose are RFLP, AFLP, SNP, SSR or KASP, for example. The term “molecular marker” relates to nucleotide sequences that are complementary or at least complementary to the greatest possible extent or homologous to genomic sequences, for example nucleic acids used as probes or primers. Markers that describe polymorphisms can be detected with use of well-established methods. These include, for example, PCR-based sequence-specific amplification, a detection of ‘restriction fragment length polymorphisms’ (RFLPs), a detection of polynucleotide polymorphisms by means of ‘allele specific hybridisation’ (ASH), a detection of amplified variable sequences of the plant genome, a detection of a ‘self-sustained sequence replication’, a detection of ‘simple sequence repeats’ (SSRs), a detection of ‘single nucleotide polymorphisms’ (SNPs), or a detection of ‘amplified fragment length polymorphisms’ (AFLPs). Furthermore, the methods for detection of ‘expressed sequence tags’ (ESTs) and SSR markers derived from EST sequences and ‘randomly amplified polymorphic DNA’ (RAPD) are also known.

The present disclosure provides a composition for topical application to a cereal plant cell, or a cereal plant or part thereof, comprising at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising (i) at least 80%, 85% or 90%, preferably at least 92%, 94% or 96%, more preferably at least 97%, 98% 99% sequence identity to the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A); or (ii) at least 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 400, 500, 700, 800, 900 or 1000 contiguous nucleotides of the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 TaWRKY19), SEQ ID NO: 9

(TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A), and a homolog thereof, preferably in sense and/or in antisense, wherein the at least one polynucleotide sequence is configured for RNA interference, preferably wherein the at least one polynucleotide sequence is configured for endogenous (post transcriptional) gene silencing or virus-induced gene silencing.

The present disclosure provides the use of one or more recombinant DNA construct(s) of the present disclosure for conferring pathogen resistance to, or increasing pathogen resistance of, a cereal plant cell, or a cereal plant or part thereof.

The present disclosure provides the use of a dsRNA molecule of the present disclosure for conferring pathogen resistance to, or increasing pathogen resistance of, a cereal plant cell, or a cereal plant or part thereof.

The present disclosure provides the use of the composition for topical application to a cereal plant cell, or a cereal plant or part thereof, of the present disclosure for conferring pathogen resistance to, or increasing pathogen resistance of, a cereal plant cell, or a cereal plant or part thereof.

In various embodiments of the present disclosure, the said nucleic acid sequence, or a complement thereof, comprising (i) at least 80% sequence identity to SEQ ID NO: 3 (TaWRKY10), or (ii) at least 20 contiguous nucleotides of SEQ ID NO: 3 (TaWRKY10), optionally in sense and/or in antisense, preferably comprises (i) at least 85%, or 90%, more preferably at least 95%, 96%, 97%, 98% or 99% sequence identity to the nucleotide sequence of SEQ ID NO: 3 (TaWRKY10), or (ii) at least 21, 22, 23, 24, 25, 30, 40 or 50 contiguous nucleotides, preferably at least 60, 70, 80, 90 or 100 contiguous nucleotides, more preferably at least 150, 200, 250, 300, 400, 500, 750 or 1000 contiguous nucleotides of SEQ ID NO: 3 (TaWRKY10), optionally in sense and/or in antisense. In particularly preferred embodiments, the said nucleic acid sequence, or a complement thereof, comprises (or consists of) the sequence of SEQ ID NO: 3 (TaWRKY10).

In various other embodiments of the present disclosure, the said nucleic acid sequence, or a complement thereof, comprising (i) at least 80% sequence identity to SEQ ID NO: 5 (TaWRKY13), or (ii) at least 20 contiguous nucleotides of SEQ ID NO: 5 (TaWRKY13), optionally in sense and/or in antisense, preferably comprises (i) at least 85%, or 90%, more preferably at least 95%, 96%, 97%, 98% or 99% sequence identity to the nucleotide sequence of SEQ ID NO: 5 (TaWRKY13), or (ii) at least 21, 22, 23, 24, 25, 30, 40 or 50 contiguous nucleotides, preferably at least 60, 70, 80, 90 or 100 contiguous nucleotides, more preferably at least 150, 200, 250, 300, 400, 500, 750 or 1000 contiguous nucleotides of SEQ ID NO: 5 (TaWRKY13), optionally in sense and/or in antisense. In particularly preferred embodiments,

the said nucleic acid sequence, or a complement thereof, comprises (or consists of) the sequence of SEQ ID NO: 5 (TaWRKY13).

In various other embodiments of the present disclosure, the said nucleic acid sequence, or a complement thereof, comprising (i) at least 80% sequence identity to SEQ ID NO: 7 (TaWRKY19), or (ii) at least 20 contiguous nucleotides of SEQ ID NO: 7 (TaWRKY19), optionally in sense and/or in antisense, preferably comprises (i) at least 85%, or 90%, more preferably at least 95%, 96%, 97%, 98% or 99% sequence identity to the nucleotide sequence of SEQ ID NO: 7 (TaWRKY19), or (ii) at least 21, 22, 23, 24, 25, 30, 40 or 50 contiguous nucleotides, preferably at least 60, 70, 80, 90 or 100 contiguous nucleotides, more preferably at least 150, 200, 250, 300, 400, 500, 750 or 1000 contiguous nucleotides of SEQ ID NO: 7 (TaWRKY19), optionally in sense and/or in antisense. In particularly preferred embodiments, the said nucleic acid sequence, or a complement thereof, comprises (or consists of) the sequence of SEQ ID NO: 7 (TaWRKY19).

In various other embodiments of the present disclosure, the said nucleic acid sequence, or a complement thereof, comprising (i) at least 80% sequence identity to SEQ ID NO: 9 (TaWRKY29), or (ii) at least 20 contiguous nucleotides of SEQ ID NO: 9 (TaWRKY29), optionally in sense and/or in antisense, preferably comprises (i) at least 85%, or 90%, more preferably at least 95%, 96%, 97%, 98% or 99% sequence identity to the nucleotide sequence of SEQ ID NO: 9 (TaWRKY29), or (ii) at least 21, 22, 23, 24, 25, 30, 40 or 50 contiguous nucleotides, preferably at least 60, 70, 80, 90 or 100 contiguous nucleotides, more preferably at least 150, 200, 250, 300, 400, 500, 750 or 1000 contiguous nucleotides of SEQ ID NO: 9 (TaWRKY29), optionally in sense and/or in antisense. In particularly preferred embodiments, the said nucleic acid sequence, or a complement thereof, comprises (or consists of) the sequence of SEQ ID NO: 9 (TaWRKY29).

In various other embodiments of the present disclosure, the said nucleic acid sequence, or a complement thereof, comprising (i) at least 80% sequence identity to SEQ ID NO: 11 (TaWRKY39), or (ii) at least 20 contiguous nucleotides of SEQ ID NO: 11 (TaWRKY39), optionally in sense and/or in antisense, preferably comprises (i) at least 85%, or 90%, more preferably at least 95%, 96%, 97%, 98% or 99% sequence identity to the nucleotide sequence of SEQ ID NO: 11 (TaWRKY39), or (ii) at least 21, 22, 23, 24, 25, 30, 40 or 50 contiguous nucleotides, preferably at least 60, 70, 80, 90 or 100 contiguous nucleotides, more preferably at least 150, 200, 250, 300, 400, 500, 750 or 1000 contiguous nucleotides of SEQ ID NO: 11 (TaWRKY39), optionally in sense and/or in antisense. In particularly preferred embodiments, the said nucleic acid sequence, or a complement thereof, comprises (or consists of) the sequence of SEQ ID NO: 11 (TaWRKY39).

In various other embodiments of the present disclosure, the said nucleic acid sequence, or a complement thereof, comprising (i) at least 80% sequence identity to SEQ ID NO: 13 (TaWRKY53B), or (ii) at least 20 contiguous nucleotides of any one of SEQ ID NO: 13 (TaWRKY53B), optionally in sense and/or in antisense, preferably comprises (i) at least 85%, or 90%, more preferably at least 95%, 96%, 97%, 98% or 99% sequence identity to the nucleotide sequence of SEQ ID NO: 13 (TaWRKY53B), or (ii) at least 21, 22, 23, 24, 25, 30, 40 or 50 contiguous nucleotides, preferably at least 60, 70, 80, 90 or 100 contiguous nucleotides, more preferably at least 150, 200, 250, 300, 400, 500, 750 or 1000 contiguous nucleotides of SEQ ID NO: 13 (TaWRKY53B), optionally in sense and/or in antisense. In particularly preferred embodiments, the said nucleic acid sequence, or a complement thereof, comprises (or consists of) the sequence of SEQ ID NO: 13 (TaWRKY53B).

In various other embodiments of the present disclosure, the said nucleic acid sequence, or a complement thereof, comprising (i) at least 80% sequence identity to SEQ ID NO: 15 (TaWRKY68A), or (ii) at least 20 contiguous nucleotides of SEQ ID NO: 15 (TaWRKY68A), optionally in sense and/or in antisense, preferably comprises (i) at least 85%, or 90%, more preferably at least 95%, 96%, 97%, 98% or 99% sequence identity to the nucleotide sequence of SEQ ID NO: 15 (TaWRKY68A), or (ii) at least 21, 22, 23, 24, 25, 30, 40 or 50 contiguous nucleotides, preferably at least 60, 70, 80, 90 or 100 contiguous nucleotides, more preferably at least 150, 200, 250, 300, 400, 500, 750 or 1000 contiguous nucleotides of SEQ ID NO: 15 (TaWRKY68A), optionally in sense and/or in antisense. In particularly preferred embodiments, the said nucleic acid sequence, or a complement thereof, comprises (or consists of) the sequence of SEQ ID NO: 15 (TaWRKY68A).

In the present disclosure, the terms “cereals”, “crops” and “cereal crops” may be used interchangeably. As described herein, the term “cereals” encompasses “cereal plants” and “cereal crops”.

A “control” or “control plant” or “control plant cell” provides a reference point for measuring changes in phenotype of a subject plant or plant cell in which genetic modification or alteration, such as transformation or mutation or knock-down or knock-out, has been effected to a gene of interest. A control plant or control plant cell may comprise, *for example*: (a) a wild-type plant or cell, *i.e.*, of the same genotype as the starting material for the genetic modification or alteration which resulted in the subject plant or cell; (b) a plant or plant cell of the same genotype as the starting material but which has been transformed with a null construct (*i.e.*, with a construct which has no known effect on the trait of interest, such as a construct comprising a marker gene); or (c) a plant or plant cell which is a non-transformed segregant among progeny of a subject plant or plant cell.

By “encoding” or “encoded” with respect to a specified nucleic acid, is meant comprising the information for translation into the specified protein. A nucleic acid encoding a protein may comprise non-translated sequences (*e.g.*, introns) within translated regions of the nucleic acid, or may lack such intervening non-translated sequences (*e.g.*, as in cDNA). The information by which a protein is encoded is specified by the use of codons. Typically, the amino acid sequence is encoded by the nucleic acid using the “universal” genetic code.

The term “down-regulation” or “knock-down” refers to a partial reduction of the expression level, the term “knock-out” to a complete reduction. For example, down-regulation of a WRKY gene in a plant or cell encompasses a reduction in expression to a level that is less than 99%, 95%, 90%, 85%, 80%, 75%, 70%, or 65%, preferably less than 60%, 55%, 50%, 45%, 40%, or 35%, more preferably less than 30%, 25%, 20%, 15%, 10%, or 5% or 0 % of the expression level of the corresponding WRKY gene in a control plant or control plant cell. Vice versa such reduction in expression level constitute a “down-regulation” or “knock-down”.

The term “up-regulation” refers to an enhancement (increase) of the expression level. For example, up-regulation of a jasmonate receptor gene in a plant or cell encompasses a enhancement (increase) in expression to a level that is more than 110%, 125%, 150%, 175%, 200%, or 250%, preferably more than 300%, 350%, 400%, 450%, or 500%, more preferably more than 600%, 700%, 800%, 900%, or 1000% of the expression level of the corresponding jasmonate receptor gene in a control plant or control plant cell.

As used herein, “nucleic acid” includes reference to a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, and unless otherwise limited, encompasses known analogues having the essential nature of natural nucleotides in that they hybridize to single-stranded nucleic acids in a manner similar to naturally occurring nucleotides (*e.g.*, peptide nucleic acids).

As used herein, the term “plant” includes reference to whole plants, plant organs (*e.g.*, leaves, stems, roots, etc.), embryos, calluses, seeds and progeny of same. Plant cell, as used herein includes, without limitation, cells in or from seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, ovules and microspores. The class of plants which can be used in the methods of the disclosure is generally as broad as the class of higher plants amenable to transformation techniques, including both monocotyledonous and dicotyledonous plants including species from the genera: *Oryza*, *Avena*, *Hordeum*, *Secale*, *Panicum*, *Zea* and *Triticum*. A particularly preferred plant is *Triticum aestivum*.

The terms “polypeptide”, “peptide” and “protein” are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more

amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers.

As used herein, the term “WRKY protein” or “WRKY polypeptide” is also inclusive of fragments, variants, homologs, alleles or precursors (e.g., preproteins or proproteins) thereof. A “WRKY protein” comprises a WRKY polypeptide.

As used herein, the term “jasmonate receptor protein” or “jasmonate receptor polypeptide” is also inclusive of fragments, variants, homologs, alleles or precursors (e.g., preproteins or proproteins) thereof. A “jasmonate receptor protein” comprises a jasmonate receptor polypeptide.

The term “subsequence” refers to a sequence of a nucleic acid that comprises a part of a longer sequence of a nucleic acid. As used herein, a subsequence suitable as molecular marker, e.g. as a hybridization probe, is about 10-140 nucleotides in length, preferably about 15-100 nucleotides in length, more preferably about 20-50 nucleotides in length; a subsequence, as used in the context of an RNA interference configuration, consists of at least 19, 20, 21, 22, 23, 24, 25, 30, 40 or 50 contiguous nucleotides, preferably at least 60, 70, 80, 90 or 100 contiguous nucleotides, more preferably at least 150, 200, 250, 300, 400, 500, 750 or 1000 contiguous nucleotides of a given longer (reference) sequence of a nucleic acid.

As used herein, “sequence identity” or “identity” in the context of two nucleic acid or polypeptide sequences includes reference to the residues in the two sequences, which are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences, which differ by such conservative substitutions, are said to have “sequence similarity” or “similarity”. Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., according to the algorithm of Meyers and Miller, (1988) *Computer Applic. Biol. Sci.* 4:1 1-17, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California, USA).

As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

The term "homology" refers to analogies or similarities in the nucleotide sequence of two nucleic acid molecules or the amino acid sequence of two proteins or peptides. The presence of homology between two nucleic acids or proteins (homologs) can be detected by comparing one position in one sequence with the corresponding position in the other sequence and determining whether identical or similar residues are present here. Two compared sequences are homologous if there is a minimum level of identical or similar nucleotides. "Identical" means that when comparing two sequences at equivalent points in each case there is the same nucleotide or the same amino acid. It may be necessary to take into account gaps in sequence to produce the best possible alignment comparison of sequences. Similar nucleotides/amino acids are non-identical nucleotides/amino acids with the same or equivalent physical and chemical properties. Exchanging a nucleotide (an amino acid) with a different nucleotide (another amino acid) with the same or equivalent physical and chemical properties is called a "conservative exchange." Examples of physico-chemical properties of an amino acid include, for example, the hydrophobicity or charge. In the context of nucleic acids there is also understood a conservative or a similar nucleotide exchange when replacing a nucleotide in a coding sequence in a codon by another, but, due to the degeneration of the genetic code, the same amino acid or a similar amino acid sequence as in the comparison of the codon affected by the exchange is encoded. The skilled worker knows which nucleotide or amino acid exchange is a conservative exchange. To determine the degree of similarity or identity between two nucleic acids, a minimum length of 60 nucleotides or base pairs is assumed, preferably a minimum length of 70, 80, 90, 100, 110, 120, 140, 160, 180, 200, 250, 300, 350 or 400 nucleotides or base pairs, more preferably the full length of the compared nucleic acids, and in the case of proteins / peptides a minimum length of 20 amino acids is assumed, preferably a minimum length of 25, 30, 35, 40, 45, 50, 60, 80, 100, 150, 200, 250 or 300 amino acids, and particularly preferably the full length of the compared amino acid sequences. The degree of similarity ("positives") or identity of two sequences can be determined using, for example, the computer program BLAST (Altschul S.F. et al (1990), Basic Local Alignment Search Tool,

J. Mol Biol 215: 403-410; see e.g. <http://www.ncbi.nlm.nih.gov/BLAST/>) using standard parameters. The determination of homology depends on the length of the compared sequences. For the purposes of the present invention a homology between two nucleic acid sequences, whose shorter one's length is at least 100 nucleotides, is established if at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 98%, or at least 99% of nucleotides are identical and/or similar ("identities" or "positives" according to BLAST), and preferably are identical. In the case of a sequence length of 50-99 nucleotides a homology between sequences is understood where there is identity or similarity of at least 80%, preferably at least 85%, 86%, 87%, 88% or 89%, with a sequence length of 15-49 nucleotides with an identity or similarity of at least 90%, preferably at least 95%, 96%, 97%, 98% or 99%. In the case of proteins a homology is assumed, when using the computer program BLAST using standard parameters and the BLOSUM62 substitution matrix (Henikoff, S., and Henikoff, J., Amino acid substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA 89: 10915-10919, 1992) an identity ("identities") and/or likeness ("positive"), preferably identity, at least 25%, at least 26%, at least 27%, at least 28%, at least 29% at least 30%, preferably at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 98%, or at least 99% is obtained, preferably the entire length of the protein/peptide, which is compared with another protein, e.g. the length of 225 amino acids in the case of SEQ ID NO: 4. The person working in this art is able with his expert knowledge to use readily available BLAST programs (e.g. BLASTn, BLASTp, BLASTx, tBLASTn or tBLASTx) to determine the homology in question. In addition, there are other programs that the expert knows, and which he can use in the case in assessing the homology of two or more comparative sequences or partial sequences. Such programs include those that can be found, for example on the website of the European Bioinformatics Institute (EMBL) (see, e.g. <http://www.ebi.ac.uk/Tools/similarity.html>).

The term "hybridizing" or "hybridization" means a process in which a single-stranded nucleic acid molecule attaches itself to a complementary nucleic acid strand, *i.e.*, agrees with this base pairing. Standard procedures for hybridization are described, for example, in Sambrook et al. (Molecular Cloning. A Laboratory Manual, Cold Spring Harbor Laboratory Press, 3rd edition 2001). Preferably this will be understood that at least 50%, more preferably at least 55%, 60%, 65%, 70%, 75%, 80% or 85%, more preferably 90%, 91%, 92%, 93%, 94% received 95%, 96%, 97%, 98% or 99% of the bases of the nucleic acid strand shows a base pairing with the complementary nucleic acid strand. The possibility of such attachment depends on the stringency of the hybridization conditions. The term "stringency" refers to hybridization conditions. High stringency is when base pairing is more difficult, low stringency, when a base-

pairing is facilitated. The stringency of hybridization conditions depends for example on the salt concentration or ionic strength and temperature. Generally, the stringency can be increased by increasing the temperature and/or decreasing salinity. "Stringent hybridization conditions" are defined as conditions in which hybridization occurs predominantly only between homologous nucleic acid molecules. The term "hybridization conditions" refers not only to the actual attachment of the nucleic acids at the prevailing conditions, but also in the subsequent washing steps prevailing conditions. Stringent hybridization conditions are, for example, conditions under which predominantly only those nucleic acid molecules having at least 70%, preferably at least 75%, at least 80%, at least 85%, at least 90% or at least 95% sequence identity hybridize. Less stringent hybridization conditions include: hybridization in 4 × SSC at 37 ° C, followed by repeated washing in 1 × SSC at room temperature. Stringent hybridization conditions include: hybridization in 4 × SSC at 65°C, followed by repeated washing in 0.1 × SSC at 65°C for a total of about 1 hour.

The term "complementary" refers to the ability of purine and pyrimidine nucleotides to form base pairs with each other via bridging hydrogen bonds. Complementary base pairs are, for example, guanine and cytosine, adenine and thymine and adenine and uracil. A complementary nucleic acid strand is accordingly a nucleic acid strand that can, by pairing with complementary bases of another nucleic acid strand, form a double strand.

Plant Transformation Methods

Numerous methods for introducing foreign or heterologous DNA into plants are known and can be used in the present disclosure, including biological and physical plant transformation protocols. See, e.g., Miki, et al., "Procedure for Introducing Foreign DNA into Plants", in *Methods in Plant Molecular Biology and Biotechnology*, Glick and Thompson, eds., CRC Press, Inc., Boca Raton, pp. 67-88 (1993). The methods chosen vary with the host plant and include chemical transfection methods such as calcium phosphate, microorganism-mediated gene transfer such as *Agrobacterium* (Horsch et al., *Science* 227:1229-31 (1985)), electroporation, micro-injection and biolistic bombardment. Expression cassettes and vectors and in vitro culture methods for plant cell or tissue transformation and regeneration of plants are known and available. See, e.g., Gruber, et al., "Vectors for Plant Transformation" in *Methods in Plant Molecular Biology and Biotechnology*, supra, pp. 89-119. The isolated polynucleotides or polypeptides may be introduced into the plant by one or more techniques typically used for direct delivery into cells. Such protocols may vary depending on the type of organism, cell, plant or plant cell, e.g., monocot or dicot, targeted for gene modification. Suitable methods of transforming plant cells include microinjection (Crossway, et al., (1986)

Biotechniques 4:320-334 and US Patent Number 6,300,543), electroporation (Riggs, et al., (1986) Proc. Natl. Acad. Sci. USA 83:5602-5606, direct gene transfer (Paszkowski et al., (1984) EMBO J. 3:2717-2722) and ballistic particle acceleration (see, for example, Sanford, et al., US Patent Number 4,945,050; WO 91/10725 and McCabe, et al., (1988) Biotechnology 6:923-926). Also see, Tomes, et al., "Direct DNA Transfer into Intact Plant Cells Via Microprojectile Bombardment", pp. 197- 213 in Plant Cell, Tissue and Organ Culture, Fundamental Methods, eds. Gamborg and Phillips, Springer-Verlag Berlin Heidelberg New York, 1995.

A generally applicable method of plant transformation is microprojectile-mediated transformation, where DNA is carried on the surface of microprojectiles measuring about 1 to 4 μm . The expression vector is introduced into plant tissues with a biolistic device that accelerates the microprojectiles to speeds of 300 to 600 m/s which is sufficient to penetrate the plant cell walls and membranes (Sanford, et al., (1987) Part. Sci. Technol. 5:27; Sanford, (1988) Trends Biotech 6:299; Sanford, (1990) Physiol. Plant 79:206 and Klein, et al., (1992) Biotechnology 10:268).

Inhibiting/reducing the Activity and/or Level of a WRKY Polypeptide

Means and methods are provided to reduce or eliminate the level or activity of a WRKY polypeptide by transforming a plant cell with an expression cassette that expresses a polynucleotide that reduces the expression of the WRKY polypeptide. The polynucleotide may reduce the expression of the WRKY polypeptide directly, by preventing transcription or translation of the WRKY messenger RNA, or indirectly, by encoding a polypeptide that reduces the transcription or translation of a WRKY gene encoding a WRKY polypeptide. Methods for reducing or eliminating the expression of a gene in a plant are well known in the art and any such method may be used in the present disclosure to reduce the expression of a WRKY polypeptide. The expression of a WRKY polypeptide is reduced or inhibited if the level of the WRKY polypeptide is less than 100%, 99%, 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5% or 1 % of the level of the same WRKY polypeptide in a control plant cell or plant. In particular embodiments, the level of the WRKY polypeptide in a modified plant is less than 60%, less than 50%, less than 40%, less than 30%, less than 20%, less than 10%, less than 5% or less than 2% of the level of the same or a related WRKY polypeptide in a control plant cell or plant. The WRKY polynucleotide expression level and/or polypeptide level and/or activity may be reduced such that the reduction is phenotypically sufficient to provide resistance against a pathogen, in particular resistance against a fungal pathogen. The level or activity of one or more WRKY polynucleotides,

polypeptides or enzymes may be impacted. The expression level of the WRKY polypeptide may be measured directly, for example, by assaying for the quantity of WRKY polypeptide expressed in the plant cell or plant, or indirectly, for example, by measuring the WRKY activity in the plant cell or plant, *i.e.*, the efficacy or ability to recognize or bind the (genomic) DNA at the corresponding *cis*-regulatory elements like the W box ((T)TGAC(C/T)) or variants thereof, or by measuring the phenotypic changes in the plant.

In certain embodiments of the disclosure, the activity of a WRKY polypeptide may be reduced or eliminated by disrupting or excising at least a part of the gene encoding the WRKY polypeptide. Mutagenized plants that carry mutations in WRKY genes also result in reduced expression of the WRKY gene and/or reduced activity of the encoded WRKY polypeptide. Thus, many methods may be used to reduce or eliminate the activity of a WRKY polypeptide. One or more methods may be used to reduce the activity of a single WRKY polypeptide. One or more methods may be used to reduce the activity of multiple WRKY polypeptides.

As described herein, the term “vector” may encompass both single-stranded and double-stranded vectors, including, but not limited to, single-stranded and double-stranded DNA vectors.

In various embodiments, a vector used for WRKY gene silencing according to the present disclosure is plasmid DNA. Plasmid DNA containing one or more target polynucleotides as described herein is readily constructed using standard techniques well known in the art. The vector may be typically constructed in a plasmid form that can then be used for transfection or transformation. The plasmid generally comprises sequences useful for replication of the plasmid in plant cells. Such plasmids are well known in the art. In addition, vectors may also include a gene whose expression confers a detectable or selectable marker such as a drug resistance. As described herein, the vector may comprise at least one regulatory expression sequence (expression control sequence).

In various embodiments, the promoter may be a tissue specific promoter. In some embodiments, the promoter is a target cell-specific promoter.

When targeting delivery of a vector to a particular target cell or target tissue, the vector genome will usually contain a promoter that is recognized by the target cell or target tissue and that is operatively linked to the sequence(s) of interest.

Promoters may be inducible, constitutive, temporally active or tissue specific. Inducible promoters are useful tools in genetic engineering because the expression of genes to which they are operatively linked can be turned on or off, *e.g.*, in a particular tissue. Inducible promoters can be grouped as chemically-regulated promoters, and physically-regulated

promoters. Typical chemically-regulated promoters and typical physically-regulated promoters are well known to the person skilled in the art.

The terms nucleic acid sequence(s) and polynucleotide(s) may be used interchangeably herein. As described herein, the term “nucleic acid sequence” may encompass both single-stranded and double-stranded nucleic acid sequences. In various embodiments, a nucleic acid sequence is DNA sequence.

It is to be acknowledged that the present invention is not limited to the particular methodology, protocols, cell lines, genera, and reagents described herein, as such may vary. It is also to be acknowledged that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting the scope of the present invention.

The following examples are offered by way of illustration and not by way of limitation.

Other embodiments and uses will be apparent to one skilled in the art in light of the present disclosures. The following examples are provided merely as illustrative of various embodiments and shall not be construed to limit the invention in any way.

EXAMPLES

Example 1: Glasshouse experiments linking WRKYs to nitrogen regimen

Wheat varieties, germination procedure and growth conditions

Sixty wheat (*Triticum aestivum*) seeds from each of two varieties (*Cordiale* and *Gallant*) were germinated in plastic trays. Four germinated seeds were planted 1 cm below the surface in each of 15 cm plastic plant pots filled with SilverSand. A fine mesh was placed in the base of the pots to contain the sand. The pots were split into 5 groups at random, and each group assigned a different nitrogen level – 100%, 90%, 70%, 50% or 30%. This gave 3 biological replicates for each nutrient level. Plants were stood in Hoagland's solution containing differing levels of nutrient according to Table 1.

Table 1: Volume (in cm³) of each stock solution added per litre of final Hoaglands solution.

Nutrient stock solution	100% N	90% N	70% N	50% N	30% N
Ca(NO ₃) ₂ ·4H ₂ O	2.5	2.25	1.75	1.25	0.75

CaCl₂	0	0.25	0.75	1.25	1.75
KNO₃	2.5	2.25	1.75	1.25	0.75
K₂SO₄	0	0.25	0.75	1.25	1.75
KH₂PO₄	1	1	1	1	1
MgSO₄·7H₂O	1	1	1	1	1
“Micronutrients”	0.5 each	0.5 each	0.5 each	0.5 each	0.5 each

Plants were grown in a controlled environment chamber under standard conditions.

Tissue collection, RNA extraction and cDNA synthesis

After 5 weeks, when plants were between the 4th to 6th leaf stages, all leaves were removed from all plants and snap frozen in liquid nitrogen. All the 4 plants in a single pot were pooled to form a single biological replicate. Leaf samples were freeze-dried for 48 hours, before being placed in 2ml Eppendorf tubes and homogenized using a TissueLyser (QIAGEN). PureLink RNA Mini Kit (Life Technology) was used for RNA extraction followed by on-column DNase treatment.

RNA was quantified using a spectrophotometer before diluting to achieve 2 µg RNA in 16 µL. cDNA synthesis was done using the iScript Reverse Transcriptase kit (Life Technologies) following the manufactures protocol.

Primer design and qRT-PCR

Primers for WRKY10, WRKY13, WRKY19, WRKY29, WRKY39, WRKY53B and WRKY68B were designed using Primer3Plus software (<http://primer3plus.com/>).

qPCR was performed using SYBR green-based dsDNA dye in the RotorGene platform (QIAGEN). The RotorDisc was heat sealed with a permanent seal, and run using the following conditions: 95°C for 300 seconds, followed by 40 cycles of 95°C for 5 second and 70°C for 10 seconds. For melt curve analysis, the temperature was increased by 10°C for between 60°C and 95°C with 5 readings per temperature.

Data analysis and statistics

Relative expression was calculated using the $\Delta\Delta CT$ method as described in Livak and Schmittgen (2001, Analysis of relative gene expression data using real-time quantitative PCR and the $2^{-\Delta\Delta CT}$ method. *methods* 25.4 (2001): 402-408) using the reference gene ubiquitin. ANOVA was used to determine if the difference in ΔCT was significant between the control and treatment. A Tukey post-hoc test was applied to determine which treatments differed significantly from the control.

Example 2: Glasshouse experiments linking the WRKYs Septoria infection

Wheat varieties, germination procedure and growth conditions

Sixty wheat (*Triticum aestivum*) seeds from each of two varieties (*Cordiale* and *Gallant*) were germinated in plastic trays. Six seeds were planted in 15cm plastic plant pots filled with John Innes No2 compost. They were grown for 3 weeks in a temperature controlled growth room under standard conditions.

Septoria infection

After 3 weeks, three of the pots from each variety were removed from the growth room for inoculation. A solution of *Zymoseptoria tritici* spores containing between 500 000 and 1 million spores per ml was made. This solution was applied to the underside of one leaf from each plant, with all other leaves removed. These pots were covered with a plastic lid to maintain humidity, and placed in a growth cabinet at 25°C. Both infected and healthy plants were watered as required, and grown for a further three weeks to allow for infection to develop.

Tissue collection, RNA extraction and cDNA synthesis

Tissue was collected from infected and controls plants by taking just the one leaf per plant, with a pool of the 5 plants from each pot making a single biological replicate. Leaves were snap frozen in liquid nitrogen. RNA extraction, cDNA synthesis, qRT-PCR and statistical analysis is as previously described.

Example 3: Field experiments linking WRKYs to *Septoria* disease and sensitivity to nitrogen

Wheat varieties, trial establishment and agronomic conditions

An experimental trial was sown at a field site near Rosemaund, Herefordshire, UK (SO 55793 48437) in September using standard agronomic practices. A total of 128 treatment plots were arranged in a complete randomised block design consisting of 8 winter wheat varieties, 2 nitrogen rates and 2 fungicide levels and 4 replicates.

Treatment conditions

Fungicide treatments consisted of treatments to selectively control for all expected diseases except *Septoria*, whereas the control treatment contained active ingredients which are effective against the disease and following normal agricultural practice.

Nitrogen treatment consisted of a reduced artificial N application relative to the control which contained ~200kg/ha of N.

Data collection and analysis

Flag leaf tissue is collected at GS39 in duplicate from 15 plants per plot and pooled to form 2 technical replicates. Leaves were snap frozen in liquid nitrogen. RNA extraction, cDNA synthesis, qRT-PCR and statistical analysis are as previously described.

Septoria disease is scored in the plots in the last 2 weeks of June according to normal practice. The plots are harvested at maturity to measure yield.

Example 4: Construction of *Agrobacterium* mediated BSMV vectors for VIGS

Barley stripe mosaic virus (BSMV) vectors suitable for cereal virus-induced gene silencing (VIGS) have been described previously (see, e.g., Yuan et. al., 2011, PLoS ONE, Vol. 6(10), e26468, and references cited therein). The tripartite genome consists of RNAs α , β , and γ , which each of the genomic (g) RNAs has a methylated 5' cap and a 3' polyadenylate sequence followed by a tyrosine accepting tRNA-like structure. RNA α of the BSMV ND18 strain encodes the methyltransferase/helicase subunit of the RNA-dependent RNA polymerase (RdRp). RNA β specifies the coat protein (CP) and three major triple gene block (TGB) proteins (TGB1, TGB2 and TGB3) that are essential for cell-to-cell movement of the virus. RNA γ encodes the polymerase (GDD) subunit of the RdRp and the γ B protein, which has significant roles in viral pathogenesis, long distance movement and suppression of host RNA silencing defences.

Each vector contains cDNA of one of the tripartite genomic RNAs (α , β and γ) between the double Cauliflower mosaic virus 35S promoter (2X35S) and a ribozyme sequence (Rz) from *Tobacco ringspot virus* (TRSV) satellite RNA (see scheme above or Figure 25, respectively). A ligation

independent cloning (LIC) site was also included after the γ cDNA for cloning in of the target PCR products.

Cloning of target PCR products

For cloning the target sequence, BSMV γ was first digested with *Apal* (Promega, Madison, USA) by incubating a 20 μ l mixture at a final concentration of 1x Buffer A (Promega), 0.1x acetylated BSA (Promega), 50 μ g/ml BSMV γ , 2.5% *Apal* in sterile distilled water at 37°C for 4 hours and then 65°C for 15 minutes.

4 μ l of this mixture was then added to 16 μ l of a reaction mixture to create a 20 μ l mixture (Mix A) at a final concentration of 5 mM dTTP, 0.1x BSA, 1x T4 buffer (NEB), 2% T4 DNA Polymerase (NEB) in sterile distilled water.

Simultaneously, a 10 μ l reaction (Mix B) was made to a final concentration of 5% Target PCR product, 5 mM dATP, 0.1x BSA, 1x T4 buffer (NEB), 2% T4 DNA Polymerase (NEB) in sterile distilled water.

Both mix A and mix B were incubated at room temperature for 30 minutes and then 75°C for 15 minutes. 2 μ l of mix A was then added to mix B and incubated at 65°C for 2 minutes then room temperature for 10 minutes, before transforming into competent DH5 α *E. coli* cells.

Example 5: Virus induced gene silencing (VIGS)

The technique is well known as a tool for delivery of dsRNA into plants (Padmanabhan, Meenu, and Savithramma P. Dinesh-Kumar. "Virus-induced gene silencing as a tool for delivery of dsRNA into plants." Cold Spring Harbor Protocols 2009.2 (2009): pdb-prot5139). As positive control for VIGS experiments the PDS (phytoene desaturase gene) gene has been used. The gene silencing constructs have been introduced into the plants by means of BMSV (Barley stripe mosaic virus) as VIGS vector. Figure 17 shows exemplary the positive control in two different wheat cultivars 'Avalon' (Av) and 'Cordiale' (Crd). Efficient gene silencing is shown by loss of greenness in leaf tissues.

A structural description of the VIGS vectors is given in the publication Yuan et al. 2011, PLoS ONE, Vol. 6(10), e26468.

Example 6: Loss-of-function studies in *Triticum aestivum*

Loss-of-function studies in *T. aestivum* were carried out through the virus-induced gene silencing (VIGS) system (Baulcombe, David C. "Fast forward genetics based on virus-induced

gene silencing." *Current opinion in plant biology* 2.2 (1999): 109-113.) based on the Barley Stripe Mosaic Virus (BSMV) as previously described (Yuan et al., 2011, PLoS ONE, Vol. 6(10), e26468). The specificity and silencing efficiency of the constructs was predicted using siRNA finder si-fi (labtools.ipk-gatersleben.de/index.html). Briefly, the LIC strategy was used to clone a series of WRKY fragments. The selected sequences were amplified with primer pairs, in which the forward primers consisted of 5'-AAGGAAGTTTAA-3' fusions to a 5' plant sequence, and the reverse primers contained 5'-AACCACCACCACCGT-3' fusions to each 3' gene sequence. PCR products were purified, treated at room temperature with T4 DNA polymerase (New England Biolabs, MA, USA) in 1X reaction buffer containing 5 mM dATP for 30 min to generate sticky ends, and heat-treated at 75°C for 10 min to inactivate the polymerase. The Apal-linearized pCa-ybLIC vector was also treated with T4 DNA polymerase in the presence of 5 mM dTTP to generate sticky ends complementary to those of the PCR products. The PCR products (~200 ng) and pCa-ybLIC vector (20 ng) were mixed, incubated at 66°C for 2 min and slowly cooled to room temperature to anneal their complementary termini. Then, 10 µl aliquots were used for cloning into *Escherichia coli* DH10B, and transformants identified by colony PCR and endonuclease digestions.

Agroinfiltration of N. benthamiana and viral inoculation of cereals

The BSMV pCa-ybLIC WRKY derivatives were transformed into *A. tumefaciens* strain GV3101. For agroinfiltration, single colonies were grown overnight at 28°C with constant shaking in 3 ml of LB containing rifampicin (25 µg/ml) and kanamycin (100 µg/ml). Then, 0.5 ml of the cultures were used to inoculate 50 ml LB containing the same antibiotics and grown at 28°C for 10 to 12 h. Bacterial cells were pelleted at 2200 g for 10 min, resuspended in infiltration buffer [10 mM MgCl₂, 10 mM 2-(N-morpholino) ethanesulfonic acid (MES), pH 5.2, and 0.1 mM acetosyringone] to 0.7 OD₆₀₀ and incubated at room temperature for at least 3 h. For agroinfiltration, equal amounts of bacteria harboring pCaBS-α, pCaBS-β and pCa-ybLIC (or its derivatives) were mixed, and infiltrated into four to eight *N. benthamiana* leaves immediately above the cotyledons with a 1-ml needleless syringe. After maintenance in a growth chamber for 5 days post infiltration (dpi), the infiltrated leaves were harvested, ground in 20 mM Na-phosphate buffer (pH7.2) containing 1% celite, and the sap was mechanically inoculated onto the two-leaf stages of wheat.

Septoria infection assays

The plants to be infected were trimmed so that only the leaf to be infected was left. The remaining leaves were then stuck down flat onto black card, leaving ~5cm of leaf to be infected.

The Septoria strain IPO323, K5090 (GFP strain) and K5097 (GFP strain) were spread onto YPD plates containing no antibiotics (IPO323) or YPD + hygromycin (K5090 and K5097, 25µg/ml) and left for 4 days to grow at 18°C. A few streaks of the Septoria were taken from the plate and dissolved into 10ml of distilled water. To measure the concentration of the Septoria spores 10µl of Septoria mixture was pipetted onto a haemocytometer slide. Using an Axkiospop microscope at x20 magnification the spores were counted. The concentration was then adjusted to, on average, 4 spores 0.05*0.05mm square (1,000,000 spores per ml). 0.1% Tween 20 was added to the Septoria mixture.

Using a cotton bud the Septoria was infected onto the leaves by rubbing the mixture onto the leaves. A new cotton bud was used for each new silenced line of wheat. The tray under the plants was filled with water and the plants were covered with a lid to generate a high humidity for the Septoria to infect. The lids were removed after 4 days. The plants infected with IPO323 were left for 28 days with pictures taken daily and samples taken weekly to check for silencing. The final infected leaves were collected for the spore count, pycnidia count and for extraction of RNA to measure the amount of a fungal gene present. The plants infected with the GFP Septoria strains (K5090 and K5097) were grown and small sections of 0.5cm² were cut and mounted on a slide to be visualized on a SP5 confocal microscope.

Spore and pycnidia count assays

The leaves were collected and suspended in a sealed box containing damp tissue to increase the humidity and cause the fungus to produce spores. This was left at 18°C for 4 days. The pycnidia were counted over a length of 2 cm of each leaf and averaged for 5 leaves. 5 leaves were then submerged in 10 ml of distilled water, vortexed for 2 minutes and left to stand for 3 hours. The leaves were vortexed again for 2 minutes and 10µl of the water loaded onto a haemocytometer slide. The spores were counted for 4 of the 0.2*0.2mm squares on the Akioskop light microscope at x20 magnification and an average taken from these 4 numbers for the spore count.

A list of exemplary WRKY VIGS fragments used for the corresponding gene silencing is given in Figure 16.

Example 7: Exemplary results on WRKY10

By knocking down TaWRKY10 in the cv. Avalon, spore and pycnidia counts were significantly reduced (Figure 18). This indicates that the infestation of the wheat plants with Septoria is efficiently inhibited and the plant defense is improved. Consequently the resistance/tolerance

of wheat against Septoria is enhanced. In addition, in TaWRKY10 silenced Avalon plants the visible symptoms of Septoria infection were delayed by around 4 days (Figure 19).

The reduced spore and pycnidia counts could be shown also in other cultivars like Cordiale (Figure 20), *KWS Santiago* (Figure 21) and *KWS Lili* (Figure 22).

The enhanced resistance has also been demonstrated in the following experiment. Naturally the cv. *KWS Santiago* is more susceptible to Septoria compared to cv. *KWS Lili*. That can be shown by spore counts (Figure 23) as well as in field trials. The resistant cv. *KWS Lili* has been transformed with an empty VIGS vector (EV) and the susceptible cv. *KWS Santiago* with BSMV:WRKY10. The result is that both the non-silenced cv. *KWS Lili* and the silenced cv. *KWS Santiago* show a comparable Septoria sporulation (Figure 23).

Comparable results as seen for WRKY10 have been achieved for WRKY13, WRKY19, WRKY29, WRKY39, WRKY53B and WRKY68A. For all of these WRKYs, it is suggested that their expression or activity is fertilizer-responsive and/or are characterized by the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid.

The present example is based on the VIGS-induced silencing of the WRKY genes. However, it is possible to achieve the same or comparable results through other methods: For example, one can build up TILLING populations of a plant and screen for mutations leading to amino acid exchanges or splicing errors. Such mutation can result in a knock-down or knock-out of the WRKY gene (e.g., if the mutation creates an early stop codon), in an altered (reduced) activity of the WRKY protein, or in a shift of the reading frame if splicing errors occur. Besides of TILLING, such mutations can be introduced/targeted by the known genome editing tools like Zinc Finger Nucleases, TAL Effector Nucleases, CRISPR/Cas etc. Another example is the introduction of a DNA construct encoding a double stranded RNA construct suitable for silencing the above WRKY genes (RNAi approach, Example 8).

Example 8: hpRNA-mediated gene-silencing of WRKYs

Effectiveness of RNAi in wheat for obtaining lines with silenced WRKY genes

RNAi is a very effective approach for obtaining WRKY silenced wheat lines.

Plasmid design and construction

For the synthesis of the RNAi vectors, conserved regions of the WRKYs are PCR-amplified from genomic DNA isolated from wheat (*Triticum aestivum*) and cloned in sense and antisense

orientation, separated by the *Ubi1* intron to form the inverted repeat (IR) sequences. The vectors are synthesized using the GATEWAY (Invitrogen) recombination technology. Different pairs of primers are used for the amplification of the IR fragments of the vectors. The expression of the IRs is driven by a constitutive promoter, with the nopaline synthase (*nos*) as terminator sequence.

Plant material and genetic transformation

Plasmids carrying the RNAi fragments are used in combination with plasmid pAHC25 containing the selectable *bar* gene (Christensen and Quail, 1996, Transgenic Res., 5, 213-218). For bombardment, plasmids are precipitated onto 0.6- μ m gold particles at 0.75 pmol/mg gold for the plasmids containing the RNAi fragments. Putative transgenic plants are transferred to soil and grown to maturity in the greenhouse. Homozygous progeny of plants containing the RNAi plasmids are identified by PCR. Then, PCR-positive transgenic plants are further analysed for pathogen resistance as described elsewhere herein.

All references and publications cited or referred to herein are incorporated by reference into the present disclosure in their entirety.

Example 9: Studies on sensitivity on jasmonic acid (JA)

Since JA is a key hormone involved in necrotrophic pathogen response, we performed JA treatment on cv. *KWS Lili* and cv. *KWS Santiago* in order to investigate their different sensitivity to JA. Root growth is an excellent model for hormone response studies, it is well established that exogenous application of JA reduces root length in many species (Staswick P, Su W, Howell S: Methyl jasmonate inhibition of root growth and induction of a leaf protein are decreased in an *Arabidopsis thaliana* mutant. PNAS 1992, 89: 6837-6840). Exploiting root growth as a model we discovered that cv. *KWS Santiago* is partially insensitive to JA treatment.

Seeds from both cvs. *KWS Lili* and *KWS Santiago* were germinated on MS medium for 3 days and then moved to MS or MS supplemented with 10 μ M of JA (Figure 27 A-C). The root lengths were recorded for the next three consecutive days (Figure 27 D). After day 1 cv. *KWS Lili* is already experiencing growth restraint caused by JA, conversely cv. *KWS Santiago* is not sensing JA effect until the succeeding day. This experiment demonstrate a partial insensitivity to JA by cv. *Santiago*.

Example 10: Gene expression of *TaCOI1* and *TaWRKY10*

Gene expression analysis has been carried out on shoot and root tissue of 4 days old seedlings, as they are both actively growing at this stage of plant development. Real-time PCR showed support for a strong downregulation of *TaCoi1* expression in cv. *Santiago* relative to cv. *Lili* in both root and shoot tissue (Figure 28). This downregulation of the JA receptor transcript explains the partial insensitivity of cv. *Santiago* to JA.

The variety *Santiago* shows a 4-fold higher level of *TaWRKY10* transcription compared to cv. *Lili* under normal conditions, with a significant decrease in transcript abundance following VIGs (Figure 29). It has been already shown that there was a gain in resistance against *Septoria* infection after silencing *TaWRKY10*.

In the same *TaWRKY10* knockdown VIGs seedlings, the expression of *TaCoi1* was also studied. *TaCoi1* showed an inverse relationship between *TaWRKY10* expression in cv. *KWS Santiago* (Figure 30). When *TaWRKY10* is knocked-down, *TaCOI1* transcript abundance was increased by 3 to 4-fold. Interestingly, this effect was seen more strongly in cv. *KWS Lili* relative to cv. *KWS Santiago*.

Santiago has a higher *WRKY10* expression, which causes a decrease in *COI1* expression, this in-turn means *Santiago* is less sensitive to JA and therefore less resistant to *Septoria* infection. Conversely, cv. *KWS Lili* has much lower *WRKY10* levels and as a consequence, *COI1* is more abundant. Since *COI1* is more abundant, this variety is more sensitive to JA and is better/faster to respond to *Septoria* infection.

In summary, *TaWRKY10* can be used as a regulator of JA signaling perception, through inhibition of *TaCOI1* receptor expression. Taken together those findings, the different levels of *TaCoi1* transcript explain the different sensitivity to *Septoria tritici* among those cultivars, and *TaCoi1* transcription is suppressed by *TaWRKY10*. Those evidence indicate that modulating either *TaWRKY10* or *TaCOI1*, or both, are useful tools in crop improvement with regard to pathogen resistance, in particular against *Septoria*.

CLAIMS

1. A cereal plant cell having introduced into its genome at least one modification inhibiting the expression or activity of at least one WRKY protein as compared to a corresponding control plant cell lacking the at least one modification, wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid, and/or at least one modification enhancing the expression or activity of a jasmonate receptor protein as compared to a corresponding control plant cell lacking the at least one modification, wherein the jasmonate receptor protein
 - a) having the amino acid sequence of SEQ ID NO: 76,
 - b) having an amino acid sequence showing an identity of at least 80% to the amino acid sequence of SEQ ID NO: 76,
 - c) is encoded by the nucleic acid sequence of SEQ ID NO: 75,
 - d) is encoded by a nucleic acid sequence showing an identity of at least 80% to the nucleic acid sequence of SEQ ID NO: 75, or
 - e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c),preferably wherein the at least one modification(s) are introduced into the at least one endogenous WRKY gene encoding the at least one WRKY protein and/or into an endogenous jasmonate receptor gene encoding the jasmonate receptor protein.
2. The cereal plant cell of claim 1, wherein the amino acid sequence motif is D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E-X-X-X3-X-X2 shown in SEQ ID NO: 2, wherein X is any amino acid, X1 is a hydrophobic amino acid, X2 is a polar, non-hydrophobic amino acid, and X3 is a polar, non-aromatic amino acid.
3. The cereal plant cell of claim 1 or 2, wherein the inhibition of the expression or activity of the at least one WRKY protein leads to an enhanced expression or activity of the jasmonate receptor protein as defined in claim 1.
4. The cereal plant cell of any one of claims 1-3, wherein the cereal plant cell is the cell of a wheat plant (*Triticum aestivum*), the cell of a rye plant (*Secale cereale*), the cell of a barley plant (*Hordeum vulgare*), or the cell of a maize plant (*Zea mays*).

5. The cereal plant cell of any one of claims 1-4, wherein
 - (i) the at least one WRKY gene comprises a nucleic acid sequence selected from the group consisting of TaWRKY10 (SEQ ID NO: 3), TaWRKY13 (SEQ ID NO: 5), TaWRKY19 (SEQ ID NO: 7), TaWRKY29 (SEQ ID NO: 9), TaWRKY39 (SEQ ID NO: 11), TaWRKY53B (SEQ ID NO: 13), and TaWRKY68A (SEQ ID NO: 15), or homologs thereof; or
 - (ii) the at least one WRKY protein comprises an amino acid sequence selected from the group consisting of TaWRKY10 (SEQ ID NO: 4), TaWRKY13 (SEQ ID NO: 6), TaWRKY19 (SEQ ID NO: 8), TaWRKY29 (SEQ ID NO: 10), TaWRKY39 (SEQ ID NO: 12), TaWRKY53B (SEQ ID NO: 14), and TaWRKY68A (SEQ ID NO: 16), or homologs thereof, or
 - (iii) the jasmonate receptor gene comprises (a) the nucleotide sequence of TaCOI1 (SEQ ID NO: 75), (b) a nucleic acid sequence showing an identity of at least 80% to the nucleic acid sequence of SEQ ID NO: 75, or (c) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (a).
6. The cereal plant cell of any one of claims 1-5, wherein the at least one modification inhibiting the expression or activity of at least one WRKY protein is caused by RNA interference, sense suppression, allele swap, insertional mutagenesis, mutagenesis or genome editing of the endogenous WRKY gene, and/or the at least one modification enhancing the expression or activity of the jasmonate receptor protein is caused by transgenic overexpression, allele swap, mutagenesis or genome editing of the endogenous jasmonate receptor gene.
7. A cereal plant, or part thereof, comprising the cereal plant cell of any one of claims 1-6, and having an increased pathogen resistance.
8. A cereal plant having an increased pathogen resistance resulting from at least one modification introduced into the genome of the cereal plant inhibiting the expression or activity of at least one WRKY protein as compared to a corresponding control plant lacking the at least one modification, wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X₁-X₂-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X₁ is a hydrophobic amino acid and X₂ is a polar, non-hydrophobic amino acid, and/or from at least one modification introduced into the genome of the cereal plant enhancing the

expression or activity of a jasmonate receptor protein as compared to a corresponding control plant cell lacking the at least one modification wherein the jasmonate receptor protein

- a) having the amino acid sequence of SEQ ID NO: 76,
- b) having an amino acid sequence showing an identity of at least 80% to the amino acid sequence of SEQ ID NO: 76,
- c) is encoded by the nucleic acid sequence of SEQ ID NO: 75,
- d) is encoded by a nucleic acid sequence showing an identity of at least 80% to the nucleic acid sequence of SEQ ID NO: 75, or
- e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c),

preferably wherein the at least one modification(s) are introduced into the at least one endogenous WRKY gene encoding the at least one WRKY protein, and/or into an endogenous jasmonate receptor gene encoding the jasmonate receptor protein.

9. The cereal plant of claim 8, wherein the increased pathogen resistance results from:
- (a) a modification in at least one endogenous WRKY gene comprising a nucleic acid sequence, or a complement thereof, comprising at least 80% sequence identity to the nucleotide sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), wherein the modification comprises one or more transposons, one or more insertions, one or more additions, one or more deletions, or one or more point mutations in the at least one endogenous WRKY gene;
 - (b) at least one introduced transgene comprising a nucleic acid sequence, or a complement thereof, comprising (i) at least 80% sequence identity to the nucleotide sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), or (ii) at least 20 contiguous nucleotides of the nucleotide sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A), and a homolog thereof, wherein the transgene is operatively linked to a promoter in a sense or antisense orientation; or
 - (c) at least one introduced polynucleotide sequence comprising one or more subsequences of a nucleic acid sequence, or a complement thereof, comprising at least

- 80% sequence identity to the nucleotide sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), wherein the at least one polynucleotide sequence is in RNA interference configuration, preferably wherein the at least one polynucleotide sequence is configured for endogenous gene silencing or virus-induced gene silencing, and/or
- (d) a modification in the endogenous jasmonate receptor gene comprising (i) the nucleotide sequence of TaCOI1 (SEQ ID NO: 75), (ii) a nucleic acid sequence showing an identity of at least 80% to the nucleic acid sequence of SEQ ID NO: 75, (iii) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (i), (iv) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (v) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80% to the amino acid sequence of SEQ ID NO: 76, wherein the modification comprises one or more transposons, one or more insertions, one or more additions, one or more deletions, or one or more point mutations in the endogenous jasmonate receptor gene; or
- (e) an introduced transgene comprising a nucleic acid sequence, or a complement thereof, comprising (i) the nucleic acid sequence of SEQ ID NO: 75, (ii) a nucleic acid sequence showing an identity of at least 80% to the nucleic acid sequence of SEQ ID NO: 75, or (iii) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (i), (iv) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or (v) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80% to the amino acid sequence of SEQ ID NO: 76, wherein the transgene is operatively linked to a promoter.
10. The cereal plant of claim 8 or 9, wherein the inhibition of the expression or activity of the at least one WRKY protein leads to an enhanced expression or activity of the jasmonate receptor protein as defined in claim 8.
11. A method for conferring pathogen resistance to, or increasing pathogen resistance of, a cereal plant cell, or a cereal plant or part thereof, the method comprising
- (I) the step of inhibiting the expression or activity of at least one WRKY protein of a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or plant or part thereof, lacking the inhibition, wherein the at least one WRKY protein is characterized by (i) a fertilizer-responsive expression or activity, and/or (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1,

wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid, preferably wherein the amino acid sequence motif is D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E-X-X-X3-X-X2 shown in SEQ ID NO: 2, wherein X is any amino acid, X1 is a hydrophobic amino acid, X2 is a polar, non-hydrophobic amino acid, and X3 is a polar, non-aromatic amino acid; and/or

(II) the step of enhancing the expression or activity of a jasmonate receptor protein of a cereal plant cell, or a cereal plant or part thereof, as compared to a corresponding control plant cell, or plant or part thereof, lacking the enhancement, wherein the jasmonate receptor protein

- a) having the amino acid sequence of SEQ ID NO: 76,
- b) having an amino acid sequence showing an identity of at least 80% to the amino acid sequence of SEQ ID NO: 76,
- c) is encoded by the nucleic acid sequence of SEQ ID NO: 75,
- d) is encoded by a nucleic acid sequence showing an identity of at least 80% to the nucleic acid sequence of SEQ ID NO: 75, or
- e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c).

12. The method of claim 11, wherein the step of inhibiting the expression or activity of at least one WRKY protein comprises introducing into the genome of the cereal plant cell, or a cereal plant or part thereof, at least one modification inhibiting the expression or activity of the at least one WRKY protein as compared to a corresponding control plant cell, or a control plant or part thereof, lacking the at least one modification, preferably wherein the at least one modification is introduced into the at least one endogenous WRKY gene encoding the at least one WRKY protein, wherein the at least one WRKY protein is selected from the group consisting of TaWRKY10 (SEQ ID NO: 4), TaWRKY13 (SEQ ID NO: 6), TaWRKY19 (SEQ ID NO: 8), TaWRKY29 (SEQ ID NO: 10), TaWRKY39 (SEQ ID NO: 12), TaWRKY53B (SEQ ID NO: 14), and TaWRKY68A (SEQ ID NO: 16), or homologs thereof, and/or

wherein the step of enhancing the expression or activity of a jasmonate receptor protein comprises introducing into the genome of the cereal plant cell, or a cereal plant or part thereof, at least one modification enhancing the expression or activity of the jasmonate receptor protein as compared to a corresponding control plant cell, or plant or part thereof, lacking the at least one modification, preferably wherein the at least one modification is introduced into an endogenous jasmonate receptor gene encoding the jasmonate receptor protein.

13. The method of claim 11 or 12, wherein the inhibition of the expression or activity of the at least one WRKY protein leads to an enhanced expression or activity of the jasmonate receptor protein.
14. A recombinant DNA construct comprising a polynucleotide sequence, or a fragment thereof, operatively linked to a heterologous promoter, wherein the polynucleotide sequence, or a fragment thereof, produces upon expression in a cereal plant cell, or cereal a plant or part thereof:
 - (a) a protein that interferes with the expression or activity of at least one endogenous WRKY protein;
 - (b) an RNA molecule that suppresses the expression of at least one endogenous WRKY protein; or
 - (c) a loss-of-function mutation in at least one endogenous WRKY gene or the protein encoded thereby,wherein the polynucleotide sequence comprises a nucleic acid sequence, or a complement thereof, comprising (i) at least 80% sequence identity to the nucleotide sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A); or (ii) at least 20 contiguous nucleotides of the nucleotide sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A).
15. A recombinant DNA construct comprising a polynucleotide sequence, or a fragment thereof, operatively linked to a heterologous promoter, wherein the polynucleotide sequence comprises
 - (a) the nucleic acid sequence of SEQ ID NO: 75,
 - (b) a nucleic acid sequence showing an identity of at least 80% to the nucleic acid sequence of SEQ ID NO: 75,
 - (c) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (a),
 - (d) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 76, or
 - (e) a nucleic acid sequence encoding an amino acid sequence exhibiting an identity of at least 80% to the amino acid sequence of SEQ ID NO: 76.

16. A double-stranded RNA (dsRNA) molecule comprising:
- (a) a first strand comprising a nucleotide sequence having a length of at least 19 nucleotides and having at least 90% sequence identity to consecutive nucleotides of a target nucleotide sequence; and
 - (b) a second strand comprising in the 5' to 3' direction a nucleotide sequence which is at least 90% complementary to the first strand and/or is able to hybridize with the first strand,
- wherein the target nucleotide sequence is a coding region of an mRNA deduced from a nucleic acid sequence, or a complement thereof, comprising at least 80% sequence identity to the nucleotide sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), and SEQ ID NO: 15 (TaWRKY68A), or homologs thereof.
17. A cereal plant cell, or a cereal plant or part thereof, comprising
- (i) the recombinant DNA construct of claim 14, and/or
 - (ii) the recombinant DNA construct of claim 15 and/or
 - (ii) the dsRNA molecule of claim 16,
- and having an increased pathogen resistance as compared to a corresponding control plant cell, or plant or part thereof, that does not comprise the said recombinant DNA construct and/or the said dsRNA molecule.
18. A method of identifying a cereal plant cell, or a cereal plant or part thereof, having an increased pathogen resistance as compared to a corresponding control plant cell, or plant or part thereof, the method comprising the step of identifying a cereal plant cell, or a cereal plant or part thereof, in which the expression or activity of at least one WRKY protein, is inhibited as compared to a corresponding control plant cell, or plant or part thereof, lacking the inhibition, wherein the at least one WRKY protein is characterized by
- (i) a fertilizer-responsive expression or activity, and/or
 - (ii) the amino acid sequence motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E shown in SEQ ID NO: 1, wherein X1 is a hydrophobic amino acid and X2 is a polar, non-hydrophobic amino acid, and/or in which the expression or activity of a jasmonate receptor protein is enhanced as compared to a corresponding control plant cell, or plant or part thereof, lacking the enhancement, wherein the jasmonate receptor protein
- a) having the amino acid sequence of SEQ ID NO: 76,

- b) having an amino acid sequence exhibiting an identity of at least 80% to the amino acid sequence of SEQ ID NO: 76,
 - c) is encoded by the nucleic acid sequence of SEQ ID NO: 75,
 - d) is encoded by a nucleic acid sequence exhibiting an identity of at least 80% to the nucleic acid sequence of SEQ ID NO: 75, or
 - e) is encoded by a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of c).
19. Use of at least one polynucleotide sequence comprising a nucleic acid sequence, or a complement thereof, comprising at least 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45 or 50 contiguous nucleotides of
- (a) the nucleic acid sequence of any one of SEQ ID NO: 3 (TaWRKY10), SEQ ID NO: 5 (TaWRKY13), SEQ ID NO: 7 (TaWRKY19), SEQ ID NO: 9 (TaWRKY29), SEQ ID NO: 11 (TaWRKY39), SEQ ID NO: 13 (TaWRKY53B), SEQ ID NO: 15 (TaWRKY68A) and SEQ ID NO: 75 (TaCOI1),
 - (b) a nucleic acid sequence exhibiting an identity of at least 80% to the nucleic acid sequence of any one of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15 and SEQ ID NO: 75, or
 - (c) a nucleic acid sequence hybridizing under stringent conditions with a nucleic acid which is complementary to the sequence of (a),
 - (d) a nucleic acid encoding the amino acid sequence of any one of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16 and SEQ ID NO: 76, or
 - (e) a nucleic acid encoding the amino acid sequence exhibiting an identity of at least 80% to the nucleic acid sequence of any one of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16 and SEQ ID NO: 76, as molecular marker for identifying a cereal plant cell, or a cereal plant or part thereof, having an increased pathogen resistance as compared to a corresponding control plant cell.
20. The cereal plant, or part thereof, according to any one of claims 7-10, the method of any one of claim 11-13 and claim 18, or the cereal plant cell, a cereal plant or part thereof, according to claim 17, or the use of at least one polynucleotide sequence according to claim 19, wherein the pathogen resistance is resistance against a fungal pathogen, preferably resistance against *Zymoseptoria tritici*.

21. The cereal plant cell of any one of claims 1-6, the cereal plant, or part thereof, according to any one of claims 7-10, or the method of any one of claim 11-13 and claim 18, wherein the fertilizer-responsive expression or activity is nitrogen-responsive expression or activity.

FIGURE 1

SEQ ID NO: 1. Amino acid sequence motif common to WRKY proteins of the invention (length: 11 amino acid residues)

D-G/E-X₁-X₂-W-R-K-Y-G-K/E/Q-K/E

wherein X₁ is a hydrophobic amino acid and X₂ is a polar, non-hydrophobic amino acid.

SEQ ID NO: 2. Amino acid sequence motif common to WRKY proteins of the invention (length: 16 amino acid residues)

D-G/E-X₁-X₂-W-R-K-Y-G-K/E/Q-K/E-X-X-X₃-X-X₂

wherein X is any amino acid, X₁ is a hydrophobic amino acid, X₂ is a polar, non-hydrophobic amino acid, and X₃ is a polar, non-aromatic amino acid.

FIGURE 2

SEQ ID NO: 3. Nucleic acid sequence of WRKY10 from *Triticum aestivum* (length: 678 nucleotides)

ATGGCAGCTTCGCTGGGACTTACCGGCCATGAGACCAGCTACCCGGCCCCACCCGGCGGCCTCCTCCTTGTACAACTTC
CAAGCCGGTGATCCCTTCGCGGCAGCGGCGGGCGGTGCCGCGGAGCTGAGCTTCCCGGAGCTCGTGGACGCCGCTCGG
CCCTCCGACTACTCGCTGCTTCCGGCGTTCGGCGCCGCTGGAGGCGAGGCGATGAACATGTACGAGCGGAGTGTCGTC
TTCCCTATGACGACCTCCTACTACTGCGACGGCGCCGGGATGTTTCGACGGCGACGCTTCGGCGAGGGCGAGAGGAGGA
GGGATCGGTGCTATGGCGGGGCGGCCGTCGGGGAGGATCGGGTTCCGGACTCGGTCGGAGGTGGAGGTGCTAGACGAC
GGGTTCGGTGGAGGAAGTACGGCAAGAAGGCGGTGAAGAGCAGCCCCAACCTGCGCAACTACTACCGGTGCTCCGCC
GAGGGGTGCGGGGTGAAGAAGCGGGTCGAGCGCGACCGCGACGACCCGCACTACGTCCTCACCACCTACGACGGCGTC
CACAACCACGTCACCCCTGGCAGCACGCCGAGGGCGTCCCCGGCGTACTCGGCGCCGGCGGCACCCGCTTGGACCTGG
AGCGAGCTGCATGCGGCGGCGGCGGGGGCTCACTCCTCGGAGTCCTACTGA

SEQ ID NO: 4. Amino acid sequence of WRKY10 from *Triticum aestivum* (length: 225 amino acid residues)

MAASLGLTGHETSYPAHPAASSLYNFQAGDPFAAAAGGAAELSFPELVDAARPSDYSLLPAFGAAGGEAMNMYERSVV
FPMTTSYYCDGAGMFDGDASARAGGGIGAMAGRPSGRIGFRTRSEVEVLDDGFRWRKYGKKAVKSSPNLRNYRCSA
EGCGVKKRVERDRDDPHYVLTTYDGVHNHVTGSTPRASPAYSAPAAPAWTWSELHAAAAAGAHSSSESY

FIGURE 3

SEQ ID NO: 5. Nucleic acid sequence of WRKY13 from *Triticum aestivum* (length: 669 nucleotides)

ATGGCCCTGGACTCCGTCCCTTCCTACCCAGCGACCTGGGATCCAGCGGCAGGGCAACCAGGACCCAGCAAAGAATC
CGGAAGGAGGAGCGAACGTGGACGGCGGACACCTACGCGCCGTACGACGACGGGCACCAGTGGAGGAAGTACGGCGAG
AAGAAGCTCTCCAACCTCCTACTTCCCGAGGTTCTACTACAGATGTACCTACAAGACTGACCTGAAGTGCCCTGCGACA
AAACAAGTCCAACAGAAGGACATGAGCGACCCACCATTGTTACGGTCACTTACTTCAACCATCACAGCTGCAACACC
ACCTCGAGGCCCATCGGCAGCGCCCCAGACACCACTGAGCAGTCGTCCTCGAGGAGGGCAGTGTCCATCTGCTTCGGG
TCGCATGCCACCGGCGAGCAGCCGACATTCCCTAACGTCGCCGGGCACACTGCAGTCACCAGCGAGCACAACCAACCAA
CAGAACGACAGAGGCGCTTACGGTCACCAGTTTCAGTGGACAGACACATCACCGTCGGCAGGCGATGCCCCAGTCAAG
ATGGAGACCGACAGTCTCGCCGGAACAGGCGCTTCGTCTGGCGCTGCTAGCGGCCATGCTCTGTCTGAGGACACTGCTG
CCGATCGGCCAGTCGAGATGCATCGAGTACTTTCAGTTCTTGTGA

SEQ ID NO: 6. Amino acid sequence of WRKY13 from *Triticum aestivum* (length: 222 amino acid residues)

MALDSVPSYPSDLGSSGRATRTQQRIRKEERTWTADTYAPYDDGHQWRKYGEKKLSNSYFPRFYRCTYKTDLKCPAT
KQVQQKDMSPPLFTVTYFNHHCNNTTSRPIGSAPDTTEQSSSRRAVSICFGSHATGEQPTFLTSPGTLQSPASTTNQ
QNDRGAYGHQFQWTDTSPSAGDAPVKMETDSL AGTGASSGAASGHALSRTLLPIGQSRCIEYFQFL

FIGURE 4

SEQ ID NO: 7. Nucleic acid sequence of WRKY19 from *Triticum aestivum* (length: 1,407 nucleotides)

ATGGCGGCGGGGAGTGGTCAGGCATCGGCGACGGCGGCGGCTCTGGGCCCCGCGCGCTCGACAGCCTCTTCCCC
GACGACCAGCCGTCGCCGGCCGCCCTCGGCGCTGGGCTTCTTCGGTGGATCCCTCGCGCAGCTCCCTTCCCCCTCCGCCG
CTCTGCGGCACCGCGCTCCTCGGGTACCCCCAGGACAACCTTTGATGTGTTCCATGAACAAGACCTAGCACAGCTGGCA
GCACAAGTAGCTCAAAAGAAAGAGTTGCGGGAAAAACAAGGGGCGGGATTGCATCACAAGATTGGACCTCAACTAGCT
TTTTCTAAATACAGTATACTTGATCAAGTGGACAACCTCTTCTTCTTCTCATTTGGCAACTTCAGTGCTGACACCTCAG
CATGTCAGTTCTTCCGTAGGCGCGGCATCAATGCAGGGACAGACTTTGCCATCACACACTGGTAGTGGTAGTGTCAAC
ACTGGACCAACTGGAGTTTTACAAGTGCTCCAAGATTTCATCCACCACTCTGGACAGTATCAACACTGGATCAACTGGA
GTTCTGGAAGCACTCCAAGGTTTCATCCATCACTCTGGATAGACCTGCTGATGATGGATACAACACTGGCGTAAGTATGGA
CAAAAGGCAGTCAAGGGTGGGAAGTATCCAAGGAGCTATTACAAATGTACCCTGAATTGCCCCGGTCAGGAAAAATGTA
GAGCACTCTGCAGATGGACGAATTATTAATAAATTTATAGAGGTGAGCACTGCCATGAACCCCCCTCAAAGAGGTTT
AAAGATTGTGGTGATTTATTTGAATGAGTTAAATGATTTCAATGATGCCAAGGAGCCTTCAACTAAATCACAATTAGGT
TGTCAAGGTTATTATGGAAAACCTATAACGCCAAATGGAATGATGACGGATGTTTTATTGCCAACGAAGGAAGAGGGG
GATGAGCAATTATCTAGTTTTAAGTGATATCCGGGAAGGTGATGGTGAAATAAGAACTGTTGATGGAGATGATGGTGAT
GCCGATGCAAAATGAAAGGAATGCACCAGGTCAAAAGATTATCGTGAGTACAACGAGCGATGTTGATCTTTTGGACGAC
GGCTATAGGTGGCGCAAGTATGGACAGAAAGTGGTGAGAGGAAATCCTCACCCAAGGAGCTATTACAAGTGCACCTTAC
CAAGGATGCGACGTCAAGAAGCATATCGAGAGATCTTCCGAGGAACCACATGCTGTGATAACTACATACGAAGGGAAG
CATACGCGATGACGTGCCGTGAGTCTAGGAACAGAAGCCAAGCCACAGGTCAACACCACTGCAAAGAGCAGACTTATTCA
GAACAATCAGCTGCAAGCTTCTGCAGTAGCTCGGAAAAGAGAAAATATGGAACAGCCATTCTGAACGATCTCGCCTTC
TAG

SEQ ID NO: 8. Amino acid sequence of WRKY19 from *Triticum aestivum* (length: 468 amino acid residues)

MAAGQWSGIGDGGGLWAPPALDSLFPDDQPSPAASALGFFGGSLAQLPSPPLCGTALLGYPQDNFDFVHEQDLAQLA
AQVAQKKELREKQAGLHHKIGPQLAFSKYSILDQVDNSSFSLATSVLTPQHVSSSVGAASMGGQTLPSHTGSGSVN
TGPTGVLQVLQDSSTLDSINTGSTGVLEALQGSSITLDRPADDGYNWRKYGQKAVKGGKYPRSYKCTLNCPVRKNV
EHSADGRIIKIIYRGQHCHEPPSKRFKDCGDLNLELNDFAKEPSTKSQLGCGQGYGKPIPTNGMMTDVLLPTKEEG
DEQLSSSLDIREGDGEIRTVDDGDADANERNAPGQKIIIVSTTSVDVLLDDGYRWRKYGQKVVRGNPHPRSYKCTY
QGCDVKKHIERSSEEPHAVITTYEGKHTHDVPESRNRSQATGQHHCKEQTYSEQSAASFCSSSEKRKYGTAILNDLAF

FIGURE 5

SEQ ID NO: 9. Nucleic acid sequence of WRKY29 from *Triticum aestivum* (length: 1,905 nucleotides)

ATGTCAGATCTGGGCCTCCCAGCCAGCTCGCCCTTTTTTATACGCGCCCCGTCCTACCGGGGAGAGACTTCAGACTCC
 TCCCTCTTTTCGGTCTCTACGACACGTTTCTTTCTCTCTCCCTCTCCCCTCGGCTACCAAGGCGTCTCTCTTTCTCCA
 AGGAGGCTCTCGATTTGCATGGACAAGGGCCACCTCGGTGGTGGCGGAGGAGGAGGAGGACTGCTAGCCCTGGACGCC
 TCGCCGCGGCAGCTCGGCTTCTTGAAC TTGCTATCGCCGCGCGCCGTTCCATAGGAGCATGGAGGCGGACGACGGCGGA
 GGCGGTGGCGGCGGCGGCAGGGGGAGGAGGTCCATCGAGGTTGACTTCTTCTCCGACGAGAAGAAGAACATGAAGAAG
 AGCCGGGCTTCGGCCGGGGCCGACGCGGAGGACCACAAGGATCAAGCCTCCGCCGCGGACTCGCCATCAAGAAGGAG
 GACCTCACCATTAACTCTCTTCCCGGGAACAACACGAGGAGCGACCGGTCCATGGTGGTTCGACGACGACGGAGCGTCC
 CGGGCCGACCAAGACAGGAACGGCAGGAACACCGGCGAGCTGGCGGTGATACAGGCCGAGCTGAGCCGCATGAACGAG
 GAGAACCAGCGGCTGCGAGGGATGTTGACCCAGGTCAACAACAGCTACCATGCGCTGCAGATGCATCTCGTCGCGCTC
 ATGCAGCAAAGGACCCAGATGCCCTCCGGTCCAGCCGCAACAACCTCCGACCCACGAGGATGGCAAGAACGAGAGTGCC
 ATCGTGCCGAGGCAAGTTCTTGGGTCTGGGCGCGTCGGGAGCCAGCGCTGACGTGGCGGAAGAGCCCTCCAACCTCGTCC
 ACGGAGGTTCGGGAGCCCGCGGCGGTCTGTCGTCCAACGGAACGAGGACCCTGAGCGCGGCGAAAACCCCTGACGGCCCCG
 TCCACCGCGGGGTGGTTGCCCGGACGCGGGATGAGCCAGCAGCAGCAGCAGCTGGGGGCGGCGGCGAAGGGCCAC
 GACCAGCAAGCGCAGGAGGCCACCATGAGGAAGGCCCGTGTCTCCGTTTCGCGCCCGATCCGAAGCCCCGATTATCGCC
 GATGGATGCCAATGGAGGAAGTACGGTCAGAAGATGGCCAAGGGAAACCCTTGCCACGCGCCTACTACCGGTGCACC
 ATGGCCACCGGCTGCCCGGTGCGCAAGCAGGTGCAACGATGCGCCGAGGACCGGACCATCTCATCACCACGTACGAG
 GGCACGCACAACCACCCGCTCCCGCCGGCCGCGCATGGCCATGGCGTCTACCACGTGCGCCGCTGCGTCCATGCTGCTC
 TCCGGCTCCATGCCAGCGCCGACGGCGCGGGGCTCATGAGCTCCAACCTTCTCGCGCGCACCGTGCTTCCGTGCTCG
 TCCAGCATGGCCACCATCTCGGCGTCCGCGCCGTTCCCGACGGTCACGCTCGACCTACCCACGCCCCCGCCGGGGCG
 CCCAACGCCATGCCGCTAAACGTCGCCCCGACCGCATGCACCGGGGCGAGTTCCATGTTCCGATGCCCGGCGGTGGGATG
 GCCCCGGCCTTCGCGATGCCGCCGCACATGCTGTACAACCAGTCCAAGTTCTCTGGGCTGCAGATGTCTCCGACTCG
 GTGGACGCCGGGCAAGTTTCGCGCAGCCTAGGCCGCCGATGGGCCTGCCAGGCCAGCTGTCCGACACCGTCAGCGCAGCG
 GCGGCCGCGATCACCGCGGACCCAACTTACAGTGGCGCTCGCCGCGGCCATCTCGTCGATCATGGCCGGCCAGCAC
 GCCGCCGGCAACAGCAACGCGAACAACAGCAACAACAACACCAGTAACAACAACGTGACGACGACTAGTAACAACACG
 ACAGCAACAACACCAACAGCGAGACCCAATGA

SEQ ID NO: 10. Amino acid sequence of WRKY29 from *Triticum aestivum* (length: 634 amino acid residues)

MSDLGLPASSPFFIRAPSYRGETSDSSLFRSLRHVSFSLPLPSATKASLSSPRRLSICMDKGHLGGGGGGGGLLALDA
 SPRQLGFLNLLSPAPFHRSMEADDGGGGGGGGGRRRSIEVDFFSDEKKNMKKSRAAGADAEDHKDQASAAGLAIKKE
 DLTINLLPGNNTRSDRSMVDDDDGASRADQDRNGRNTGELAVIQAELSRMNEENQRLRGMLTQVNNSYHALQMHLVAL
 MQQRTQMPPVQPOQPPTHEGKNEAIVPRQFLGLGPSGASADVAEPEPSNSTEVGSPRRSSSNGNEDPERGENPDGP
 STAGWLPGRGMSQQQQQQLGAAAKGHDQQAQEATMRKARVSVRARSEAPIIADGCQWRKYGQKMAKNPCPRAYYRCT
 MATGCPVRKQVQRCADRTILITTYEGTHNHPLPPAAMAMASTTSAAASMLLSGSMPSADGAGLMSSNFLARTVLPSC
 SSMATISASAPFPTVTLDLTHAPPGAPNAMPLNVARPHAPGQFHVPMPPGGMAPAFAMPPHMLYNQSKFSGLQMSDS
 VDAGQFAQPRPPMGLPGQLSDTVSAAAAAITADPNFTVALAAAISSIMAGQHAAGNSNANNSSNNNTSNNNVTTTSNNT
 TSNNNTSETQ

FIGURE 6

SEQ ID NO: 11. Nucleic acid sequence of WRKY39 from *Triticum aestivum* (length: 660 nucleotides)

ATGGACGAGCAGTGGATGATGGGGCAGACTTCCCTCAGCCTCGGCCTCAACGTCGGCCGGCCGACGGCGCGGCGGGGT
GCCCCCTCCGGTGACCAAGATCCTCGTGGAGGAGGACTTCATGTCTCTCAAGAAGAATCACGAGGTCGAGGCGCTGGAG
GCCGAGCTCCGGCGCGTGGGCGAGGAGAACAGGAGGCTCAGCGACATGCTCCGCGCGCTGGTGGCCAAGTACTCCGAC
CTTCAGGGCAGGGTCAGCGGCATGATGGCGGGCGGCGGCCGCGGCCAACAACCGCCAGTCACCCACGACGTCTGAGGGC
GGCTCCGCGGCCCTCGCCGTCCAGGAAGCGCGCTCGCAGCGACAGTCCCGACACCGCAGTCCAGGAAGCGTACCCTGCC
AGCGGCGGCTTCGCCGTCAAGCTCGGCCCCGACCAGGCGGAGTGCACGTCCGTCCACGAGCCGGGCAACAGC
AAGCGCGTCCGCGCCGACGAGTGCAAGGCCAGCCGGGTCTCCAAGCTCTACGTCCACGCCGACCCGCGCGACCTCAGC
CTCGTGGTGAAGGATGGGTACCAATGGCGAAAGTACGGCCAAGAAGGTGACCAAGGACAACCCATGCCCCGAGGGCCTA
CTCCGGTGCTCCGTTTCGCGCCGTCTGCCAGGTGA

SEQ ID NO: 12. Amino acid sequence of WRKY39 from *Triticum aestivum* (length: 219 amino acid residues)

MDEQWMMGQTSLSLGLNVGRPTARRGAPPVTKILVEEDFMSSKKNHEVEALEAELRRVGEENRRLSDMLRALVAKYSD
LQGRVSGMMAAAAAANNRQSPTTSEGGSAASPSRKRARSDSPDTAVQEAYPASGGFAVSVNVGPDQAECTSVHEPGNS
KRVRADCKASRVSKLYVHADPADLSLVVKDGYQWRKYQEGDQGPMPGELLPVLRSRPAR

FIGURE 7

SEQ ID NO: 13. Nucleic acid sequence of WRKY53B from *Triticum aestivum* (length: 1,323 nucleotides)

ATGTCCTCCTCCACGGGGAGCTTGGACCACGCAGGGTTCACGTTACGCCGCCGCGTTCATCACGTCTTCACCGAG
CTTCTGTCGGGGTCCGGCGCCGGCGACGCGGAGCGGTTCGCCGAGGGGGTTCAACCGAGGGGGCCGGGCGGGGCGCCC
AAGTTCAAGTCCGCGCAGCCGCCCAGCCTGCCCATCTCGTCGCCCTTCTCTGCTTCTCCGTCCCTGCAGGTCTCAGC
CCTGCCGAGCTGCTCGACTCCCCCGTTCTCTCAACTACTCTCACATCTTGGCGTCTCCGACTACCGGTGCGATCCCT
GCGCAGAGGTGCGACTGGCAGGTGAGCGCCGATCTGAACACCTTTTCAGCAGGATGAGCTCGGCCTCTCTGGCTTCTCC
TTTCACGCAGTCAAGTCCAACGCCACGGTCAACGCTCAAGCAAACCTGCTTACCTTTATTCAAGGAGCAGCAGGAGCAA
CAACAAGAAGAAGTGGTTCAAGTGAGCAACAAGAGCAGCAGCAGCAGCGCAACAACAAGCAGGTTGAGGACGGATAC
AATTGGAGGAAGTACGGGCAGAAGCAAGTTAAGGGGAGCGAGAACCCGCGGAGCTACTACAAGTGCACCTACAACAAT
TGCTCCATGAAGAAGAAAGTGGAGCGCTCTCTCGCCGACGGCCGCATCACGCAGATCGTCTACAAGGGCGCACATGAC
CACCCGAAGCCCCCTCTCCACGCGCCGCAACTCTCCGGCTGCGCGGCGGTCTGTTGCGGAGGATCACACCAACGGCTCG
GAGCACTCTGGCCCGACGCCCGAGAATTATCCGTCACCTTCGGAGACGATGAGGCCGACAAGCCCGAGACCAAGCGC
CGGAAGGAGCATGGTGACAACGAGGGCAGTTCAAGCGGCACCGGCGGCTGCGGGAAGCCCGTGC GCGGAGCCCGAGGCTC
GTGGTGCAGACGCTGAGCGATATAGACATACTCGACGACGGCTTCCGGTGGAGGAAGTACGGGCAGAAGGTTGTCAAG
GGCAATCCCAACCCAGGAGCTACTACAAGTGCACAACGGTGGGCTGCCCGGTGCGCAAGCATGTGGAGCGGGCCTCG
CACGACAACCGCGCGGTGATCACCACCTACGAGGGTAAGCACAGCCACGACGTGCCGATCGGCCGGGGCCGCGCGCTG
CCGCGCTCATCTTCTCCGACAGCTCGGCCGTCTGCGCTGCCGCCGCGGTGCAAGCCCGTGCACCCCTCGAGATG
CTCGCCGGACACCCAGGCTACGCGGCCAAGGACGAGCCCCGGGACGACATGTTCTGTCGAGTCGCTCCTCTGCTAG

SEQ ID NO: 14. Amino acid sequence of WRKY53B from *Triticum aestivum* (length: 440 amino acid residues)

MSSSTGSLDHAGFTFTPPPFITSFTELLSGSGAGDAERSPRGFNRGGRAGAPKFKSAQPPSLPISSPFSCFSVPAGLS
PAELLDSPVLLNYSHILASPTTGAI PAQRCDWQVSADLNTFQQDELGLSGFSFHAVKSNATVNAQANCLPLFKEQQEQ
QQEEVVQVSNKSSSSSGNNKQVEDGYNWRKYGQKQVKSENPRSYKCTYNNCSMKKKVERSLADGRITQIVYKGAHD
HPKPLSTRNSSGCAAVVAEDHTNGSEHSGPTPENSSVTFGDDEADKPETKRRKEHGDNEGSSGGTGGCGKPVREPR
VVQTLSDIDILDDGFRWRKYGQKVVKGPNPNRSYKCTTVGCPVRKHVERASHDNRAVITTYEGKHS HDVP IGRGRAL
PASSSSDSSAVIWPAAAVQAPCTLEMLAGHPGYAAKDEPRDDMFVESLLC

FIGURE 8

SEQ ID NO: 15. Nucleic acid sequence of WRKY68A from *Triticum aestivum* (length: 987 nucleotides)

ATGGCCGTGGACCCCATGGGCTGCTACACCCCTCGCCGCGCCGACGACCAGCTCGCCATCCAGGAGGCCGCCACCGCC
GGCCTCCGCAGCCTGGAGCTCCTCGTCTCCTCCCTCTCCGGCGCGGCGCCGTCCAAGGCGCCGAGCAGCACCTGCAG
CAGCCGTTTCGGCGAGATCGCCGACCAGGCCGTCTCCAAGTTCGCAAGGTGATCTCCATCCTCGACCCGACCGGCCAC
GCCCCGTTCCGCGCGGGCCCCGTCCAGTCGCCTACCCCGCCTCCTCCGGCTCCGGTCGCTCCTCCGCGCGCCCCACCG
CGCCCTCTGGCCGTGCTCGAGCCGGCCAGGCCCGCTCCCTTGACCGCCGTGGCGCCGGTGTTCGGTGGCCGCCCCGGTC
CCTCTCCCGCAGCCGCAGAGCCTGACGCTGGACTTCACCAAGCCGAACCTGACCATGTCAGGCGCGACGTCCGTGACG
TCCACGTCTTCTTTCTCTCGGTGACCGCCGGCGAGGGCAGCGTGTCCAAGGGCCGACGCTGGTCTCCGCGGCAAG
CCGCGCGTGTCCGGGCACAAGAGAAAGCCGTGCGCCGGCGCGCACTCGGAGGCCAACACCACCGGCAGCCGATGCCAC
TGCTCCAAGAGAAGGAAGAACC CGTGAAGACGACGGTGAGGGTGCCCGCGGTGAGCGCGAAGATCGCCGACATCCCG
CCGGACGAGTACTCGTGGAGGAAGTACGGCCAGAAGCCCATCAAGGTATCCCCTTACCCACGGGGGCTACTACAAGTGC
AGCACAGTGCGAGGGTGCCCGGCGCGGAAGCACGTGGAGCGCGCCCTGGACGACCCGGCGATGCTGGTGGTGACGTAC
GAGGGCGAGCACC GCCACTCGCCGGGGCCGATGCCGATGCAGATGGCGCCGTCGCCGGTGCCGATTCCGATGCCGATG
GGCGCGCCCGTAGCCGTAGCTAGTGTGTCCGCCGGCAACGGGCACGTCTGA

SEQ ID NO: 16. Amino acid sequence of WRKY68A from *Triticum aestivum* (length: 328 amino acid residues)

MAVDPMGCYTPRRADDQLAIQEAATAGLRSLLELLVSSLGAAPSKAPQQHLQQPFGEIADQAVSKFRKVISILDRTGH
ARFRRGPVQSPTPPPPAPVAPPPPPRPLAVVEPARPAPLTAVAPVSVAAPVPLPQPQSLTLDFTKPNLTMSGATSVT
STSFFLSVTAGEGSVSKGRSLVSAGKPPLSGHKRKPCAGAHSEANTTGSRCHCSKRRKNRVKTTVRVPAVSAKIADIP
PDEYSWRKYGQKPIKVSPYPRGYKCVTVRGC PARKHVERALDDPAMLVVTYEGEHRHSPGPMPMQMAPSPVPI PMPM
GAPVAVASVSAGNGHV

FIGURE 9

SEQ ID NO: 17. Nucleic acid sequence of WRKY6 from *Triticum aestivum* (91.1% sequence identity to the nucleic acid sequence of TaWRKY10 shown in SEQ ID NO: 3) (length: 672 nucleotides)

ATGGCGGCTTCGCTAGGACTTACCAGCCATGAAGCCTGCTGCACGGTCCACCCACCGGCTCCTCCTTGTACAACTTC
CAAGCCGATGACCCCTTCGTGGCAGCAGCGGACGGTGCCGCGGAGCTGAGCTTCCCGGAGCTCGTGGAAGCCGCTCGG
GCCTCCGACTACTCGCCGCTTCCGGCGTTCGGCGTTCGCTGGAGGCGAGACGATGAACATGTACGGGCGGAGCGTCGTC
TTCCCTATGACGACCTCGTACTACTGCGACGGCGCCGGGATGTTTCGACGGCGACGNCTTCGGCGAGGGGGAGATAGGG
GAAGGGATCGGTGCTATGACCGGGCGGCCGTGCGGGAGGATCGGGTTCGGGACTCGGTTCGGAGGTGGAGGTGATGGAC
GACGGGTTCGGGTGGAGGAAGTACGGCAAGAAGGCGGTGAAGAGCAGCCCCAACCTGCGGAACCTACTACCGGTGCTCC
GCCGAGGGGTGCGGGGTGAAGAAGCGGATCGAGCGCGACCGCGACGACCCGCGCTACGTCCTCACCACCTACGACGGC
GTCCACAACCACGTCACCCCGGCAGCACGTCGTCGAGGGCAGCGCCGGCGTACTCGGCGCCGACGGCGCCCGCTTGG
ACCTGGAGCGAGCTGCATGCGGCGGCGCACTCCTCGGAGTCCTACTGA

SEQ ID NO: 18. Amino acid sequence of WRKY6 from *Triticum aestivum* (83.7% sequence identity to the amino acid sequence of TaWRKY10 shown in SEQ ID NO: 4) (length: 223 amino acid residues)

MAASLGLTSHEACCTVHPTGSSLYNFQADDPFVAAADGAAELSFPELVEAARASDYSPLPAFGVAGGETMNMVGRSVV
FPMTTSYYCDGAGMFDGDXFGEIGEIGIGAMTGRPSGRIGFRTRSEVEVMDDGFRWRKYGKKAVKSSPNLRNYYRCS
AEGCGVKRIERDRDDPRYVLTITYDGVHNHVTGSTSSRAAPAYSAPTAPAWTWSELHAAAHSSSEY

SEQ ID NO: 19. Nucleic acid sequence of WRKY10A from *Triticum aestivum* (90.9% sequence identity to the nucleic acid sequence of TaWRKY10 shown in SEQ ID NO: 3) (length: 669 nucleotides)

ATGGCGGCTTCGCTAGGACTTACCCCGAGCCATGAAGCCTACTACTCGGCCCACCCGGCGGCCTCCTCCTTGTACAAT
TTCGAAGCCGGTGATCCCTTCGTGGCAGCGGCGGACGGTGCCGCGGAGCTGAGCTTCCCGGAGCTCGTGAGGCCGCT
CGTGCCCTCCGACTACTCGCCGCTTCCGGCGTTCGGCGCCGCTGGAGGCGAGACGATGAACATGTACGGGCGGAGCGTC
GTCTTCCCTATGACGGCCTCGTACTACTGCGACGGCGCGTGGATGTTTCGAGGACGACGCGGCGGCGAGGGCGAGAGGA
GGAGGGATCGGTGCTATGGCAGGGCGGCCGTGCGGGAGGATCGGGTTCGGGACTCGGTTCGGAGGTGGAGGTGATGGAC
GACGGATTCCGGTGGAGGAAGTACGGCAAGAAGGCGGTGAAGAGCAGCCCCAACCTGCGCAACTACTACCGGTGCTCC
GCCGAGGGGTGCGGGGTGAAGAAGCGGGTTCGAGCGGGACCGCGACGACCCGCTCTACGTCCTCACCACCTACGACGGC
GTCCACAACCACGTCACCCCGGCAGCACGTCGTCGAGGGCGGCGCCGGCGTACTCGGCGCCGACGGCGCCCGCTTGG
ACCTGGAGCGAGCTGCAAGCGGCGGCGCACTCCTCGGAGTCCTAG

SEQ ID NO: 20. Amino acid sequence of WRKY10A from *Triticum aestivum* (86.8% sequence identity to the amino acid sequence of TaWRKY10 shown in SEQ ID NO: 4) (length: 222 amino acid residues)

MAASLGLTPSHEAYYSAHPAASSLYNFEAGDPFVAAADGAAELSFPELVEAARASDYSPLPAFGAAGGETMNMVGRSV
VFPMTASYYCDGAWMFEDDAAARARGGGIGAMAGRPSGRIGFRTRSEVEVMDDGFRWRKYGKKAVKSSPNLRNYYRCS
AEGCGVKRVERDRDDPLYVLTITYDGVHNHVTGSTSSRAAPAYSAPTAPAWTWSELQAAAHSSSES

SEQ ID NO: 21. Nucleic acid sequence of TaWRKY10-homolog from *Secale cereale* (91.4% sequence identity to the nucleic acid sequence of TaWRKY10 shown in SEQ ID NO: 3) (length: 672 nucleotides)

ATGGCGACTTCGCTGGGACTTACCACCAGCCATGAAGCCTGCTTCTCGGCCCACCCGGCGGGCTCCTCCTTGTACAAC
TTTCAAGCTGATGATCACTTCCCTGGCAGCGGCGGACGGTGCCGCGGCGCTGAGCTTCCCGGAGCTCGTCGACGCCGCT
CGGGCCTCCAAC TACCCGCCGCTTCCGGCGTTCCGGCGCCGCTGGAGGCGAGGCGATGAACATGTACGAGCGGAGTGTC
GTCTTCCCCATGACGTCCCTCGTACTACTGCGACGGCGCTGGGATGTTGACGGCGACGCTTCGGCGAGGGCGAGAGGA
GGAGGGATCGGCGCTATGGCCGGGCGGCCGTCGGGGAGGATCGGGTTCCGGACCCGGTCGGAGGTGGAGGTGATGGAC
GACGGGTTCGGGTGGAGGAAGTACGGCAAGAAGGCGGTGAAGAGCAGCCCCAACCTGCGGAAC TACTACCGGTGCTCC
GCCGAGGGGTGCGGGGTGAAGAAGCGGGTCGAGCGGGACCGCGACGACCCGCTCTACGTGCTACCCACCTACGACGGC
GTCCACAACCACGTCACCCCGGCAGCACGTCGTCGCGGGCGGCGCCGGCGTACTCGGCGCCGGCCGCGCCCGCTTGG
ACCTGGAGCGAGCTGCATGCGGCGGCGCACTCCTCGGAGTCCTACTGA

SEQ ID NO: 22. Amino acid sequence of TaWRKY10-homolog from *Secale cereale* (88.5% sequence identity to the amino acid sequence of TaWRKY10 shown in SEQ ID NO: 4) (length: 223 amino acid residues)

MATSLGLTTSHEACFSAHPAASSLYNFQADDHFLAAADGAAALSFPFLVDAARASNYPPLPAFGAAGGEAMNMYERSV
VFPMTSSYYCDGAGMFDGDASARARGGGIGAMAGRPSGRIGFRTRSEVEVMDDGFRWRKYGKKAVKSSPNLRNYYRCS
AEGCGVKRVERDRDDPLYVLTITYDGVHNHVT PGSTSSRAAPAYSAPAAPAWTWSELHAAAHSSESY

SEQ ID NO: 23. Nucleic acid sequence of TaWRKY10-homolog from *Hordeum vulgare* (91.2% sequence identity to the nucleic acid sequence of TaWRKY10 shown in SEQ ID NO: 3) (length: 690 nucleotides)

ATGGCGGCCTCGCTGGGACTTACCAGCCATGAAGAAGCCTGCTACTCTGCCCACCCGGCCGGCTCCTCCCTGTACAAC
TTCCAAGACGGCGAACCCTTCGGGGCGGCGGCCGACGGTGCCGCGGCGCCGAGCTTCCAGGAGCTCGTGACGCCGCT
CGACCTCCGACTACGCGCCGCTTCCGGCGTTCCGGCGCCGCTGGAGGCGAGGCGATGAGCATGTACGAGCGGAGCGTC
GTCTTCCCTATGACGACGTCCCTCGTACTACTGCGACGGCGCCGGGATGTTGACGACGACGCGGCGGGCGAGGGCGAGA
GGGGGAGGGGTTCGGTGCATGGCAGGGCGGCCGTCGGGGAGGATCGGGTTCCGGACCCGGTCGGAGGTGGAGGTGATG
GACGACGGGTTCGGGTGGAGGAAGTACGGCAAGAAGGCGGTGAAGAGCAGCCCCAACCTGCGGAAC TACTACCGCTGC
TCCGCCGACGGGTGCGGGGTGAAGAAGCGGGTCGAGCGGGACCGCGACGACCCGCGCTACGTCTCACCACCTACGAC
GGCGTCCACAACCACGTCGCCCCCGGCGGCGGCACGCCGTCGCGGGCGGCGCCGGCGTACTCGGCGCCGGCCGCGCCA
GCTTGACCTGGAGCGAGCTGCATGCGGCGGCGGCGGCGGCGGCTCACTCCTCGGAGTCCTACTGA

SEQ ID NO: 24. Amino acid sequence of TaWRKY10-homolog from *Hordeum vulgare* (87.3% sequence identity to the amino acid sequence of TaWRKY10 shown in SEQ ID NO: 4) (length: 229 amino acid residues)

MAASLGLTSHEEACYSAPAGSSLYNFQDGEFPGAADGAAAPSFQELVDAARPSDYAPLPAFGAAGGEAMSMYERSV
VFPMTSSYYCDGAGMFDGDDAAARARGGGVGAMAGRPSGRIGFRTRSEVEVMDDGFRWRKYGKKAVKSSPNLRNYYRC
SADGCGVKRVERDRDDPRYVLTITYDGVHNHVPAGGGT PSRAAPAYSAPAAPAWTWSELHAAAAAAHSSESY

FIGURE 10

SEQ ID NO: 25. Nucleic acid sequence of WRKY46 from *Triticum aestivum* (100% sequence identity to the nucleic acid sequence of TaWRKY13 shown in SEQ ID NO: 5) (length: 669 nucleotides)

ATGGCCCTGGACTCCGTCCCTTCCTACCCAGCGACCTGGGATCCAGCGGCAGGGCAACCAGGACCCAGCAAAGAATC
CGGAAGGAGGAGCGAACGTGGACGGCGGACACCTACGCGCCGTACGACGACGGGCACCAAGTGGAGGAAGTACGGCGAG
AAGAAGCTCTCCAACCTCCTACTTCCCGAGGTTCTACTACAGATGTACCTACAAGACTGACCTGAAGTGCCCTGCGACA
AAACAAGTCCAACAGAAGGACATGAGCGACCCACCATTGTTACGGTCACTTACTTCAACCATCACAGCTGCAACACC
ACCTCGAGGCCCATCGGCAGCGCCCCAGACACCACTGAGCAGTCGTCTCGAGGAGGGCAGTGTCATCTGCTTCGGG
TCGCATGCCACCGGCGAGCAGCCGACATTCCTAACGTGCGCCGGGCACACTGCAGTCACCAAGCAGCACAACCAACCAA
CAGAACGACAGAGGCGCTTACGGTCACCAAGTTTCAGTGGACAGACACATCACCGTCGGCAGGCGATGCCCCAGTCAAG
ATGGAGACCGACAGTCTCGCCGGAACAGGCGCTTCGTCTGGCGCTGCTAGCGGCCATGCTCTGTGAGGACACTGCTG
CCGATCGGCCAGTCGAGATGCATCGAGTACTTTCAGTTCTTGTGA

SEQ ID NO: 26. Amino acid sequence of WRKY46 from *Triticum aestivum* (100% sequence identity to the amino acid sequence of TaWRKY13 shown in SEQ ID NO: 6) (length: 222 amino acid residues)

MALDSVPSYPSDLGSSGRATRTQQRIRKEERTWTADTYAPYDDGHQWRKYGEKKLSNSYFPRFYRCTYKTDLKPAT
KQVQQKDMSPPLFTVTYFNHHCNTTSRPIGSAPDTTEQSSSRAVSICFGSHATGEQPTFLTSPGTLQSPASTTNQ
QNDRGAYGHQFQWTDTSPSAGDAPVKMETDSLGTGASSGAASGHALSRTLPIGQSRCEYFQFL

SEQ ID NO: 27. Nucleic acid sequence of TaWRKY13-homolog from *Secale cereale* (86.4% sequence identity to the amino acid sequence of TaWRKY13 shown in SEQ ID NO: 5) (length: 591 nucleotides)

AGGAAGGAGGAGCGGACGTGGACGGCGGACACCTACGCGCCGTACGACGACGGGCACCAAGTGGAGGAAGTACGGCGAG
AAGAAGCTCTCCAACCTCCAACCTCCCGAGGTTCTACTACAGATGTACGTACAAGACTGACCTGAAGTGCCCTGCGACA
AAACAAGTCCAGCAGAAGGACATGAGCGACCCACCATTGTTACGGTCACTTACTTCAACCATCACAGCTGCAACACC
ACCTCGAGGCCCATCGGCAGCGCCCCAGACACCAACCGAGCAGTCCTCTCGAGGAGGGCAGTGTCATCTGCTTCGGG
TCGCATGCCACTGGCGAGCAGCCGACATTCCTAACGTGCGCCGGGCACACTGCAGTCACCAAGCAGCACAACCAACCAA
CAGAGCGACAGAGGCGCTTACGGTCACCAAGTTTCAGTGGACAGACACATCACCGTCGGCAGGCGATGCCCCAGTCAAG
ATGGAGACCGACAGTCTCGCCGGAACAGGCTCGTCGTCTGGCGCTGCTAGCGGCCATGCTCTGTGAGGACACTTCTG
CCGATCGGCCAGTCGAGATGCATCGAGTACTTTCAGTTCTTGTGA

SEQ ID NO: 28. Amino acid sequence of TaWRKY13-homolog from *Secale cereale* (86.9% sequence identity to the amino acid sequence of TaWRKY13 shown in SEQ ID NO: 6) (length: 196 amino acid residues)

RKEERTWTADTYAPYDDGHQWRKYGEKKLSNSNFRFYRCTYKTDLKPATKQVQQKDMSPPLFTVTYFNHHCNT
TSRPIGSAPDTTEQSSSRAVSICFGSHATGEQPTFLTSPGTLQSPASTTNQSDRGAYGHQFQWTDTSPSAGDAPVK
METDSLGTGSSSGAASGHALSRTLPIGQSRCEYFQFL

SEQ ID NO: 29. Nucleic acid sequence of TaWRKY13-homolog from *Hordeum vulgare* (95.7% sequence identity to the nucleic acid sequence of TaWRKY13 shown in SEQ ID NO: 5) (length: 672 nucleotides)

ATGGCCCTGGACTCCGTCCCGTCCTACCCCAGCGACCTGGGATCCAGCAGCAGTAGGACAACCAGGACCCAGCAAAGA
ATCCGGAAGGAGGAGCGGACGTGGACGGCGGACACCTACGCACCGTACGACGACGGGCACCAGTGGAGGAAGTACGGC
GAGAAGAAGCTCTCCAACCTCCAACCTCCCGAGGTTCTACTACAGATGTACCTACAAGACTGACCTGAAGTGCCCTGCG
ACAAAACAAGTCCAGCAGAAGGACATGAGCGACCCACCATTGTTTACAGTCACTTACTTCAACCATCACAGCTGCAAC
ACCACCTCGAGGCCCCATCGGCAGCGCCCCAGACACCACCGAGCAGTCGTCTCGAGGAGGGCGGTGTCCATCTGCTTC
GGGTCGCATGCCACCGGCGAGCAGCCAACGTTCTTAACGTCGCCGGGTACACTACAGTCACCAGCAAGCACAAACCAAC
CAACAGAGCGACATAGGCGCTTACGGTCACCAAGTTTCAGTGGACAGATACATCACCGTCGGCAGACGATGCCCCGGTC
AAGATGGAGACCGACAGTCTCGCAGGAACAGGTGCTTCGTCTGGCGGTGCTAGCGGCCATGCTCTGTCTGAGGACACTG
CTGCCGATCGGCCAGTCGAGATGCATCGAGTACTTCCACTTCTTGTGA

SEQ ID NO: 30. Amino acid sequence of TaWRKY13-homolog from *Hordeum vulgare* (96.0%
sequence identity to the amino acid sequence of TaWRKY13 shown in SEQ ID NO: 6) (length:
223 amino acid residues)

MALDSVPSYPSDLGSSSSRTTRTQQRIRKEERTWTADTYAPYDDGHQWRKYGEKKLSNSNFPFRFYRCTYKTDLKCPA
TKQVQQKDMSDPPLFTVTYFNHHCNTTSRPIGSAPDTTEQSSSRRAVSICFGSHATGEQPTFLTSPGTLQSPASTTN
QQSDIGAYGHQFQWTDTSPSADDAFVKMETDSLACTGASSGGASGHALSRTLLPIGQSRCIEYFHFLL

FIGURE 11

SEQ ID NO: 31. Nucleic acid sequence of WRKY19C from *Triticum aestivum* (90.0% sequence identity to the nucleic acid sequence of TaWRKY19 shown in SEQ ID NO: 7) (length: 1,293 nucleotides)

CCGCCGCTGGCCGCTCGGCGCTCGGCTTCTTCGGGGGACCCCTATCCCTCGCGCAGCTCCCTTCCCCTCCGCCGCTC
CTCGGGTACCCCCAGGACAACCTTTGATGTGTTCCATGAACAAGACCTAGCACAGCTGGCAGCACAAAGTAGCTCAAAAG
AAAGAGTTGCGGGAAAAACAAGGGGCGGGATTGCATCACAAGATTGGACCTCAACTAGCTTTTTTCGAAATACAGTATA
CTTGATCAAGTGGACAACCTTCTTCTTCTTCATTGGCAACTTCAGTGCTGACACCTCAGCATGTCAGTTCTTCCGTA
GGCGCGGCATCAATGCAGGGACAGACTTTGCCATCACACACTGGTAGTGGTAGTGTCAACACTGGACCAACTGGAGTT
TTACAAGTGCTCCAAGATTCACCACTCTGGACAGTATCAACACTGGATCAACTGGAGTTCTGGAAGCACTCCAA
GGTTCATCCATCACTCTGGATAGACCTGCTGATGATGGATACAACCTGGCGTAAGTATGGACAAAAGGCAGTCAAGGGT
GGGAAGTATCCAAAGAGCTATTACAAATGCACCCTGAAGTGGCCGGTCAGGAAAAATGTAGAGCACTCTGCAGATGGA
CGAATTATTTAAATAATTTATAGAGGTCAGCACTGCCATGAACCCCCCTCAAAGAGGTTTAAAGATTGTGGTGATTTA
TTGAATGAGTTAAATGATTTCAATGATGCCAAGGAGCCTTCAACTAAATCACAATTAGGTTGTCAAGGTTATTATGGA
AAACCTATAACGCCAAATGGAATGATGACGGATGTTTTATTGCCAACGAAGGAAGAGGGGGATGAGCAATTATCTAGT
TTAAGTGATATCCGGGAAGGTGATGGTGAAATAAGAACTGTTGATGGAGATGATGGTGATGCCGATGCAAATGAAAGG
AATGCACCAGGTCAAAAGATCATCGTGAGTACAACGAGCGATGTTGATCTTTTGGACGACGGCTATAGGTGGCGCAAG
TATGGACAGAAAGTGGTGAGAGGAAATCCTCACCCAAGGAGCTATTACAAGTGCACTTACCAAGGCTGCGACGTCAAG
AAGCATATCGAGAGATCTTCCGAGGAACCATGCTGTGATAACCATACGAAGGGAAGCATACCCATGACGTGCCT
GAGTCTGGAACAGAAGCCAAGGCACAGGTCAACACCACTGCAAAGAGCAGACTTATTTCAGAACAAACAGCTGCTAGCT
TCTGCAGTAGCTCGGAAAAGAGAAAATACGGAACAGCCATTCTGA

SEQ ID NO: 32. Amino acid sequence of WRKY19C from *Triticum aestivum* (83.6% sequence identity to the amino acid sequence of TaWRKY19 shown in SEQ ID NO: 8) (length: 430 amino acid residues)

PPLAASALGFFGGPLSLAQLPSPPLLGYPDNFDVFHEQDLAQLAAQVAQKKELREKQAGLHHKIGPQLAFSKYSI
LDQVDNSSSFLATSVLTPQHVSSSVGAASMGGQTLPSHTGSGSVNTGPTGVLQVLQDSSTTLDSINTGSTGVLEALQ
GSSITLDRPADDGYNWRKYGQKAVKGGKYPKSYKCTLNCPRKNVEHSADGRIIKIIYRGQHCHEPPSKRFKDCGDL
LNELNDFNDAKEPSTKSQLGCGYGYGKPIIPNGMMDVLLPTKEEGDEQLSSLSDIREGDGEIRTVDDGDDADANER
NAPGQKIIIVSTSDVDLLDDGYRWRKYGQKVVRGNPHPRSYKCTYQGC DVKKHIERSSEEPHAVITTYEGKHTHDVP
ESGTEAKAQVNTTAKSRLLIQNNQLLASAVARKRENTEQPF

SEQ ID NO: 33. Nucleic acid sequence of TaWRKY19-homolog from *Secale cereale* (84.3% sequence identity to the nucleic acid sequence of TaWRKY19 shown in SEQ ID NO: 7) (length: 1,218 nucleotides)

GACAATTTTGATGTGTTCCATGAACAAGACCTAGCACAGCTGGCAGCACAAAGTAGCTCAAAAGAAAGAGTTGCGGGAA
AGACAAGGGGCGGGATTGCTTCACAAGATTGGACCTCAACTAGCTTTTTCAAATACAGTATACTTGATCAAGTGGGC
AACTCTTCTTCTTCTTCATTGGCAACTTCAGTGCTAACACCTCAGCATGTTAGTTCTTCCGTAGGCGCGTCATCAATG
CAGGGACAGACTTTGCCATCACACACTGGTAGTGGTAGTGTCAACACTGAACCAACTGGAGTTTACAAGTGCTCCAA
GATTCATCCACCCTCTGGACAGTATCAACACTGGATCAGCTGGAGTTCTGGAAGCACTCCAAGGTGCATCCATCACT
CTGGATAGACCTGCTGATGATGGATACACTTGGCGTAAGTATGGACAAAAGGCAGTCAAGGGTGGGAAGTATCCAAAG
AGCTATTACAAATGCACCCTGAAGTGGCCGGTCAGGAAAAATGTAGAGCACTCTGCAGATGGACGAATTATTTAAATA
ATTTATAGAGGTCAGCACTGCCATGAACCTCCCTCAAAGAGGTTTAAAGATTGTGGTGATTTATTGAATGAGTTAGAT
GATTTCAATGATGCCAAGGAGCCTTCAACTGGATCACAATTAGGTTGTCAAGGTTATTATGGAAAACCTATAACGCCA
AATGGCACGATGGCGGATGGTTTATTGCCAACGAAGGAAGAGGGAGATGAGCAATTATCTAGTTTAAAGTGATATCCGG
GAAGGTGATGATGAAATAAGAACTGTTGATGGAGATGTTGGTGATGCCGATGCAAATGAAAGGAATGCACCAGGTCAA
AAGATAATCGTGAGTACAACGAGCGATGTTGATCTTTTGGACGACGGCTATAGGTGGCGCAAGTATGGACAGAAAGTG
GTGAGAGGAAATCCTCACCCAAGGAGCTATTACAAGTGCACTTACCAAGGCTGCGACGTCAAGAAGCATATCGAGAGA

TCTTCCGAGGAACCATGCTGTGATAACTACATACGAAGGGAAGCATACCCATGACGTGCCTGAGTCTAGGACCAGA
AGCCAAGCCACAGGTCAACACCCTGCAAAGAGCAGACTTATTCAGAACAACCAGCTGCTAGCTTCTGCAGTAGCTCG
GAAAAGAGAAAATACGGAACAGCCATTCTGAACGATCTCGCCTTCTAG

SEQ ID NO: 34. Amino acid sequence of TaWRKY19-homolog from *Secale cereale* (82.7% sequence identity to the amino acid sequence of TaWRKY19 shown in SEQ ID NO: 8) (length: 405 amino acid residues)

DNFDVFHEQDLAQLAQVAQKKELRERQGAGLLHKIGPQLAFSKYSILDQVGNSSSFSLATSVLTPQHVSSSVGASSM
QGQTLPSHTGSGSVNTEPTGVQLQDSSTTLDSINTGSAGVLEALQGASITLDRPADDGYTWKRYGQKAVKGGKYPK
SYYKCTLNCPVRKNVEHSADGRIIKIIYRGQHCHEPPSKRFKDCGDLNDELDFNDAKEPSTGSQLGCQGYGKPIPT
NGTMADGLLPTKEEGDEQLSSLSDIREDGDEIRTVGDVGDADANERNAPGQKIIVSTTSDVDLLDDGYRWRKYGQKV
VRGNPHPRSYKCTYQGC DVKKHIERSSEEPHAVITTYEGKHTHDVPESRTRSQATGQHHCKEQTYSQPAASFCSSS
EKRYGTAILNDLAF

SEQ ID NO: 35. Nucleic acid sequence of TaWRKY19-homolog from *Hordeum vulgare* (84.5% sequence identity to the nucleic acid sequence of TaWRKY19 shown in SEQ ID NO: 7) (length: 1,341 nucleotides)

ATGGCGGCCGCGCCAGTGGTCGGCCATCGGCGACGGCGCGGCCCTCTGGTCCCCGAGGCGCTCGAGAGCCTCTTCCCC
GACGAGCAGCCGCGCGCGCGCAGCTGGGCTTCTTCGGGGGGTCCCTCGCGCAGCTCGCTCCCCCTCCGCGCTCTGC
GCCATCGCGCTCCTCGGGTACCCCCAGGATAACTTTGATGTGTTCAATGAACAAGACCTAGCACAGGTGGCAGCACAG
GTAGCTCAAAAGAAGGAGTTGCAGGAAAAACAAGCGGCGTTATTACATCCGAAGGGTATGTCGACTTTGCCATCATAT
ACTGGTAGTGGTAGTATGAACACTGGACCAACTGGAATTCTACAAGTGCTCCAAGGTTTCATCCACCACTCTGGACAGT
ATCAACACTGGATCAGCTGGAGTTCTACAAGTGCTCCAAGGTTTCATCCACCACTCTGGACAGTATCAACACTGGATCA
GCTGGATTTCTGGAAGCACTCCAAGGTTCTTCCATCACTCTGGATAAACCTGCTGATGATGGCTACAATTGGCGTAAA
TATGGACAGAAGGCAGTCAAGGGCGGGAAGTGTCGAAGGAGCTATTACAAATGTACCCTGAAGTGGCGGTGAGAAAA
AATGTGGAGCACTCTGCAGATGGACGAATTATTAATAAGTATTTATAGAGGTGAGCACTGTGATGAACCTCCCTCAAAG
AGGTTTAAAGATTGTGGTGATTTATTGAACGAGTTAGATGAAGTCAATGATGCCGAGGAACCTTCAACCAGATCACTA
TTAGGTTGTCAAGTTATTATGGAAGCAACCAAAACCTATAACGCCAAATGGCAGCATGGTGGATGGTTTATTGCCAACG
AAGGAAGAGGGAGATGAGCAATTATCTAGTTTAAAGTGATATCCGGGAAGATGATGGTGAAATAAGAACTGTTGATGGA
GATGTTGGTGATGCCGATGCAATGAAAGGAATGCACCAGGTCAAAAAATTATTGTGAGTACAACAAGCGATGTTGAT
CTTTTGGACGATGGCTATAGGTGGCGCAAGTATGGACAGAAAGTGGTGAGAGGAAATCCTCACCCAAGGAGCTATTAC
AAGTGCACTTACCAAGGCTGCGACGTCAAGAAGCATGTCGAGAGATCTTCCAGGAACCATGCTGTGATAACTACA
TACGAAGGGAAGCATACCCATGACGTGCCTGAGTCTAGGAACAGAAGCCAGGCCACAGGTTACACCACTGCAAAGAG
CAGACTTATTCAGAACAACCAGCTGCTAGCTTCTGCAGTAGCTCGGAAAAAAGAAAATACGGAACGGTCATTCTGAAC
GATCTCGCTTTCTAG

SEQ ID NO: 36. Amino acid sequence of TaWRKY19-homolog from *Hordeum vulgare* (77.6% sequence identity to the amino acid sequence of TaWRKY19 shown in SEQ ID NO: 8) (length: 446 amino acid residues)

MAAGQWSAIGDGGGLWSPQALES LFPDEQPAAAQLGFFGGSLAQLAPPPPLCAIALLGYPQDNFDVFNEQDLAQVAAQ
VAQKKELEKQAALLHPKGMSTLPSHTGSGSMNTGPTGILQVLQGSSTTLDSINTGSAGVLEALQGSSTTLDSINTGS
AGFLEALQGSSTITLDKPADDGYNWRKYGQKAVKGGKCPRSYYKCTLNCPVRKNVEHSADGRIIKIIVYRGQHCHEPPSK
RFKDCGDLNDELNDAAEPSTRSLLGCQGYGKPKPIPTNGTMVDGLLPTKEEGDEQLSSLSDIREDGDEIRTVDG
DVGDADANERNAPGQKIIVSTTSDVDLLDDGYRWRKYGQKVVRGNPHPRSYKCTYQGC DVKKHVERSSEQEPHAVITTY
YEGKHTHDVPESRNRSQATGSHHCKEQTYSQPAASFCSSSEKRYGTVILNDLAF

FIGURE 12

SEQ ID NO: 37. Nucleic acid sequence of TaWRKY29-homolog from *Secale cereale* (89.9% sequence identity to the nucleic acid sequence of TaWRKY29 shown in SEQ ID NO: 9) (length: 1,785 nucleotides)

CTCTCCCTCCCCCTCTCGGCTAGCAAGCGTCTCTTCTCCCAGGAGGCTCTCGATTTGCATGGACAAGGGCCACCACGGT
GGTGGCGGAGGAGGAGGAGGAGTGTCTCGCCCTGGACGCCTCGCCGCGGCAGCTCGGCTTCTTGAACCTTGCTATCGCCG
GCGCCGTTCCACAGGAGCATGGAGGCGGACGACGGCGGTGGCGGTGGCGGCGGCAGGGGGAGGAGGTCCATCGAGGTT
GACTTCTTCTCCGACGAGAAGAAGAACATGAAGAAGAGCCGGGCATCGGCCGCTGCCGACGCGGAGGACCAGAAAGAT
CAGGCATCCGCCCGCGGACTCGCCATCAAGAAGGAGGACCTCACCATTAACTCTCTTCCCGGGAACAACACGAGGAGC
GACCGGTCCATGGTGGTTCGACGACGACGCGGGGCTCCCGGGCAGACGACGCGCAGGAACACCGGCGAGCTCGCGGCGATG
CAGGCCGAGCTGAGCCGCATGAACGAGGAGAACCAGCGGCTGCGAGGGATGTTGACCCAGGTCAACAGCAGCTACCAT
GCGCTGCAGATGCATCTCGTCGCGCTCATGCAGCAAAGGACCCAGATGCCTCCGGTCCAACCGCAACAACCTCCGACC
CACGAGGATGGCAAGAACGAGAGTGCCATCGTGCCGAGGCAGTTCTTGGGTCTGGGCCCATCCGGAGCCAGCGCTGAC
GTGGCGGAGGAGCCGTCCAACCTCGTCCACGAGGTGCGGAGCCCGCGCCGCTCGTCTGTCGAACGGGAACGAGGACCT
GAGCGCGGCGACAACCTGACGGCCCGTCCACCGCGGGGTGGTTGCCCGGACGCGGGATGACCCAGCAGCAGCAGCAG
CAGCAGCAGCTGGGAGCGGCGGCGAAGGGCCACGACCAGCAAGCGCAGGAGGCCACCATGAGGAAGGCCCGTGTCTCC
GTTTCGCGCAGATCCGAAGCACCGATTATCGCCGATGGATGCCAATGGAGGAAGTACGGCCAGAAGATGGCCAAGGGA
AACCCTTGCCACGCGCCTACTACCGCTGCACCATGGCCACCGGCTGCCCGGTGCGCAAGCAGGTGCAACGATGCGCT
GAGGACCGGACTATCCTCATCACACGTACGAGGGCAGCACAACCACCCGCTCCCGCCGGCCGCCATGGCCATGGCG
TCTACCACGTGCGCCGCCGCTCCATGCTGCTCTCGGGCTCCATGCCAGCGCCGACGGCGCGGGGCTCATGAGCTCC
AACTTCTCGCGCGCACCGTGTGCTGCCGTGCTCGTCCAGCATGGCCACCATCTCGGCGTCCGCGCCGTTCCCCGACGGTC
ACGCTCGACCTCACCCACGCCCCGCCCGGGGCGCCCAACGCCATGCCGCTGAACGTGCTCGACCGCATGCACCGGGG
CAGTTCCATGTTCCGATGCCCGGCGGTGGGATGGCCCCGGCCTTCGCGATGCCGCGGCACATGCTGTACAACAGTCA
AAGTTCTCTGGTCTGCAGATGTCTCCGACTCGGTGGACCCCGGGCAATTTCGCGCAGCCTAGGCCGCGAGATGGGCCTG
CCAGGCCAGCTGTCCGACACCGTCAGCGCAGCGGCGGCTGCGATCACC CGGACCCGAACCTTACCGTGGCACTTGCC
GCGGCCATCTCGTCGATCATGGCCGGCCAGCACGCCGCGGGCAACAGCAACGCGAACAACAGCAACAACACACCACC
AGTAACAACAACGTGACGACGACCAGTAACAACACGACGAGCAACAACACCAACAGCGAGACTCAATGA

SEQ ID NO: 38. Amino acid sequence of TaWRKY29-homolog from *Secale cereale* (90.6% sequence identity to the amino acid sequence of TaWRKY29 shown in SEQ ID NO: 10) (length: 594 amino acid residues)

LSLPSRLASVSSPRRLSICMDKGHHGGGGGGGGLLALDASPRQLGFLNLLSPAPFHRSMEADDGGGGGGGRGRRSIEV
DFFSDEKKNMKSRASAGADAEDQKDQASAAGLAIKKEDLTINLLPGNNTRSDRSMVDDDDGASRADDGRNTGELAAM
QAELSRMNEENQRLRGMILTQVNSSYHALQMHLLVALMQORTQMPFVQPPQPPTHEDGKNESAIVPRQFLGLGPSGASAD
VAEPPSNSSTEVGSPRRSSSNGNEDPERGDNPDGPSTAGWLPGRGMTQQQQQQQQLGAAAKGHDQQAQEATMRKARVS
VRARSEAPIIADGCQWRKYGQKMAKGNPCPRAYYRCTMATGCPVRKQVQRCAEDRTILITTYEGTHNHPLPPAAMAMA
STTSAAASMLLSGSMPSADGAGLMSNFLARTVLPCCSSMATISASAPFPTVTLDLTHAPPGAPNAMPLNVARPHAPG
QFHVPMPPGGMAPAFAMPPHMLYNQSKFSGLQMSDSDVDPGQFAQPRPQMGLPGQLSDTVSAAAAAITADPNFTVALA
AAISSIMAGQHAAGNSNANNSSNNNTTSNNVTTTTSNNTTSNNTNSETQ

SEQ ID NO: 39. Nucleic acid sequence of TaWRKY29-homolog from *Hordeum vulgare* (90.0% sequence identity to the nucleic acid sequence of TaWRKY29 shown in SEQ ID NO: 9) (length: 1,833 nucleotides)

ACTTCAGACTCCTCCCTCTTTTCGGTCTCTACGACACGTTTCTCTCTCCCCCTCCCTCTCCCCCTCCCTCTCGTTCCCTC
CCCTCGGCTAGCGTCTCTCTTCTTCTCCAAGAGGCTCTCGATTTGCATGGACAAGGGCCACCTCGGTGGTGGCGGAGGA
GGAGGAGGGCTGCTCGCTCTGGACGCGTCGCGCGGCAGCTTGGCTTCTTGAACCTTGCTTTTCGCCGCGCGCGTTCTCTC
AGGAACATGGAGGCGGACGACGCGGTGGCGGCGGCAGGGGCAGGAGGTCTATCGAGGTTGACTTCTTCTCCGACGAG
AAGAAGAACATGAAGAAGAGCCGGCTTCGGCCGCTGCCGACGCGGACGACCAGAAGGATCAGGCCTCCGCCGCCGGA

CTCGCCATCAAGAAGGAGGACCTCACCATTAACTCCTTTCCGGGAACAACACGAAGCGCGACCGGTCCATGGTAGTC
GACGACGACGGGGCGTCCCGGGCCGATGAGGACAGTAACGGCAGGAACACCGGCGAGCTCGCGGCGATGCAGGCCGAG
CTGAGCCGCATGAACGACGAGAACCAGCGGCTGCGAGGGATGTTGACCCAGGTCAATAACAGCTACCATGCGCTGCAG
ATGCATCTCGTCACGCTCATGCAGCAAAGGACCCAGATGCCTCCGGCCCCAACCGCAACAGCCTCCGACTCACGAGGAG
GGCAAGAACGAGAGTGCCATCGTGCCGAGGCAGTTCTGGGTCTGGGCCCCGTCCGGAGCCAGCGCTGAGGTGGCGGAA
GAGCCGTCCAACTCGTCCACGGAGGTGGGAGCCCCGCGCCGGTCTGTCATCCAACGGAAACGAGGACCCTGAGCGTGGC
GACAACCCAGACGGCCCCGTCCACCGCGGGGTGGTTGCCCGGACGCGGGATGACCCAGCAGCAGCAGCTGGGAGCGGCG
GCCAAGGGCCACGACCAGCAAGCCCAGGAGGCCACCATGAGGAAGGCCCGTGTCTCCGTTTCGCGCACGATCAGAAGCC
CCGATTATCGCCGATGGATGCCAATGGAGGAAGTACGGTCAGAAGATGGCGAAGGGAAACCCCTTGCCACGCGCCTAC
TACCGCTGCACCATGGCCACCGGCTGCCCGGTGCGCAAGCAGGTGCAACGATGCGCCGAGGACCGGACCATCCTCATC
ACCACGTACGAGGGCACGCACAACCACCCGCTCCCGCCGGCCGCCATGGCCATGGCGTCTACCACGTGCGCCGCGCGCG
TCCATGCTGCTCTCGGGCTCCATGCCCAGCGCCGACGGCGCGGGGCTCATGAGCTCCAACCTTCTCGCGCGCACCGTG
CTGCCGTGCTCGTCCAGCATGGCCACCATCTCGGCGTCCGCGCCGTTCCCGACTGTCACCCTCGACCTACCCACGCC
CCGCCGGGTGCGCCCAACGCCATGCCGCTAAACGTCGCCCCGACCGCATGCACCGGGGCGAGTTCCATGTTCCGATGCCC
GGCGGTGGGATGGCCCCGGCCTTCGCCATGCCCGCCGAGATGCTCTACAACAGTCGAAGTTCTCTGGTCTGCAGATG
TCCTCCGACTCGGTGGACGCCGGGCGAGTTTCGCGCAGCCTAGGCAGCCCATGGGCCTGCCAGGCCAGCTGTCCGACAGC
GTCAGTGACGCGGGCGTGCATCACCAGCAGACCCAACTTACGGTGGCGCTCGCCGCGGCAATCTCGTCCATCATG
GCCGGCCAGCACGCCGCCGGCAACAGCAACGCGAACAACAACACCACTAAGAACAACGTGACGACGACCAGTAAC
AACACGACGAGCAACAACACCAACAGCGAGACTCAATGA

SEQ ID NO: 40. Amino acid sequence of TaWRKY29-homolog from *Hordeum vulgare* (89.1% sequence identity to the amino acid sequence of TaWRKY29 shown in SEQ ID NO: 10) (length: 610 amino acid residues)

TSDSSLFRSLRHVSLSPSLSPSPRSLPSASVSLFSKRLSICMDKGHLGGGGGGGLLALDASPRQLGFLNLLSPAPFL
RNMEADDGGGGGRGRRSIEVDFFSDEKKNMKKSRASAGADADDQKDQASAAGLAIKKEDLTINLLSGNNTKRDRSMVV
DDDGASRAEDSNGRNTGELAA MQAELSRMNDENQRLRGLMTQVNNSYHALQMHLVTLMQORTQMPPAQPPQPPTHEE
GKNESAIVPRQFLGLGPSGASAEVAE EPSNSSTEVGSPRRSSNGNEDPERGDNPDGPSTAGWLPGRGMTQQQQLGAA
AKGHDQQAQEATMRKARVSVRARSEAPI IADGCQWRKYGQKMAKNPCPRAYYRCTMATGCPVRKQVQRC AEDRTILI
TTYEGTHNHPLPPAAMAMASTTSAASMLLSGSMPSADGAGLMSSNFLARTVLP CSSSMATISASAPFPTVTLDLTHA
PPGAPNAMPLNVARPHAPGQFHVPMPPGGMAPAFAMPPQMLYNQSKFSGLQMSDSVDAGQFAQPRQPMGLPGQLSDS
VSAAAAAITADPNFTVALAAAISSIMAGQHAAGNSNANNNTTKNNVTTTSNNTTSNNTNSETQ

FIGURE 13

SEQ ID NO: 41. Nucleic acid sequence of WRKY43 from *Triticum aestivum* (90.4% sequence identity to the nucleic acid sequence of TaWRKY39 shown in SEQ ID NO: 11) (length: 636 nucleotides)

ATGGACGAGCAGTGGATGATGGGGCAGACTTCCCTCAGCCTCGGCCTCAACGTCGGCCGGCCGACGGCGCCGCGGGGT
GCCCCCTCCGGTGACCAAGGTTCTCGTGGAGGAGGACTTCATGTCTCCAAGAAGAATCACGAGGTCGAGGCGCTGGAG
GCGGAGCTCCGGCGCGTGGGCGAGGAGAACAGGAGGCTTAGCGACATGCTCCGCGCGCTGGTGGCCAAGTACTGCGAC
CTGCAGGGCAGGGTCAGCGGCATGATGGCGGCGGCGGTGGCGGCCAACCAACCACAGTCACCCACGACATCTGAGGGC
GGCTCCGCGGCCCTCGCCGTCCAGGAAGCGCGCCCGCAGCGATAGCCCCGACACCGCCGTCCAGGAAGCGCGCCCTGCC
AGCGGCGGCTTCGCCGTGAGCGTCAACGTCGGCCCCGACCAGGCGGAGTGCACGTCCGTCCACGAGCCGTGCAACAGC
AAGCGCGTCCGCGCCGACGAGTGCANGGCCAGCAGGGTATCCAAGCTGTATGTCCACGCCGATCCCTCGGACCTCAGC
CTCGTCTGAAAGATGGGTACNCATGGCGAAAGTACGGGCAGAAGGTGACCCAAGAACAACCCTTTGCCCTGAGGGCT
ACTTCCGGGTGC

SEQ ID NO: 42. Amino acid sequence of WRKY43 from *Triticum aestivum* (87.2% sequence identity to the amino acid sequence of TaWRKY39 shown in SEQ ID NO: 12) (length: 212 amino acid residues)

MDEQWMMGQTSLSLGLNVGRPTAPRGAPPVTKVLVEEDFMSSKKNHEVEALEAELRRVGEENRRLSDMLRALVAKYCD
LQGRVSGMMAAAVAANNHQSPTTSEGGSAASPSRKRARSDSPDTAVQEARPASGGFAVSVNVGPDQAECTSVHEPCNS
KRVRADECXASRVSKLYVHADPSDLSLVKDGXWRKYGQKVTQEOPFALRATSGC

SEQ ID NO: 43. Nucleic acid sequence of WRKY79 from *Triticum aestivum* (90.7% sequence identity to the nucleic acid sequence of TaWRKY39 shown in SEQ ID NO: 11) (length: 660 nucleotides)

ATGGACGAGCAGTGGATGATCGGGCAGACTTCGCTGAGCCTCGGCCTCAACGTCGGCCGGCCGACGGCGCGGCGGGGT
GCCCCCTCCGGTGACCAAGGTTCTCGTGGAGGAGGACTTCATGTCTTCCAAGAAGAACACGAGGTCGAGGCGCTGCAG
GCGGAGCTCCGGCGCGTGGGCGAGGAGAACAGGAGGCTCAGCGACATGCTCCGCGCGCTCGTGGCCAAGTACTCCGAC
CTCCAGGGCAAGGTCAGCGGCATGATGGCGGCGGCGGCCGCGGCCAACCAACCACAGTCGTTGTCTACGTCTGAGGGC
GGCTCCGCGGCCCTCGCCCTCCAGGAAGCGCGCCCGCAGCGACAGCCTCGACACCGCCGGCCGCAATCCTTCGCCGCCG
CTCGCCGCGGCCGTGAGCATCAACGTCGTCCCCGACCAGGCGACAGGTGGAGTGCACGTCCGTCCATGAGCCGTGCAAC
AGCAAGCGCGTCCGAGCCGACGAGTGAAGGCCAGCAGGGTCTCCAAGCTCTACGTCCACGCCGACCCCTCCGACCTC
AGCCTCGTCTGTAAGGATGGGTACCAATGGCGGAAGTACGGGCAGAAGGTGACCAAGGACAACCCGTGCCCGAGGGCC
TACTTCCGGTGCTCGTTCGCGCCGTCTGTGCCAGGTG

SEQ ID NO: 44. Amino acid sequence of WRKY79 from *Triticum aestivum* (79.4% sequence identity to the amino acid sequence of TaWRKY39 shown in SEQ ID NO: 12) (length: 220 amino acid residues)

MDEQWMIGQTSLSLGLNVGRPTARRGAPPVTKVLVEEDFMSSKKNHEVEALQAEELRRVGEENRRLSDMLRALVAKYSD
LQGVSGMMAAAAAANNHQSLSLSTSEGGSAASPSRKRARSDSLDTAGRNPSPLAAAVSINVVPDRDQVECTSVHEPCN
SKRVRADECKASRVSKLYVHADPSDLSLVKDGXQWRKYGQKVTKDNPFCPRAYFRCSFAPSCQV

SEQ ID NO: 45. Nucleic acid sequence of WRKY79A from *Triticum aestivum* (99.7% sequence identity to the nucleic acid sequence of TaWRKY39 shown in SEQ ID NO: 11) (length: 657 nucleotides)

ATGGACGAGCAGTGGATGATGGGGCAGACTTCCCTCAGCCTCGGCCTCAACGTCGGCCGGCCGACGGCGCGGCGGGGT
GCCCCCTCCGGTGACCAAGATCCTCGTGGAGGAGGACTTCATGTCTCTCCAAGAAGAATCACGAGGTCGAGGCGCTGGAG
GCCGAGCTCCGGCGCGTGGGCGAGGAGAACAGGAGGCTCAGCGACATGCTCCGCGCGCTGGTGGCCAAGTACTCCGAC
CTTCAGGGCAGGGTCAGCGGCATGATGGCGGGCGGCGGCGCGGCCAACCAACCGCCAGTCACCCACGACGTCTGAGGGC
GGCTCCGCGGCCTCGCCGTCCAGGAAGCGCGCTCGCAGCGACAGTCCCGACACCGCAGTCCAGGAAGCGTACCCTGCC
AGCGGCGGCTTCGCCGTCCAGCGTCAACGTCGGCCCCGACCAGGCGGAGTGCACGTCCGTCCACGAGCCGGGCAACAGC
AAGCGCGTCCGCGCCGACGAGTGCAAGGCCAGCCGGGTCTCCAAGCTCTACGTCCACGCCGACCCCGCCGACCTCAGC
CTCGTGGTGAAGGATGGGTACCAATGGCGAAAGTACGGCAAGAAGGTGACCAAGGACAACCCATGCCCGAGGGCCTAC
TTCCGGTGCTCCTTCGCGCCGTCTGCCAGGTG

SEQ ID NO: 46. Amino acid sequence of WRKY79A from *Triticum aestivum* (90.0% sequence identity to the amino acid sequence of TaWRKY39 shown in SEQ ID NO: 12) (length: 219 amino acid residues)

MDEQWMGQTSLSLGLNVGRPTARRGAPPVTKILVEEDFMSSSKKNHEVEALEAELRRVGEENRRLSDMLRALVAKYSD
LQGRVSGMMAAAAAANNRQSPTTSEGGSAASPSRKRARSDSPDTAVQEAYPASGGFAVSVNVGPDQAECTSVHEPGNS
KRVRADCKASRVSKLYVHADPADLSLVVKDGYQWRKYGKKVTKDNPCPRAYFRCSFAPSCQV

SEQ ID NO: 47. Nucleic acid sequence of TaWRKY39-homolog from *Secale cereale* (88.6% sequence identity to the nucleic acid sequence of TaWRKY39 shown in SEQ ID NO: 11) (length: 687 nucleotides)

ATGGACGAGCAGTGGATGATCGGGCAGACTTCCCTCAGCCTCGGCCTTAACATCGCCCGGCCGACGGCGCGGCTAGGT
GCTCCCCCGGTGACCAAGGTCTCTCGTGGAGGAGGACTTCATGTCTCTCAGGAAGAATCACGAGGTCGAGGCACTGGAG
GCGGAGCTCCGGCGAGTGGGCGAGGAGAACCGGAGGCTCAGCGACATGCTCCGCGCGCTGGTGGCCAAGTACGCTGAC
CTGCAGGGCAAGGTCAGCGGCATGATGGCGGGCGGCGTCAGCCGCTGCCAACCAACCGCCAGTCGTCCACCACGTCTGAG
GGCGGCTCCGCGGCCCTCGCCGTCCAGGAAGCGCGCCCGCAGCGACAGCCTCGACACCGCCGGCCGCAATCCTTCGCCG
CCGCTCGCCCGCGGCCGCAAGTGGCGGCTTCGCCGTCCAGCGTCAACGTCAACGTCCGCCCCGACCGCGATCAGGCGGAG
TGCACGTCCGTTACGAGCACGGCAACAGCAAGCGTGTCCGCGCCGACGAGTGCAAGGCCAGCAGGGTCTCAAAGCTC
TACGTCCACGCCGACCCCTCCGACCTCAGCCTCGTCTGAAGGATGGGTACCAATGGCGAAAGTACGGGCAGAAGGTG
ACCAAGGACAACCCGTGCCCGAGGGCCTACTTCCGGTGCTCGTTTCGCGCCGTCTGTGCCAGGTG

SEQ ID NO: 48. Amino acid sequence of TaWRKY39-homolog from *Secale cereale* (79.2% sequence identity to the amino acid sequence of TaWRKY39 shown in SEQ ID NO: 12) (length: 229 amino acid residues)

MDEQWMIGQTSLSLGLNIARPTARLGAPPVTKVLVEEDFMSSSRKNHEVEALEAELRRVGEENRRLSDMLRALVAKYAD
LQGVSGMMAAASAAANNRQSSTTSEGGSAASPSRKRARSDSLDTAGRNPSPLAAAASGGFAVSVNVNVPDRDQAE
CTSVHEHGNSKRVRADCKASRVSKLYVHADPSDLVLVKDGYQWRKYGQKVTKDNPCPRAYFRCSFAPSCQV

SEQ ID NO: 49. Nucleic acid sequence of TaWRKY39-homolog from *Hordeum vulgare* (88.0% sequence identity to the nucleic acid sequence of TaWRKY39 shown in SEQ ID NO: 11) (length: 684 nucleotides)

ATGGACGAGCAGTGGATGATGGGGCAGACTTCCCTCAGCCTCGGCCTCAACGTGGGCCGGCCGACGGCGCGGGGAGGG
GGTCCCTCCGGTGCCGTCCAAGGTGCTCGTGGAGGAGGACTTCATGTCCTCCAAGAAAAGCCACGAGGTTCGAGGCGCTG
GAGGCGGAGCTCCGGCGTGTGGGCGAGGAGAACAGGAGGCTGGGCGACATGCTCCGCGCGCTGGTGGTAAAGTACTCC
GACCTGCAGGGCAAGGTCAGCGGCATGATGGCGGCGGCGGCGGCCAATAACCACCAGTCGTTGACGTTGACTACGTCT
GAGGGCGGCTCCGCGGCCTCGCCGTCCAGGAAGCGCGCCCGTAGCGACAGCCTCGACACCGCCGGCCGCAATCCTTCG
CCTCCGCTCGCCGCGGCCGCCACCGGCGGCTTCGCCATCAGCGTCAACGTTCGGCCCCGGCCGCGACACGAGGCGGAGTGC
ACGTCCGTCCACGAGCCGTGCAACAGCAAGCGCGTCCGCGCCGACGAGTGCAAGGCCAGCAGGGTCTCCAAGCTCTAC
GTCCACGCCGACCCCTCCGACCTCAGCCTCGTGGTGAAGGATGGGTACCAATGGCGGAAGTACGGGCAGAAGGTGACC
AAGGACAATCCGTGCCCCGAGGGCCTACTTCCGGTGCTCGTTCGCGCCGTATGCCAGGTG

SEQ ID NO: 50. Amino acid sequence of TaWRKY39-homolog from *Hordeum vulgare* (77.5% sequence identity to the amino acid sequence of TaWRKY39 shown in SEQ ID NO: 12) (length: 228 amino acid residues)

MDEQWMMGQTSLSLGLNVGRPTARGGGPPVPSKVLVEEDFMSSKKSHEVEALEAELRRVGEENRRRLGDMRLRALVVKYS
DLQGVSGMMAAAAANNHQLTLTTSEGGSAASPSRKRARSDSLDTAGRNPSPLAAAATGGFAISVNVGPGRDQAEC
TSVHEPCNSKRVRADCKASRVSKLYVHADPSDLSLVVKDGYQWRKYGQKVTKDNPCPRAYFRCSFAPSCQV

FIGURE 14

SEQ ID NO: 51. Nucleic acid sequence of WRKY53 from *Triticum aestivum* (92.1% sequence identity to the nucleic acid sequence of TaWRKY53b shown in SEQ ID NO: 13) (length: 1,233 nucleotides)

ATGTCCTCCTCCACGGGGAGCTTGGACCACGCAGGGTTCACGTTACGCCGCCGCCGTTTCATCACGTCTTCACCGAG
CTTCTGTCGGGGTCCGGCGCCGGCGACGCGGAGCGGTTCGCCGAGGGGGTTCAACCGAGGGGGCCGGGCGGGGCGCCC
AAGTTCAAGTCCGCGCAGCCGCCAGCCTGCCCATCTCGTCGCCCTTCTCCTGCTTCTCCGTCCCTGCAGGTCTCAGC
CCTGCCGAGCTGCTCGACTCCCCCGTTCTCCTCAACTACTCTCACATCTTGGCGTCTCCGACTACGGGTGCGATCCCT
GCGCAGAGGTGCGACTGGCAGGCGAGCGCCGATCTGAACACCTTTTTCAGCAGGATGAGCTCGGCCCTCTCTGGCTTCTCC
TTTTCACGCAGTCAAGTCCAACGCCACGGTCAACGCTCAAGTAACTACTTACCTTTTATTCAAGGAGCAGCAGGAGCAA
CAACAAGAAGAAGTGGTTCAAGTGAGCAACAAGAGCAGCAGCAGCAGCGGCAACAACAAGCAGGTTGAGGACGGATAC
AATTGGAGGAAGTACGGGCAGAAGCAAGTTAAGGGGAGCGAGAACCCGCGGAGCTACTACAAGTGCACCTACAACAAT
TGCTCCATGAAGAAGAAAGTGGAGCGCTCTCTCGCCGACGGCCGCATCACGCAGATCGTCTACAAGGGCGCACATGAC
CACCCGAAGCCCCCTCTCCACGCGCCGCAACTCCTCCGGCTGCGCGCGGTCGTTGCGGAGGATCATAACACGGCTCG
GAGCACTCTGGCCCGACGCCCGAGAATTTCATCCGTCACTTTTCGAGACGATGAGGCCGACAAGCCCGAGACCAAGCGC
CGGAAGGAGCATGGTGACAACGAGGGCAGTTTTCAGGCGGCACCGCGGCTGCGGGAAGCCCGTGC GCGAGCCAGGCTC
GTGGTGCAGACGCTGAGCGATATAGACATACTCGACGACGGCTTCCGGTGGAGGAAGTACGGGCAGAAGGTTGTCAAG
GGCAATCCCAACCCAGGAGCTACTACAAGTGCACAACGGTGGGCTGCCCGGTGCGCAAGCATGTGGAGCGGGCCTCG
CACGACAACCGCGCGGTGATCACCACCTACGAGGGCCCCGTGCACCCTCGAGATGCTCGCCGGACACCCAGGCTACGC
GGCCAAGGACGAGCCCCGGGACGACATGTTTCGTGAGTCGCTCCTCTGCTAGCTAGGCAGGCT

SEQ ID NO: 52. Amino acid sequence of WRKY53 from *Triticum aestivum* (86.1% sequence identity to the amino acid sequence of TaWRKY53b shown in SEQ ID NO: 14) (length: 411 amino acid residues)

MSSSTGSLDHAGFTFTPPPFITSFTELLSGSGAGDAERSPRGFNRRGRAGAPKFKSAQPPSLPISSPFSCFSVPAGLS
PAELLDSPVLLNYSHILASPTTGAI PAQRCDWQASADLNTFQQDELGLSGFSFHAVKSNATVNAQVNYLPLFKEQQEQ
QQEEVVQVSNKSSSSSGNNKQVEDGYNWRKYGQKQVKGSENPRSYKCTYNNCSMKKKVERSLADGRITQIVYKGAHD
HPKPLSTRNNSGCAAVVAEDHTNGSEHS GPTPENSSVTFGDDEADKPETKRRKEHGDNEGSSGGTGGCGKPVREPR
LVQTLSDIDILDDGFRWRKYGQKVVKGNPNPRSYKCTTVGCPVRKHVERASHDNRAVITTYEGPVHPRDARRTPRLR
GQGRAPGRHVRRVAPLLARQA

SEQ ID NO: 53. Nucleic acid sequence of WRKY53A from *Triticum aestivum* (87.7% sequence identity to the nucleic acid sequence of TaWRKY53b shown in SEQ ID NO: 13) (length: 1,416 nucleotides)

ATGTCCTCCTTCACGGGGAGCTTGGACCACGCAGGGTTCACGTTACGCCGCCGCCGTTTCATCACGTCTTGACTGAG
CTTCTATCAGGGTCTGGCGCCGGCGACGTGGAGGGGTTCGCCAAGGGGGTTCAACCGAGGGGGTTCGACCGGGGTGCCC
AAGTTCAAGTCCGCGCAGCCGCCAGCCTGCCCATCTCGTCGCCAGCGTCGCCCTTCTCCTGCTTCTCCATCCCTGCA
GGTCTCAGCCCTGCTGAGCTGCTCCACTCTCCGTTCTCCTCAACTACTCTCATATATTGGCGTCTCCGACTACAGGT
GCGATCCCTGCGCGGAGATACGACTGGCAGGCGAGCGCCGATCTGAACACCTTTTCAGCAGGATGAGGTGCGCCGTGGA
GACAGCGCCCTTTTGGCTTCTCCTTTTCACGCAGTGAAGCCCAACGCCACGGTCAACGCTCAAACAAATTACTTACCT
TTATTCAAGGAACATCAGCAGCAGCAGCAACAACAAGTGGTAGAAGTGAGCAACAAGAGCAGCAGCGGCGACAAC
AACAAGCAGGTTGAGGACGGATACAATTGGAGGAAGTACGGGCAGAAGCAAGTTAAGGGCAGCGAGAACCCGCGGAGC
TACTACAAGTGCACCTACAACAATTGCTCCATGAAGAAGAAAGTGAACGCTCTCTTGCAGACGGCCGCATCACGCAG
ATTGCTCTACAAGGGCGCGCATGATACCCGAAGCCCCCTCCACGCGCCGCAACTCCTCCGGCTGTGCGGCGGTCATT
GCGGAGGATCATAACACGGCTCGGAGCACTCTGGCCCGACGCTGAGAATTTCATCCGTACATTTCGGAGACGATGAG
ACCGACAATGGCGCTGAGCCTGAGACCAAGCGCCGGAAGGAGCACGGTGACAACGAGGGCAGTTTCGGGTGGCACCGGC

GCCTGCGTGAAGCCCGTGC GCGAGCCCAGGCTTGTGGTGCAGACGCTGAGCGATATAGACATACTCGACGACGGCTTC
CGGTGGAGGAAGTACGGGCAGAAGGTTGTCAAGGGCAATCCCAACCCAGGAGCTACTACAAGTGACAACGGTGGGT
TGCCCGGTGCGCAAGCACGTGGAGCGGGCCTCGCACGACAACCGCGCGGTGATTACCACCTACGAGGGTAGGCACAGC
CACGACGTGCCGGTCCGCGAGGGGGGCGGTGCTAGCCGCGCGCTGCCGACGTCTGCTTCTCCTCCGACAGCTCGGTGCTC
GTCTGTCTGCCGCCGCCGGGCGAGGCCCCGTACACCCTCGAGATGCTCGCCAACCCTGCCGCCGGACACCGAGGCTAC
GCGGCCAAGGACGAACCCCGGGGCGGCGCCTTCCAGCGCACCAAGGACGAGCCCCGGGACGACATGTTTCGTGAGTCG
CTCCTCTGCTAG

SEQ ID NO: 54. Amino acid sequence of WRKY53A from *Triticum aestivum* (85.2% sequence identity to the amino acid sequence of TaWRKY53b shown in SEQ ID NO: 14) (length: 471 amino acid residues)

MSSFTGSLDHAGFTFTPPPFITSLTELLSGSGAGDVEGSPRGFNRGGRTGVPKFKSAQPPSLPISSPASPFSCFSIPA
GLSPAELLHSPVLLNYSHILASPTTGAI PARRYDWQASADLNTFQQDEVGRGDSGLFGFSFHAVKPNATVNAQTNYLP
LFKEHQQQQQQQVVEVSNKSSSGDNNKQVEDGYNWRKYGQKQVKGSENPRSYKCTYNNCSMKKKVERS LADGRITQ
IVYKGAHDHPKPPSTRNSSGCAAVIAEDHTNGSEHS GPTPENSSVTFGDDETNGAEPETKRKRKEHGDNEGSSGGTG
ACVKPVREPRLVQTLSDIDILDDGFRWRKYGQKVKGNPNPRSYKCTTVGCPVRKHVERASHDNRAVITTYEGRHS
HDVPVGRGAGASRALPTSSSDSSVVVCPAAAGQAPYTLEMLANPAAGHRGYAAKDEPRGGAFFQRTKDEPRDDMFVES
LLC

SEQ ID NO: 55. Nucleic acid sequence of TaWRKY53B-homolog from *Secale cereale* (83.9% sequence identity to the nucleic acid sequence of TaWRKY53B shown in SEQ ID NO: 13) (length: 1,410 nucleotides)

ATGTCGTCCTCCTCCACAGGGAGCTTGGACCACGTAGGGTTACCTTCACGCCGCCGCGTTCATCACGTCCTTACC
GAGCTTCTGT CAGGGTGTGGCGCCGGCGACATGGAGCGGTTCAACCGAGGGGTCGGGCCGGGGCGCCCAAGTTCAAG
TCGGCGCAGCCGCCAGCCTGCCCATCTCGCCGCCCTTCTCCTGCTTCTCCATCCCTGCAGGTCTCAGCCCTGCTGAG
CTGCTCGACTCTCCCGTTCTCCTCAACTACTCTCATATCTTGGCGTCTCCGACTACAGGTGCGATCCCTGCGCAGAGA
CAGAGATACGACTGGCAGGCGAGCGCCGATCTCAACACCTTTCAGCAGCAGGATGAGCTCTGCCGAGGAGTGTGTTGTGCAGGAG
CTCTTTGGCTTCTCCTTTACGCAGTCAAGTCCAACGCCACAGTCATGAGCTCTGCCGAGGAGTGTGTTGTGCAGGAG
CAGCAACAACAACAAGAAGTGGTAGAAGTGAGCAACAACAGCAGCAGCGGCAACAACAACAGCAGGTTGAGGAC
GGATACAAC TGGAGGAAGTACGGACAGAAGCAAGTCAAGGGGAGCGAGAACCCGCGGAGCTACTACAAGTGCACCTAC
AACAAATTGCTCCATGAAGAAGAAAGTGAACGCTCTCTTGGCGACGGCCGCATCACGGAGATTGTGTACAAGGGCGCG
CATGACCACCCCAAGCCCTCTCCACGCGCCGCAACTCCTCCTCCGGCTGTGCGGCGGCGGTGCTTGCAGGATCAT
GCCAACGGCTCGGAGCACTCCGGCCCGACGCCCGCAATTTCATCTGTCACTTTCGAGACGATGAGGCCGACAACGGG
TTGCAGCTCAGTGATGGGGCTGAGCCCGAGGCCAAGCGCCGGAAGGAGCATGGTGACAACAACGAGGGCAGTTCAGGT
GGCACC GGCGGCGGTGCGGGAAGCCCGTGC GCGAGCCCAGGCTTGTGGTGCAGACGCTGAGCGATATAGACATACTC
GACGACGGCTTCCGGTGGAGGAAGTACGGGCAGAAGGTTGTCAAGGGCAATCCCAACCCAGGAGCTACTACAAGTGC
ACAACGGTGGGTTGTCCGGTGC GCAAGCATGTGGAGCGGGCCGCGCACGACAACCGCGCGGTGATCACACCTACGAG
GGTAAGCACAACCACGACATGCCGGTCCGGCCGGGTGCCGGTGCCAGCCGGGCGCTGCCGACGTCATCTTCTCCTCGGAC
AGCTCGGTGCTAACC TGGCCTGCCGCCGTGCAGGCCCGGTACACCCTCGAGATGCTCACC AACCCTGCCGCCGGCCAC
CGAGGCTATGCAGCCGGCGGCGCCTTCCAGCGCACCAAGGACGAGCCCCGGGACGACATGTTTCGTGAGTCGCTCCTC
TGCTAG

SEQ ID NO: 56. Amino acid sequence of TaWRKY39-homolog from *Secale cereale* (82.8% sequence identity to the amino acid sequence of TaWRKY53B shown in SEQ ID NO: 14) (length: 469 amino acid residues)

MSSSSTGSLDHVGF TFTPPPFITSTTELLSGCGAGDMERFNRGGRAGAPKFKSAQPPSLPISPPFSCFSIPAGLSPA
ELDSPVLLNYSHILASPTTGAI PAQRQRYDWQASADLNTFQQQDELRCGDSGLFGFSFHAVKSNATVMSSAEELFVQE
QQQQQQEVVEVSNSSSGNNNKQVEDGYNWRKYGQKQVKGSENPRSYKCTYNNCSMKKKVERS LADGRITEIVYKGA

HDHPKPLSTRNSSSGCAA VVAEDHANGSEHSGPTPANSSVTFGDDEADNGLQLSDGAEPEAKRRKEHGDNNEGSSG
GTGGGCGKPVREPRLVVQTLSDIDILDDGFRWRKYGQKVVKGNPNPRSYKCTTVGCPVRKHVERAAHDNRAVITTYE
GKHNHDMPVGRGAGASRALPTSSSSDSSVVTWPAAVQAPYTLEMLTNPAAGHRGYAAGGAFQRTKDEPRDDMFVESLL
C

FIGURE 15

SEQ ID NO: 57. Nucleic acid sequence of WRKY9 from *Triticum aestivum* (94.1% sequence identity to the nucleic acid sequence of TaWRKY68A shown in SEQ ID NO: 15) (length: 948 nucleotides)

ATGGCCGTGGACCTCATGGGCTGCTACACCCCTCGCCGCGCCGACGACCAGCTCGCCATCCAGGAGGCCGCCACCGCC
GGCCTCCGCAGCCTGGAGCTCCTCGTCTCCTCCCTCTCCGGCGCGGCGCCGTCCAAGGCGCCGACGAGCACCCGCAG
CAGCCGTTCCGGCGAGATCGCCGACCAGGCCGTCTCCAAGTTCGCAAGGTGATCTCCATCCTCGACCGCACCCGGCCAC
GCCCCGTTCCGCCGCGGCCCGCTCCAGTCGCCTACCCCGCCTCCTCCGGCTCCGGTCGCTCCTCCGCCGCCCCACCG
CGCCCTCTGGCCGTCGTCGAGCCGCCAGGCCCGCTCCCTTGACCGTCGTGGCGCCGGTGTCTGGTGGCCGCCCCGGTC
CCGCAGCCCGAGAGCCTGACGCTGGACTTCACCAAGCCGAACCTGACCATGTCTGGGCGCGACGTCCGTCACGTCCACG
TCCTTCTTCTCGTCTGGTGACCGCCGCGGAGGGCAGCGTGTCCAAGGGCCGACGCTGGTCTCCGCCGCAAGCCGCCG
CTGTCCGGGCACAAGAGAAAGCCCTGCGCCGCGCGCACTCGGAGGCCAACACCACCGGCAGCCGATGCCACTGCTCC
AAGAGAAGGAAGAACC GCGTGAAGACGACGGTGAGGGTGCCCGCGGTGAGCGCGAAGATCGCCGACATCCCGCCGGAC
GAGTACTCGTGGAGGAAGTACGGCCAGAAGCCCATCAAGGGATCCCTTACCCACGGGGTACTACAAGTGCAGCACAG
TGCGGGGGTGCCCGGCGCGGGAAGCACGTGGAGCGCGCCCTGGACGACCCGGCGATGCTGGTGGTGACCTACGAGGGC
GGAGCACCGCCACTCGCCGGGGCCGATGCCGATGCAGATGGCGCCGTCGCCTATGCCGATGCCGATGGGCGCTCCCGT
CGCCGTAGCTAG

SEQ ID NO: 58. Amino acid sequence of WRKY9 from *Triticum aestivum* (80.4% sequence identity to the amino acid sequence of TaWRKY68A shown in SEQ ID NO: 16) (length: 315 amino acid residues)

MAVDLMGCTPRRADDQLAIQEAATAGLRSLLELLVSSLGSAAPSKAPQQHPQQPFGEIADQAVSKFRKVISILDRTGH
ARFRRGPVQSPTPPPPAPVAPPPPPRPLAVVEPARPAPLTVVAPVSVAAPVPQPQSLTLDFTKPNLMSGATSVTST
SFFSSVTAGEGSVSKGRSLVSAGKPPLSGHKRKPACAGAHSEANTTGSRCHCSKRRKNRVKTTVRVPAVSAKIADIPPD
EYSWRKYGQKPIKGSPPYRGTTSAAQCGGARRGKHVERALDDPAMLVVTYEGGAPPLAGADADADGAVAYADADGRSR
RRS

SEQ ID NO: 59. Nucleic acid sequence of WRKY68 from *Triticum aestivum* (99.0% sequence identity to the nucleic acid sequence of TaWRKY68A shown in SEQ ID NO: 15) (length: 987 nucleotides)

ATGGCCGTGGACCTCATGGGCTGCTACACCCCTCGCCGCGCCGACGACCAGCTCGCCATCCAGGAGGCCGCCACCGCC
GGCCTCCGCAGCCTGGAGCTCCTCGTCTCCTCCCTCTCCGGCGCGGCGCCGTCCAAGGCGCCGACGAGCACCCGCAG
CAGCCGTTCCGGCGAGATCGCCGACCAGGCCGTCTCCAAGTTCGCAAGGTGATCTCCATCCTCGACCGCACCCGGCCAC
GCCCCGTTCCGCCGCGGCCCGCTCCAGTCGCCTACCCCGCCTCCTCCGGCTCCGGTCGCTCCTCCGCCGCCCCACCG
CGCCCTCTGGCCGTCGTCGAGCCGCCAGGCCCGCTCCCTTGACCGTCGTGGCGCCGGTGTCTGGTGGCCGCCCCGGTC
CCTCTCCCGCAGCCGAGAGCCTGACGCTGGACTTCACCAAGCCGAACCTGACCATGTCTAGGCGCGACGTCCGTGACG
TCCACGTCTCTTCTCTCGTCTGGTGACCGCCGGCGAGGGCAGCGTGTCCAAGGGCCGACGCTGGTCTCCGCCGCAAG
CCGCCGCTGTCCGGGCACAAGAGAAAGCCGTGCGCCGCGCGCACTCGGAGGCCAACACCACCGGCAGCCGATGCCAC
TGCTCCAAGAGAAGGAAGAACC GCGTGAAGACGACGGTGAGGGTGCCCGCGGTGAGCGCGAAGATCGCCGACATCCCG
CCGGACGAGTACTCGTGGAGGAAGTACGGCCAGAAGCCCATCAAGGGATCCCTTACCCACGGGGTACTACAAGTGC
AGCACAGTGGCAGGGGGCCCGGCGCGGAAGCACGTGGAGCGCCCCCTGGACGACCCGGCGATCCTGGTGGTGACGTAC
GAGGGCGAGCACCGCCACTCCCGGGGGCCGATGCCGATGCAGATGGCGCCGTCGCCGGTGCCGATTCCGATGCCGATG
GGCGCGCCCGTAGCCGTAGCTAGTGTGTCCGCCGGCAACGGGCACGTCTGA

SEQ ID NO: 60. Amino acid sequence of WRKY68 from *Triticum aestivum* (97.6% sequence identity to the amino acid sequence of TaWRKY68A shown in SEQ ID NO: 16) (length: 328 amino acid residues)

MAVDLMGCYTPRRADDQLAIQEAAATAGLRSLLELLVSSLGAAPSKAPQQHPQQPFGEIADQAVSKFRKVISILDRTGH
ARFRRGPVQSPTPPPPAPVAPPPPPRPLAVVEPARPAPLTVVAPVSVAAPVPLPQPQSLTLDFTKPNLTMSGATSVT
STSFFSSVTAGEGSSVSKGRSLVSAGKPPLSGHKRKPACAGAHSEANTTGSRCHCSKRRKNRVKTTVRVPAVSAKIADIP
PDEYSWRKYGQKPIKGSYPYRGYYKCSTVRGGPARKHVERPLDDPAILVVTYEGEHRHSPGPMQMAMAPSPVPIPMMPM
GAPVAVASVSAGNGHV

SEQ ID NO: 61. Nucleic acid sequence of WRKY68C from *Triticum aestivum* (88.8% sequence identity to the nucleic acid sequence of TaWRKY68A shown in SEQ ID NO: 15) (length: 945 nucleotides)

ATGGCCGTGGACCTCATGGGCTGCTACACCCCTCGCCGCGCCGACGACCAGCTCGCCATCCAGGAGGCCGCCACCGCC
GGCCTCCGCAGCCTGGAGCTCCTGGTCTCCTCCCTCTCCGGCGCGGCGCCGTCCAAGGCGCCCCAGCAGCACCCGCAG
CAGCCGTTCCGCGAGATCGCCGACCAGGCCGTCTCCAAGTTCGCAAGGTGATCTCCATCCTCGACCCGACCCGGTCAC
GCCCCGTTCCGCGCGCGCCCCGTCCAGTCGGCGCCGCGCCGCCGCTCCTCCAGCACCCGGTCGCTCCACCTCCTCCC
CCACCTTTGACCGTCGTGGCGCCGGTGTGGTGGCCGCCCGCTCCCGCAGCCGCAGAGCCTGACGCTGGACTTCACC
AAGCCGAACCTGACCATGTCTGGGCGCGACGTCCGTGACATCCACGTCTTCTTCTCTTCCGTGACCGCCGGCGAGGGC
AGCGTGTCCAAGGGCCGGAGCCTGGTCTCCGCCGGCAAGCCGCCGCTGTCCGGGCACAAGAGAAAGCCCTGCGCCGGC
GCGCACTCCGAGGCCAACACCACCGGCAGCCGATGCCACTGCTCCAAGAGAAGGAAGAACCAGCGTGAAGACAACGGTG
AGGGTGCCGGCGGTGAGCGCGAAAATCGCCGACATCCCGCCGACGAGTACTCGTGGAGGAAGTACGGCCAGAAGCCC
ATCAAGGGATCCCCTTACCCACGGGGGCTACTACAGTGCAGCACAGTGCAGGGGTGCCCTGCCCGGAAGCACGTGGAG
CGCGCCCTGGACGACCCGCCGATGCTGGTGGTGAATTACGAGGGCGTCGCACGCCACTCGCCGGGGCCGATGCCGATG
CAGATTGCGCGCTCGCCGATGCCAATGCGATGGGCGCTCCGTAGCCGTGCTAGTGTGTCCGCGGGCACGGGCAGTCTG
ACTAGTTAA

SEQ ID NO: 62. Amino acid sequence of WRKY68C from *Triticum aestivum* (85.5% sequence identity to the amino acid sequence of TaWRKY68A shown in SEQ ID NO: 16) (length: 314 amino acid residues)

MAVDLMGCYTPRRADDQLAIQEAAATAGLRSLLELLVSSLGAAPSKAPQQHPQQPFGEIADQAVSKFRKVISILDRTGH
ARFRRGPVQSAPPPPPPPAPVAPPPPPPLTVVAPVSVAAPLPQPQSLTLDFTKPNLTMSGATSVTSTSFFSSVTAGEG
SVSKGRSLVSAGKPPLSGHKRKPACAGAHSEANTTGSRCHCSKRRKNRVKTTVRVPAVSAKIADIPDEYSWRKYGQKPI
KGSYPYRGLLQCS TVRGC PARKHVERALDDPMLVVTYEGVARHSPGPMPMQIAASPMPMRWALRSRASVSAGTGSL
TS

SEQ ID NO: 63. Nucleic acid sequence of TaWRKY68A-homolog from *Secale cereale* (94.1% sequence identity to the nucleic acid sequence of TaWRKY68A shown in SEQ ID NO: 15) (length: 978 nucleotides)

ATGGCCGTGGACCTCATGGGCTGCTACACCCCTCGCCGCGCCGACGACCAGCTCGCCATCCAGGAGGCCGCCACCGCC
GGCCTCCGCAGCCTGGAGCTCCTGGTCTCCTCCCTCTCCGGCGCGGCGCCGTCCAAGGCGCCGAGCAGCACCCAGCAG
CAGTTCGCGGAGATCGCCGACCAGGCCGTCTCCAAGTTCGCAAGGTGATCTCCATCCTCGACCCGACCCGGACACGCC
CGCTTCCGCCGCGGCCCGTCCAGTCCCGCCGCGCCGCTCCTCCTCCAGCTCCGGTCGCTCCTCCCCGCCACACCG
CGCCCTCTGGCCATCGAGCCAGCCAGGCCGCTCCCTTGACCGTCGTGGCGCCGGTGTGGTGGCCGCCCGCCGGTCCCG
CAGCCGAGAGCCTGACGCTGGACTTCACCAAGCCGAACCTGACCATGTCTGGGCGCGACGTCCTGTCGAGCCGCGCTG
TTCTTCTCGTTCGGTGACCGCCGGCGAGGGCAGCGTGTCCAAGGGCCGAGCAGCTGGTCTCCGCGGCAAGCCCGCGCTG
TCCGGGCACAAGAGAAAGCCCTGCGCGGGCGCGCACTCGGAGGCCAACACCACGGGCAGCCGATGCCACTGCTCCAAG
AGAAGGAAGAACCAGGTGAAGACGACGGTGAGGGTGCCGCGCGTGAGCGCGAAGATCGCCGACATCCCGCGGACGAG
TACTCGTGGAGGAAGTACGGGCAGAAGCCCATCAAGGGATCCCCATACCCACGGGGCTACTACAAGTGCAGCACCGTG

CGAGGGTGCCCGGCCCGGAAGCACGTGGAGCGCGCCCTGGACGACCCGGCGATGCTGGTGGTGACCTACGAGGGCGAG
CACCGCCACTCGCCGGCGCCGATGCCGATGCCGATGCAGATGGCCCCGTCGCCGGTGCCGATGCCGATGGGCGCTCCC
GTAGCCGTAGCTAGTGTGTCCGCCGGCAACGGGCACGTCTGA

SEQ ID NO: 64. Amino acid sequence of TaWRKY68A-homolog from *Secale cereale* (93.9%
sequence identity to the amino acid sequence of TaWRKY68A shown in SEQ ID NO: 16) (length:
325 amino acid residues)

MAVDLMGCYTPTRRADDQLAIQEAAATAGLRSLLELLVSSLGAAPSKAPQQHQQQFGEIADQAVSKFRKVISILDRTGHA
RFRRGPVQSPPPPPPAPVAPPPPPRPLAIEPARPAPLTVVAPVSVAAPVPQPQSLTLDFTKPNLTMSGATSVTSTS
FFSSVTAGEGSVSKGRSLVSAGKPPLSGHKKRKCAGAHSEANTTGSRCHCSKRRKNRVKTTVRVPAVSAKIADI PADE
YSWRKYGQKPIKGSFYPRGYKCVTRGCPARKHVERALDDPAMLVVTYEGEHRHSPAPMPMPMQMAPSPVPMMPMGAP
VAVASVSAGNGHV

FIGURE 16**SEQ ID NO: 65. Nucleic acid sequence of fragment A from TaWRKY10 for WRKY gene silencing (97 nucleotides)**

actgaactgagctactgatcgatcagtagctgtagctgtggtagttttatgatcgattacggttcagaaatct
cacggatgcatgtacacga

SEQ ID NO: 66. Nucleic acid sequence of fragment A from TaWRKY13/46 for WRKY gene silencing (164 nucleotides)

ggtcacttacttcaaccatcactcgaggaggcggtgtccatctgcttcgggtcgcatgccacggcgagcagccgac
attcctaacgtcgccgggcacactgcagtcaccagcgagcacaaccaaccaacagaacgacagaggcgcttacgggtca
ccagtttc

SEQ ID NO: 67. Nucleic acid sequence of fragment B from TaWRKY13/46 for WRKY gene silencing (174 nucleotides)

cttacgggtcaccagtttcagtggacagacacatcacggtcggcaggcgatgccccagtcagatggagaccgacagtc
tcgccggaacaggcgcttcgtctggcgctgctagcggccatgctctgtcgaggacactgctgccgatcggccagtcga
gatgcatcgagtactttc

SEQ ID NO: 68. Nucleic acid sequence of fragment A from TaWRKY19 for WRKY gene silencing (99 nucleotides)

ttggtccccgtgtcttctttaccgaccacggtggtggctcgcgaaagaaagaaacacaaattcgattggttcttc
ggtgacgggctgttattgctc

SEQ ID NO: 69. Nucleic acid sequence of fragment B from TaWRKY19 for WRKY gene silencing (83 nucleotides)

tgctctgtttgctgtatattccccactccagtaataactcttgcatatgcagaaattgtaactgttgaaatgatggg
tggtc

SEQ ID NO: 70. Nucleic acid sequence of fragment A from TaWRKY29 for WRKY gene silencing (105 nucleotides)

tgttgtagccgtacaaacataattgagacaatgttttcattgtcagtagttgttttaggaggaaaacatcttggttt
tggataatggaaatcgaagagggtgct

SEQ ID NO: 71 Nucleic acid sequence of fragment A from TaWRKY53B for WRKY gene silencing (70 nucleotides)

ccgcggcccttcgttccccctgtggcgtttacatgtgggtccacgtgtacaatataatagatgctacatg

SEQ ID NO: 72. Nucleic acid sequence of fragment A from TaWRKY68A for WRKY gene silencing (80 nucleotides)

ttcgttcgctcgcaatctgtctgatgtccgtgtaaagaagaagaaagatcgtagagagacggagaggggaaacttaatg
cc

FIGURE 17

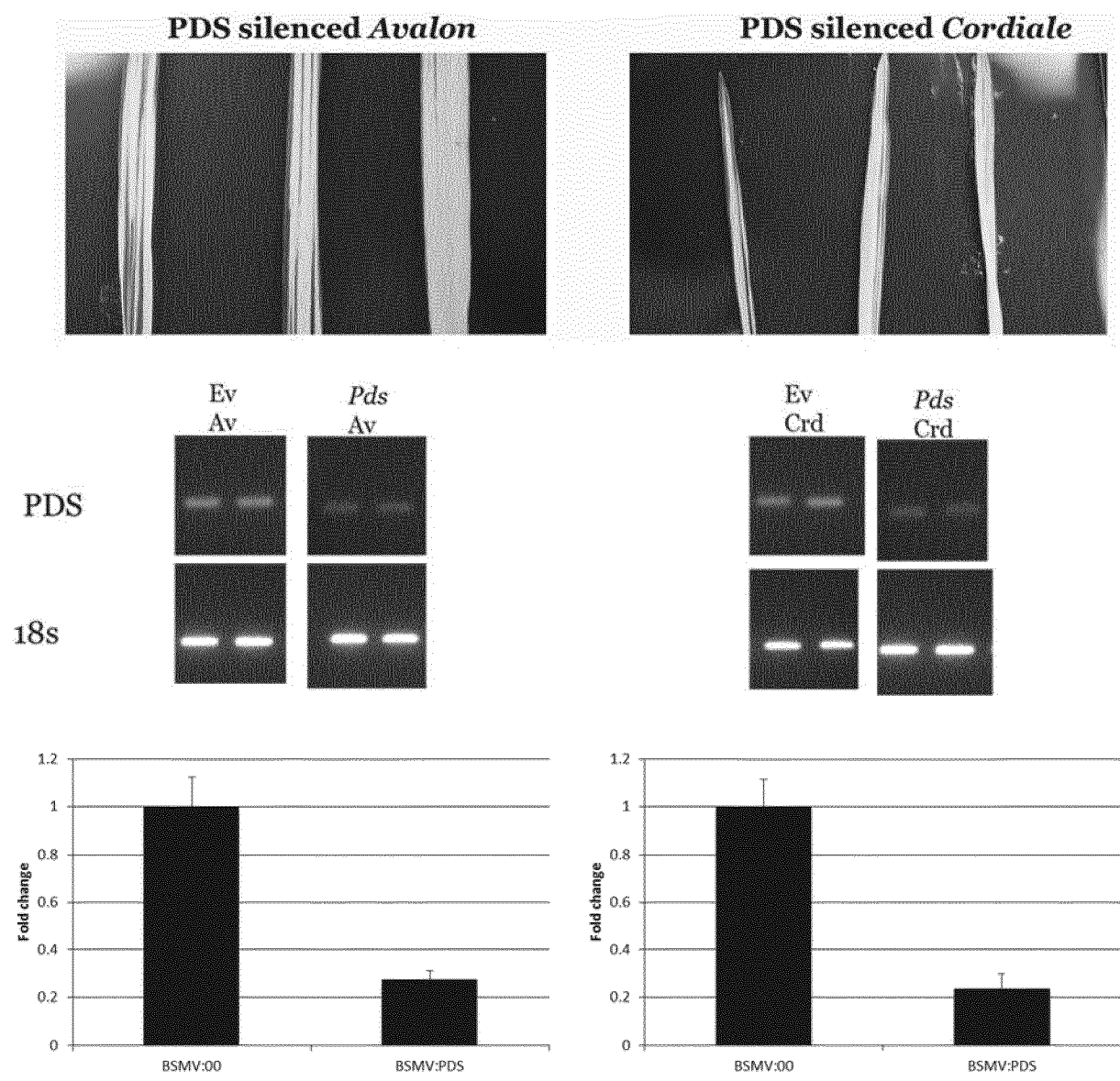
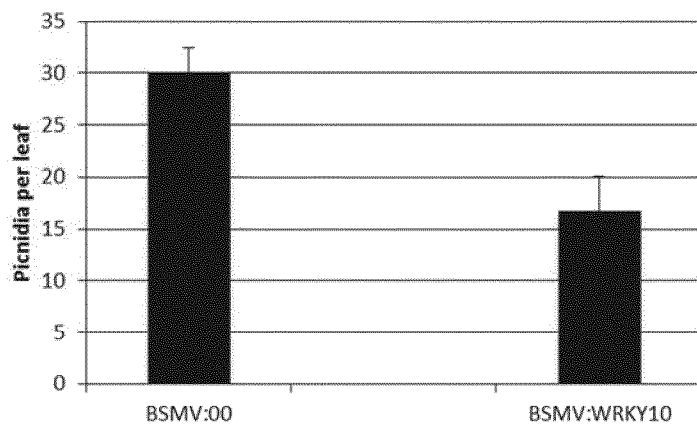
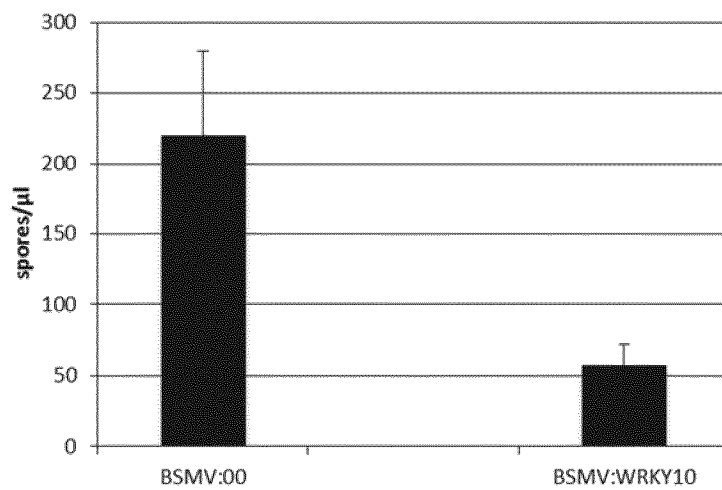


FIGURE 18

Picnidia and spores count data indicates that WRKY10 is important for Septoria defence in cv. *Avalon*



pvalue=0.003



pvalue=0.016

FIGURE 19

WRKY10 silencing leads to later onset of symptoms of Septoria infection on cv. Avalon

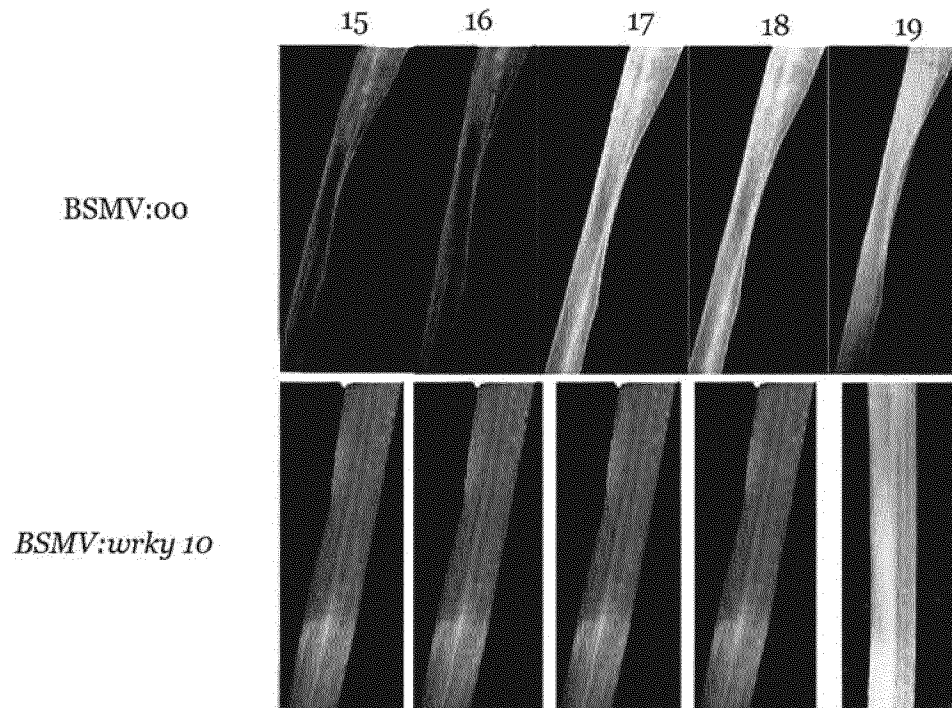
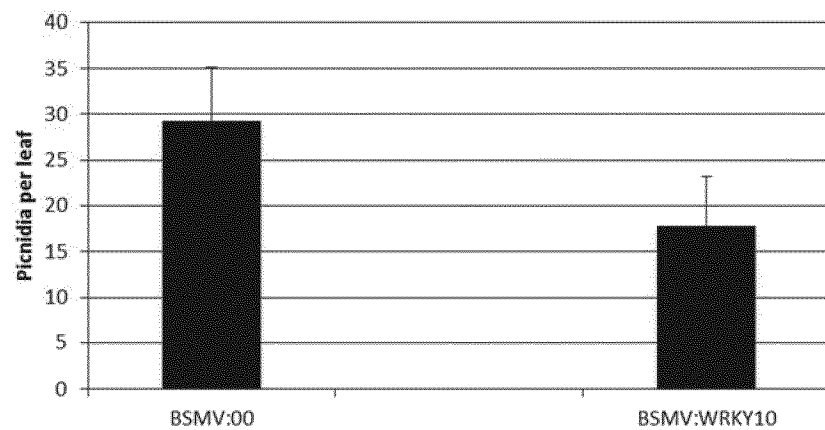
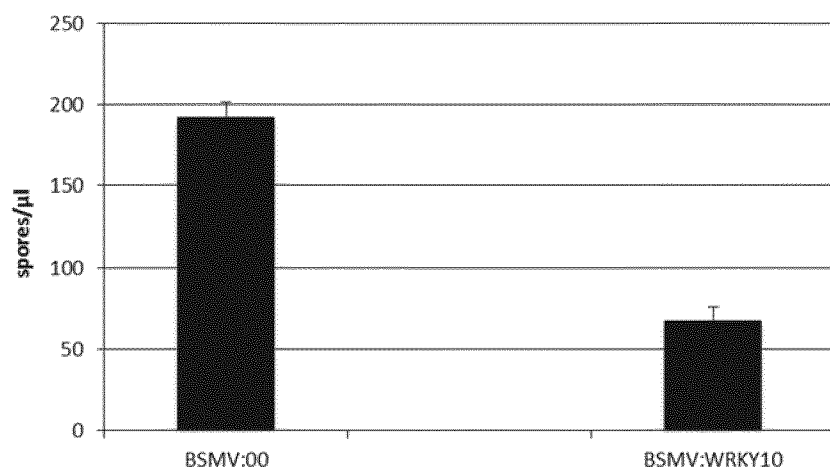


FIGURE 20

Picnidia and spores count data indicates that also in cv. *Cordiale* WRKY10 has a role during *Septoria* defense



pvalue=0.02



pvalue=<0.001

FIGURE 21

Picnidia and spore count data indicates that WRKY10 is important for Septoria defence in cv. *Santiago*

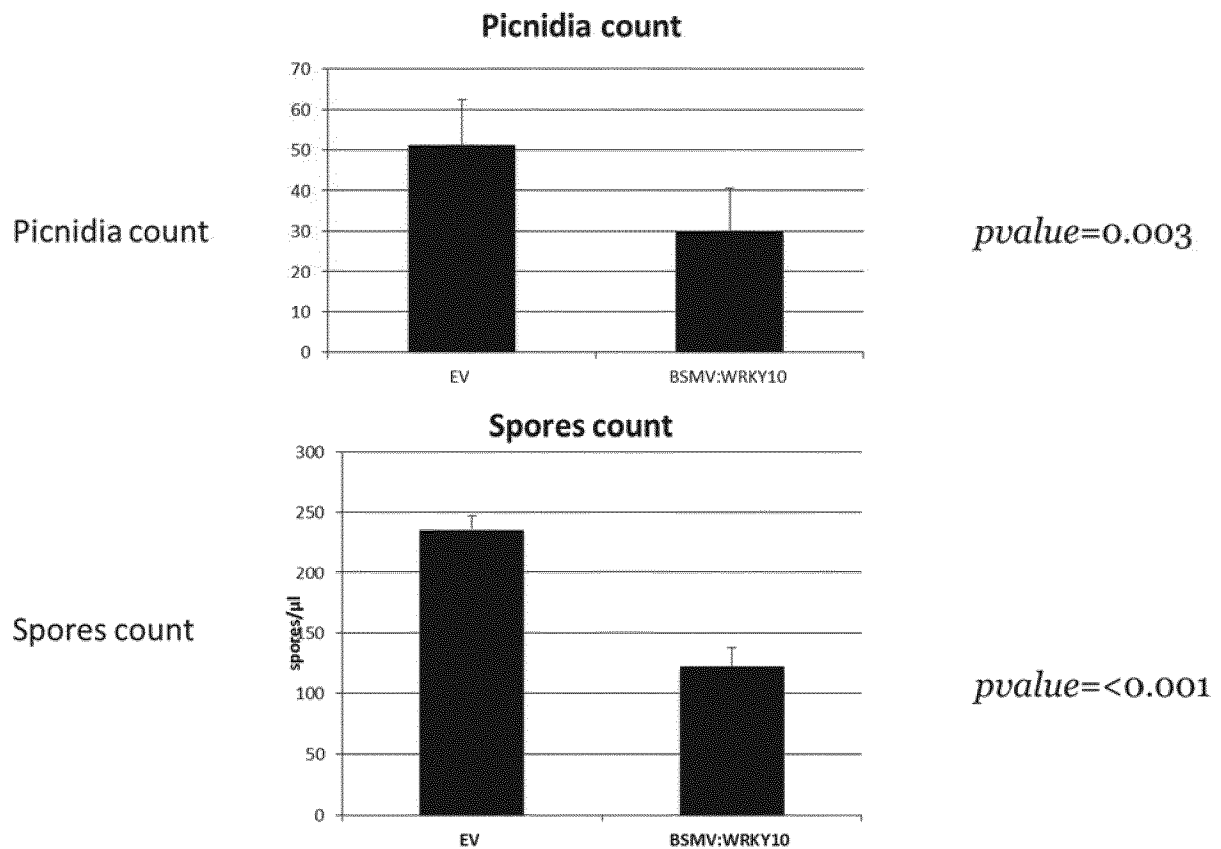


FIGURE 22

Picnidia and spores count data indicates that in cv. *Lili*
WRKY10 has a role during *Septoria* defence

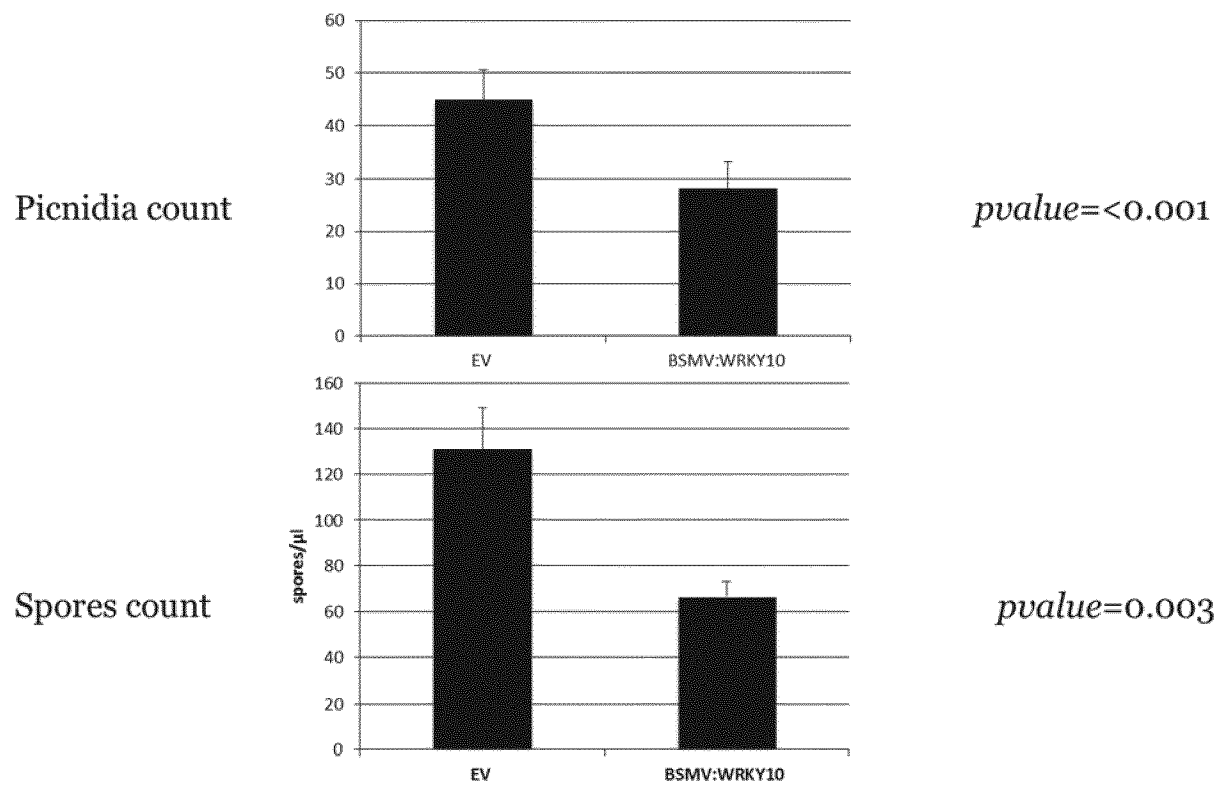


FIGURE 23

cv. Santiago is more susceptible to *Septoria* compared to
cv. Lili

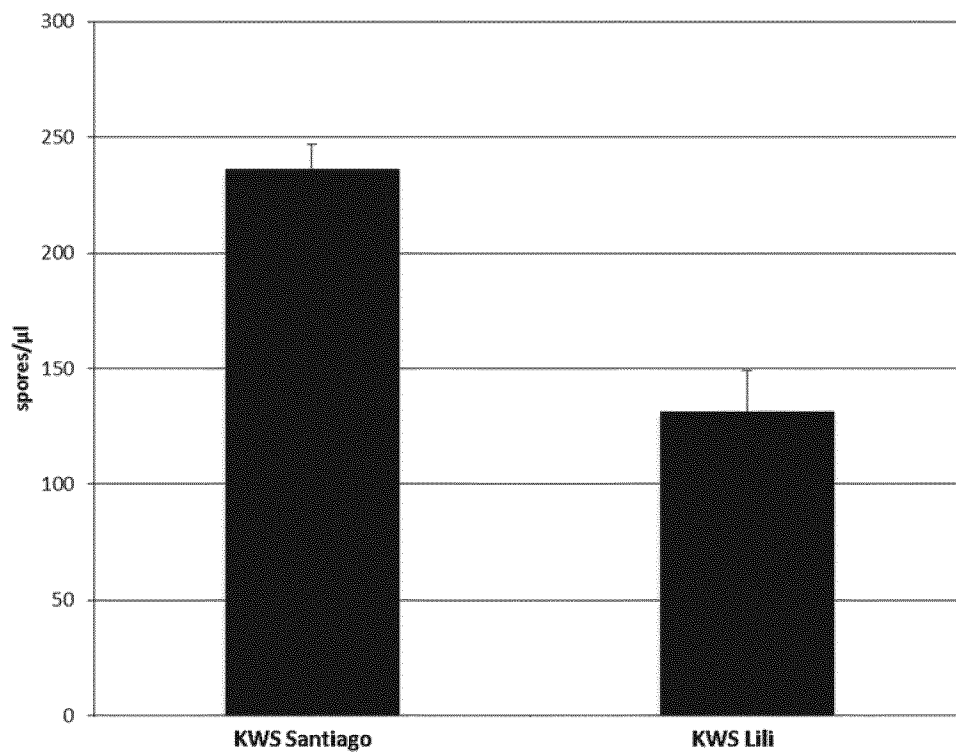


FIGURE 24

Septoria Sporulation in *WRKY10* silenced *cv. Santiago* is comparable to *cv. Lili* with full *WRKY10* expression

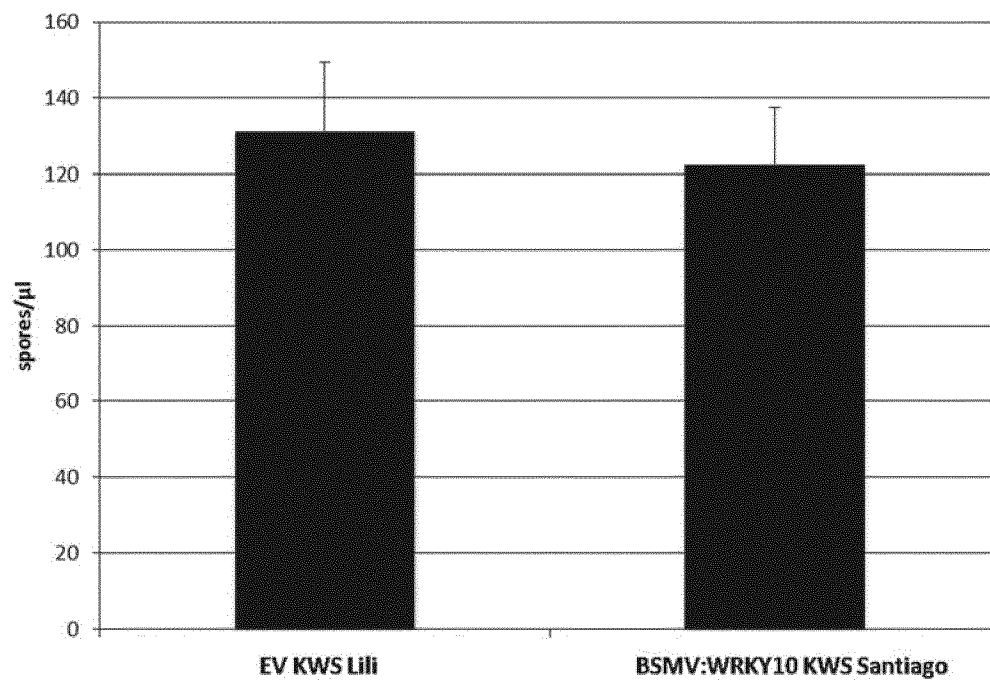


FIGURE 25

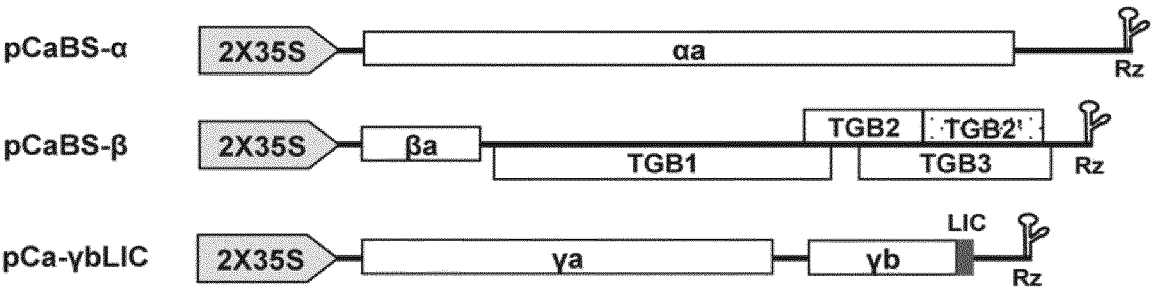


FIGURE 26

TaWRKY10:

Nucleotide position according to SEQ ID NO: 3	Nucleotide	Mutation	Effect
11	C	A	STOP Codon
16	G	T	STOP Codon
31	G	T	STOP Codon
42	C	A,G	STOP Codon
68	T	A	STOP Codon
72	C	A,G	STOP Codon
79	C	T	STOP Codon
121	G	T	STOP Codon
136	G	T	STOP Codon
168	C	A,G	STOP Codon
170	C	A	STOP Codon
196	G	T	STOP Codon
202	G	T	STOP Codon
219	C	A,G	STOP Codon
220	G	T	STOP Codon
255	C	A,G	STOP Codon
258	C	A,G	STOP Codon
261	C	A	STOP Codon
293	C	A	STOP Codon
304	A	T	STOP Codon
307	G	T	STOP Codon
310	G	T	STOP Codon
341	C	A	STOP Codon
368	C	A	STOP Codon
370	G	T	STOP Codon
376	G	T	STOP Codon
401	G	A	STOP Codon
402	G	A	STOP Codon
406	A	T	STOP Codon
411	C	A,G	STOP Codon
415	A	T	STOP Codon
418	A	T	STOP Codon
427	A	T	STOP Codon
453	C	A,G	STOP Codon
456	C	A,G	STOP Codon
462	C	A	STOP Codon
469	G	T	STOP Codon

477	C	A	STOP Codon
484	A	T	STOP Codon
487	A	T	STOP Codon
496	G	T	STOP Codon
522	C	A,G	STOP Codon
537	C	A,G	STOP Codon
594	C	A,G	STOP Codon
596	C	A	STOP Codon
617	G	A	STOP Codon
618	G	A	STOP Codon
623	G	A	STOP Codon
624	G	A	STOP Codon
628	G	T	STOP Codon
665	C	A	STOP Codon
667	G	T	STOP Codon
675	C	A,G	STOP Codon

TaWRKY13:

Nucleotide position according to SEQ ID NO: 5	Nucleotide	Mutation	Effect
27	C	A,G	STOP Codon
40	G	T	STOP Codon
67	C	T	STOP Codon
70	C	T	STOP Codon
73	A	T	STOP Codon
82	A	T	STOP Codon
85	G	T	STOP Codon
88	G	T	STOP Codon
91	C	T	STOP Codon
98	G	A	STOP Codon
99	G	A	STOP Codon
114	C	A,G	STOP Codon
123	C	A,G	STOP Codon
136	C	T	STOP Codon
140	G	A	STOP Codon
141	G	A	STOP Codon
145	A	T	STOP Codon
150	C	A,G	STOP Codon
154	G	T	STOP Codon
157	A	T	STOP Codon
160	A	T	STOP Codon

177	C	A,G	STOP Codon
192	C	A,G	STOP Codon
195	C	A,G	STOP Codon
196	A	T	STOP Codon
201	T	A	STOP Codon
207	C	A,G	STOP Codon
208	A	T	STOP Codon
220	A	T	STOP Codon
225	C	A	STOP Codon
235	A	T	STOP Codon
238	C	T	STOP Codon
244	C	T	STOP Codon
247	C	T	STOP Codon
250	A	T	STOP Codon
272	T	A	STOP Codon
288	C	A,G	STOP Codon
306	C	A	STOP Codon
317	C	A	STOP Codon
349	G	T	STOP Codon
352	C	T	STOP Codon
356	C	A	STOP Codon
362	C	A	STOP Codon
384	C	A	STOP Codon
392	C	A	STOP Codon
406	G	T	STOP Codon
409	C	T	STOP Codon
428	C	A	STOP Codon
442	C	T	STOP Codon
446	C	A,G	STOP Codon
466	C	T	STOP Codon
469	C	T	STOP Codon
478	A	T	STOP Codon
489	C	A,G	STOP Codon
496	C	T	STOP Codon
502	C	T	STOP Codon
506	G	A	STOP Codon
507	G	A	STOP Codon
518	C	A,G	STOP Codon
524	C	A	STOP Codon
544	A	T	STOP Codon
550	G	T	STOP Codon
568	G	T	STOP Codon
581	C	A	STOP Codon
611	C	A	STOP Codon

634	C	T	STOP Codon
638	C	A	STOP Codon
640	A	T	STOP Codon
645	C	A	STOP Codon
649	G	T	STOP Codon
654	C	A,G	STOP Codon
658	C	T	STOP Codon
665	T	A	STOP Codon

TaWRKY19:

Nucleotide position according to SEQ ID NO: 7	Nucleotide	Mutation	Effect
13	C	T	STOP Codon
17	G	A	STOP Codon
18	G	A	STOP Codon
20	C	A,G	STOP Codon
47	G	A	STOP Codon
48	G	A	STOP Codon
85	C	T	STOP Codon
92	C	A	STOP Codon
104	C	A	STOP Codon
124	G	T	STOP Codon
136	C	T	STOP Codon
162	C	A	STOP Codon
183	C	A,G	STOP Codon
187	C	T	STOP Codon
211	G	T	STOP Codon
214	C	T	STOP Codon
226	C	T	STOP Codon
238	C	T	STOP Codon
247	C	T	STOP Codon
250	A	T	STOP Codon
253	A	T	STOP Codon
256	G	T	STOP Codon
260	T	A	STOP Codon
265	G	T	STOP Codon
268	A	T	STOP Codon
271	C	T	STOP Codon
280	G	T	STOP Codon
284	T	A	STOP Codon
292	A	T	STOP Codon

298	G	T	STOP Codon
304	C	T	STOP Codon
319	A	T	STOP Codon
324	C	A,G	STOP Codon
337	C	T	STOP Codon
362	C	A,G	STOP Codon
365	T	A	STOP Codon
374	C	A,G	STOP Codon
388	C	T	STOP Codon
419	C	A,G	STOP Codon
424	C	T	STOP Codon
427	G	T	STOP Codon
430	C	T	STOP Codon
437	T	A	STOP Codon
443	C	A,G	STOP Codon
472	G	T	STOP Codon
481	A	T	STOP Codon
488	T	A,G	STOP Codon
490	C	T	STOP Codon
499	C	T	STOP Codon
506	C	A,G	STOP Codon
535	G	T	STOP Codon
539	C	A,G	STOP Codon
544	G	T	STOP Codon
553	G	T	STOP Codon
562	C	T	STOP Codon
569	C	A,G	STOP Codon
586	A	T	STOP Codon
601	G	T	STOP Codon
606	C	A,G	STOP Codon
611	G	A	STOP Codon
612	G	A	STOP Codon
616	A	T	STOP Codon
621	T	A,G	STOP Codon
622	G	T	STOP Codon
625	C	T	STOP Codon
628	A	T	STOP Codon
637	A	T	STOP Codon
646	A	T	STOP Codon
651	T	A,G	STOP Codon
663	T	A,G	STOP Codon
666	C	A,G	STOP Codon
667	A	T	STOP Codon
672	T	A	STOP Codon

684	C	A	STOP Codon
694	A	T	STOP Codon
703	G	T	STOP Codon
718	G	T	STOP Codon
721	C	T	STOP Codon
730	A	T	STOP Codon
741	T	A,G	STOP Codon
742	A	T	STOP Codon
748	C	T	STOP Codon
756	C	A	STOP Codon
760	G	T	STOP Codon
770	C	A,G	STOP Codon
772	A	T	STOP Codon
781	A	T	STOP Codon
789	T	A	STOP Codon
797	T	A,G	STOP Codon
800	T	A	STOP Codon
805	G	T	STOP Codon
809	T	A,G	STOP Codon
829	A	T	STOP Codon
832	G	T	STOP Codon
839	C	A,G	STOP Codon
844	A	T	STOP Codon
848	C	A,G	STOP Codon
850	C	T	STOP Codon
854	T	A,G	STOP Codon
861	T	A	STOP Codon
862	C	T	STOP Codon
870	T	A,G	STOP Codon
873	T	A,G	STOP Codon
874	G	T	STOP Codon
877	A	T	STOP Codon
895	G	T	STOP Codon
914	T	A,G	STOP Codon
917	T	A	STOP Codon
925	A	T	STOP Codon
928	G	T	STOP Codon
931	G	T	STOP Codon
940	G	T	STOP Codon
943	C	T	STOP Codon
947	T	A,G	STOP Codon
956	T	A,G	STOP Codon
970	G	T	STOP Codon
982	G	T	STOP Codon

988	A	T	STOP Codon
1000	G	T	STOP Codon
1027	G	T	STOP Codon
1045	C	T	STOP Codon
1048	A	T	STOP Codon
1085	T	A	STOP Codon
1098	T	A,G	STOP Codon
1103	G	A	STOP Codon
1104	G	A	STOP Codon
1108	A	T	STOP Codon
1113	T	A,G	STOP Codon
1114	G	T	STOP Codon
1117	C	T	STOP Codon
1120	A	T	STOP Codon
1129	A	T	STOP Codon
1132	G	T	STOP Codon
1155	T	A,G	STOP Codon
1158	C	A,G	STOP Codon
1159	A	T	STOP Codon
1164	C	A	STOP Codon
1170	C	A,G	STOP Codon
1171	C	T	STOP Codon
1174	G	T	STOP Codon
1179	C	A	STOP Codon
1186	A	T	STOP Codon
1189	A	T	STOP Codon
1198	G	T	STOP Codon
1201	A	T	STOP Codon
1210	G	T	STOP Codon
1213	G	T	STOP Codon
1239	C	A,G	STOP Codon
1240	G	T	STOP Codon
1246	A	T	STOP Codon
1267	G	T	STOP Codon
1279	A	T	STOP Codon
1285	C	T	STOP Codon
1297	C	T	STOP Codon
1308	C	A	STOP Codon
1309	A	T	STOP Codon
1312	G	T	STOP Codon
1315	C	T	STOP Codon
1323	T	A,G	STOP Codon
1325	C	A,G	STOP Codon
1327	G	T	STOP Codon

1330	C	T	STOP Codon
1334	C	A,G	STOP Codon
1350	C	A	STOP Codon
1358	C	A	STOP Codon
1360	G	T	STOP Codon
1363	A	T	STOP Codon
1366	A	T	STOP Codon
1369	A	T	STOP Codon
1374	T	A,G	STOP Codon
1375	G	T	STOP Codon

TaWRKY29:

Nucleotide position according to SEQ ID NO: 9	Nucleotide	Mutation	Effect
5	C	A,G	STOP Codon
29	C	A	STOP Codon
57	C	A,G	STOP Codon
61	G	T	STOP Codon
64	G	T	STOP Codon
71	C	A,G	STOP Codon
97	C	T	STOP Codon
128	C	A	STOP Codon
136	A	T	STOP Codon
167	C	A	STOP Codon
174	C	A	STOP Codon
181	A	T	STOP Codon
202	G	T	STOP Codon
205	G	T	STOP Codon
208	G	T	STOP Codon
211	G	T	STOP Codon
214	G	T	STOP Codon
236	C	A	STOP Codon
244	C	T	STOP Codon
257	T	A	STOP Codon
263	T	A	STOP Codon
269	C	A	STOP Codon
295	G	T	STOP Codon
310	G	T	STOP Codon
349	G	T	STOP Codon
370	G	T	STOP Codon
373	A	T	STOP Codon

376	A	T	STOP Codon
385	A	T	STOP Codon
388	A	T	STOP Codon
401	C	A	STOP Codon
418	G	T	STOP Codon
427	A	T	STOP Codon
433	C	T	STOP Codon
448	G	T	STOP Codon
460	A	T	STOP Codon
463	A	T	STOP Codon
466	G	T	STOP Codon
538	G	T	STOP Codon
556	C	T	STOP Codon
583	G	T	STOP Codon
598	C	T	STOP Codon
604	G	T	STOP Codon
622	G	T	STOP Codon
625	G	T	STOP Codon
631	C	T	STOP Codon
640	C	T	STOP Codon
650	T	A	STOP Codon
655	C	T	STOP Codon
672	C	A,G	STOP Codon
682	C	T	STOP Codon
706	C	T	STOP Codon
709	C	T	STOP Codon
718	C	T	STOP Codon
733	C	T	STOP Codon
739	C	T	STOP Codon
742	C	T	STOP Codon
757	G	T	STOP Codon
766	A	T	STOP Codon
772	G	T	STOP Codon
793	C	T	STOP Codon
815	C	A	STOP Codon
817	G	T	STOP Codon
838	G	T	STOP Codon
841	G	T	STOP Codon
854	C	A	STOP Codon
862	G	T	STOP Codon
884	C	A	STOP Codon
887	C	A	STOP Codon
895	G	T	STOP Codon
901	G	T	STOP Codon

910	G	T	STOP Codon
919	G	T	STOP Codon
950	G	A	STOP Codon
951	G	A	STOP Codon
953	T	A	STOP Codon
958	G	T	STOP Codon
973	C	T	STOP Codon
976	C	T	STOP Codon
979	C	T	STOP Codon
982	C	T	STOP Codon
985	C	T	STOP Codon
988	C	T	STOP Codon
1006	A	T	STOP Codon
1018	C	T	STOP Codon
1021	C	T	STOP Codon
1027	C	T	STOP Codon
1030	G	T	STOP Codon
1045	A	T	STOP Codon
1069	C	T	STOP Codon
1075	G	T	STOP Codon
1096	G	T	STOP Codon
1101	C	A	STOP Codon
1102	C	T	STOP Codon
1106	G	A	STOP Codon
1107	G	A	STOP Codon
1111	A	T	STOP Codon
1116	C	A,G	STOP Codon
1120	C	T	STOP Codon
1123	A	T	STOP Codon
1132	A	T	STOP Codon
1135	G	T	STOP Codon
1146	C	A	STOP Codon
1158	C	A,G	STOP Codon
1161	C	A,G	STOP Codon
1167	C	A	STOP Codon
1185	C	A	STOP Codon
1195	A	T	STOP Codon
1198	C	T	STOP Codon
1204	C	T	STOP Codon
1207	C	T	STOP Codon
1212	C	A	STOP Codon
1216	G	T	STOP Codon
1245	C	A,G	STOP Codon
1246	G	T	STOP Codon

1304	C	A	STOP Codon
1401	C	A	STOP Codon
1403	C	A	STOP Codon
1424	C	A	STOP Codon
1510	C	T	STOP Codon
1528	C	T	STOP Codon
1596	C	A,G	STOP Codon
1600	C	T	STOP Codon
1606	A	T	STOP Codon
1621	C	T	STOP Codon
1637	C	A	STOP Codon
1651	C	T	STOP Codon
1660	C	T	STOP Codon
1690	C	T	STOP Codon
1772	C	A	STOP Codon
1775	C	A	STOP Codon
1789	C	T	STOP Codon
1894	G	T	STOP Codon
1900	C	T	STOP Codon

TaWRKY39:

Nucleotide position according to SEQ ID NO: 11	Nucleotide	Mutation	Effect
7	G	T	STOP Codon
10	C	T	STOP Codon
14	G	A	STOP Codon
15	G	A	STOP Codon
25	C	T	STOP Codon
94	A	T	STOP Codon
106	G	T	STOP Codon
109	G	T	STOP Codon
127	A	T	STOP Codon
130	A	T	STOP Codon
139	G	T	STOP Codon
145	G	T	STOP Codon
154	G	T	STOP Codon
160	G	T	STOP Codon
178	G	T	STOP Codon
181	G	T	STOP Codon
223	A	T	STOP Codon
228	C	A,G	STOP Codon

238	C	T	STOP Codon
289	C	T	STOP Codon
293	C	A,G	STOP Codon
307	G	T	STOP Codon
326	C	A	STOP Codon
337	A	T	STOP Codon
373	C	T	STOP Codon
376	G	T	STOP Codon
384	C	A,G	STOP Codon
430	C	T	STOP Codon
436	G	T	STOP Codon
441	C	A	STOP Codon
454	G	T	STOP Codon
469	A	T	STOP Codon
487	G	T	STOP Codon
492	C	A	STOP Codon
493	A	T	STOP Codon
511	A	T	STOP Codon
519	C	A,G	STOP Codon
556	A	T	STOP Codon
567	C	A,G	STOP Codon
568	C	T	STOP Codon
572	G	A	STOP Codon
573	G	A	STOP Codon
574	C	T	STOP Codon
577	A	T	STOP Codon
582	C	A,G	STOP Codon
586	C	T	STOP Codon
589	G	T	STOP Codon
598	C	T	STOP Codon
601	G	T	STOP Codon
604	C	T	STOP Codon
616	G	T	STOP Codon
641	C	A	STOP Codon

TaWRKY53B:

Nucleotide position according to SEQ ID NO: 13	Nucleotide	Mutation	Effect
23	T	A	STOP Codon
76	G	T	STOP Codon
86	C	A	STOP Codon

109	G	T	STOP Codon
116	C	A	STOP Codon
133	C	T	STOP Codon
157	A	T	STOP Codon
163	A	T	STOP Codon
172	C	T	STOP Codon
194	C	A	STOP Codon
197	C	A	STOP Codon
210	C	A	STOP Codon
241	G	T	STOP Codon
273	C	A,G	STOP Codon
284	T	A	STOP Codon
316	C	T	STOP Codon
324	C	A	STOP Codon
329	G	A	STOP Codon
330	G	A	STOP Codon
331	C	T	STOP Codon
358	C	T	STOP Codon
361	C	T	STOP Codon
367	G	T	STOP Codon
403	A	T	STOP Codon
427	C	T	STOP Codon
438	C	A	STOP Codon
440	T	A,G	STOP Codon
446	T	A,G	STOP Codon
451	A	T	STOP Codon
454	G	T	STOP Codon
457	C	T	STOP Codon
460	C	T	STOP Codon
463	G	T	STOP Codon
466	C	T	STOP Codon
469	C	T	STOP Codon
472	C	T	STOP Codon
475	G	T	STOP Codon
478	G	T	STOP Codon
487	C	T	STOP Codon
499	A	T	STOP Codon
526	A	T	STOP Codon
529	C	T	STOP Codon
535	G	T	STOP Codon
541	G	T	STOP Codon
546	C	A,G	STOP Codon
551	G	A	STOP Codon
552	G	A	STOP Codon

556	A	T	STOP Codon
561	C	A,G	STOP Codon
565	C	T	STOP Codon
568	A	T	STOP Codon
571	C	T	STOP Codon
577	A	T	STOP Codon
586	G	T	STOP Codon
603	C	A,G	STOP Codon
606	C	A,G	STOP Codon
607	A	T	STOP Codon
612	C	A	STOP Codon
618	C	A,G	STOP Codon
627	C	A	STOP Codon
634	A	T	STOP Codon
637	A	T	STOP Codon
640	A	T	STOP Codon
646	G	T	STOP Codon
676	C	T	STOP Codon
687	C	A,G	STOP Codon
688	A	T	STOP Codon
709	A	T	STOP Codon
744	C	A	STOP Codon
760	G	T	STOP Codon
779	C	A	STOP Codon
781	G	T	STOP Codon
802	G	T	STOP Codon
809	C	A,G	STOP Codon
823	G	T	STOP Codon
832	G	T	STOP Codon
841	A	T	STOP Codon
847	G	T	STOP Codon
853	A	T	STOP Codon
862	A	T	STOP Codon
865	G	T	STOP Codon
880	G	T	STOP Codon
890	C	A,G	STOP Codon
909	C	A	STOP Codon
913	A	T	STOP Codon
925	G	T	STOP Codon
943	C	T	STOP Codon
986	G	A	STOP Codon
987	G	A	STOP Codon
991	A	T	STOP Codon
996	C	A,G	STOP Codon

1000	C	T	STOP Codon
1003	A	T	STOP Codon
1012	A	T	STOP Codon
1038	C	A,G	STOP Codon
1041	C	A,G	STOP Codon
1042	A	T	STOP Codon
1047	C	A	STOP Codon
1062	C	A	STOP Codon
1072	A	T	STOP Codon
1081	G	T	STOP Codon
1091	C	A	STOP Codon
1122	C	A,G	STOP Codon
1123	G	T	STOP Codon
1129	A	T	STOP Codon
1178	C	A,G	STOP Codon
1196	C	A	STOP Codon
1208	G	A	STOP Codon
1209	G	A	STOP Codon
1225	C	T	STOP Codon
1236	C	A	STOP Codon
1243	G	T	STOP Codon
1255	G	T	STOP Codon
1269	C	A,G	STOP Codon
1276	A	T	STOP Codon
1282	G	T	STOP Codon
1306	G	T	STOP Codon
1310	C	A	STOP Codon
1320	C	A	STOP Codon

TaWRKY68A:

Nucleotide position according to SEQ ID NO: 15	Nucleotide	Mutation	Effect
24	C	A	STOP Codon
27	C	A,G	STOP Codon
49	C	T	STOP Codon
61	C	T	STOP Codon
64	G	T	STOP Codon
94	G	T	STOP Codon
133	A	T	STOP Codon
142	C	T	STOP Codon
145	C	T	STOP Codon

154	C	T	STOP Codon
157	C	T	STOP Codon
169	G	T	STOP Codon
181	C	T	STOP Codon
193	A	T	STOP Codon
202	A	T	STOP Codon
259	C	T	STOP Codon
263	C	A	STOP Codon
331	G	T	STOP Codon
353	T	A	STOP Codon
374	C	A	STOP Codon
400	C	T	STOP Codon
406	C	T	STOP Codon
430	A	T	STOP Codon
449	C	A,G	STOP Codon
488	C	A	STOP Codon
502	G	T	STOP Codon
517	A	T	STOP Codon
544	A	T	STOP Codon
565	A	T	STOP Codon
568	A	T	STOP Codon
571	A	T	STOP Codon
579	C	A	STOP Codon
593	C	A	STOP Codon
595	G	T	STOP Codon
616	C	T	STOP Codon
621	C	A	STOP Codon
627	C	A	STOP Codon
631	A	T	STOP Codon
634	A	T	STOP Codon
640	A	T	STOP Codon
652	A	T	STOP Codon
685	A	T	STOP Codon
709	G	T	STOP Codon
714	C	A,G	STOP Codon
716	C	A	STOP Codon
719	G	A	STOP Codon
720	G	A	STOP Codon
724	A	T	STOP Codon
729	C	A,G	STOP Codon
733	C	T	STOP Codon
736	A	T	STOP Codon
745	A	T	STOP Codon
759	C	A,G	STOP Codon

771	C	A,G	STOP Codon
774	C	A,G	STOP Codon
775	A	T	STOP Codon
780	C	A	STOP Codon
790	C	T	STOP Codon
798	C	A	STOP Codon
808	A	T	STOP Codon
817	G	T	STOP Codon
858	C	A,G	STOP Codon
859	G	T	STOP Codon
865	G	T	STOP Codon
878	C	A	STOP Codon
898	C	T	STOP Codon
911	C	A	STOP Codon

FIGURE 27

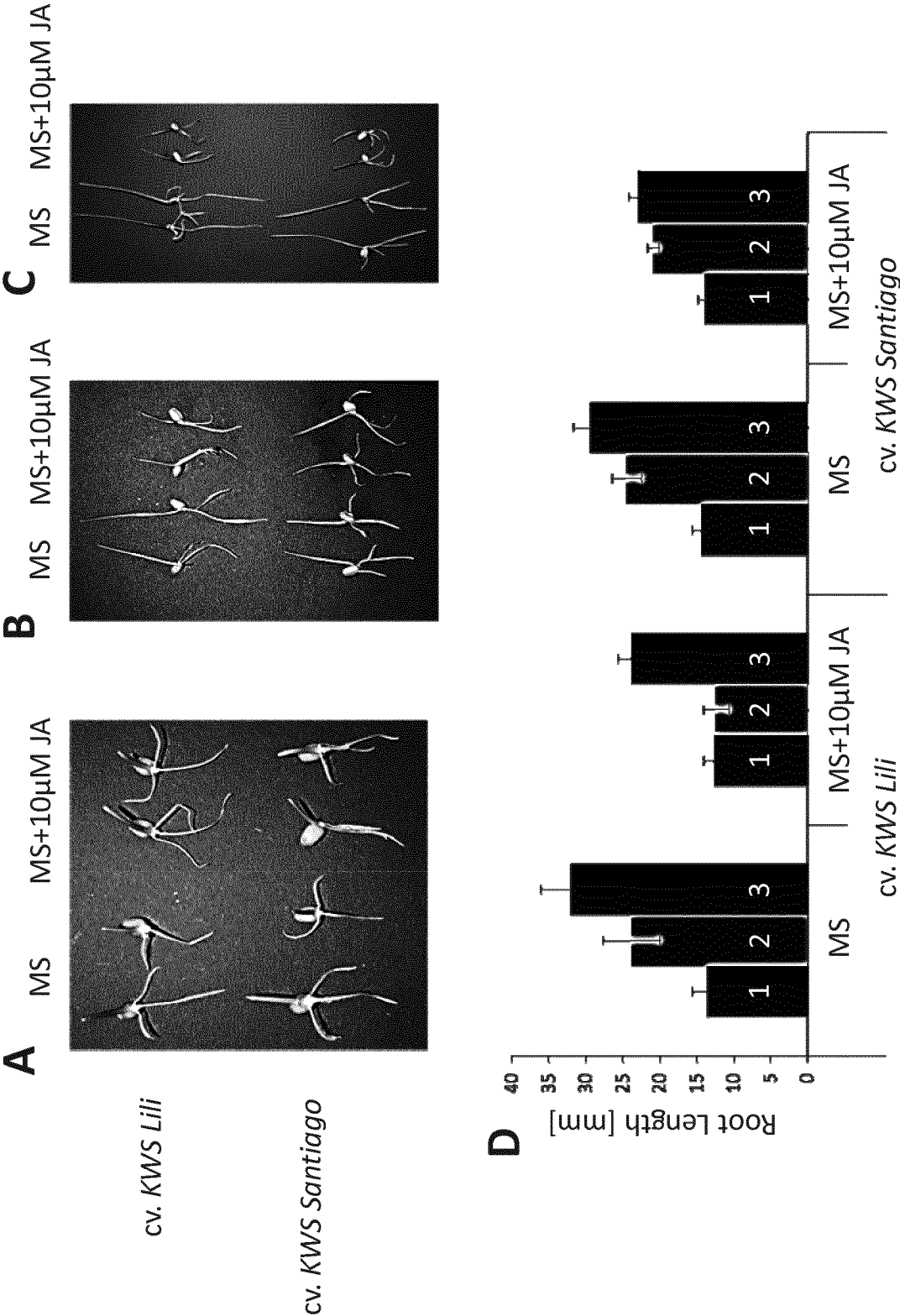


FIGURE 28

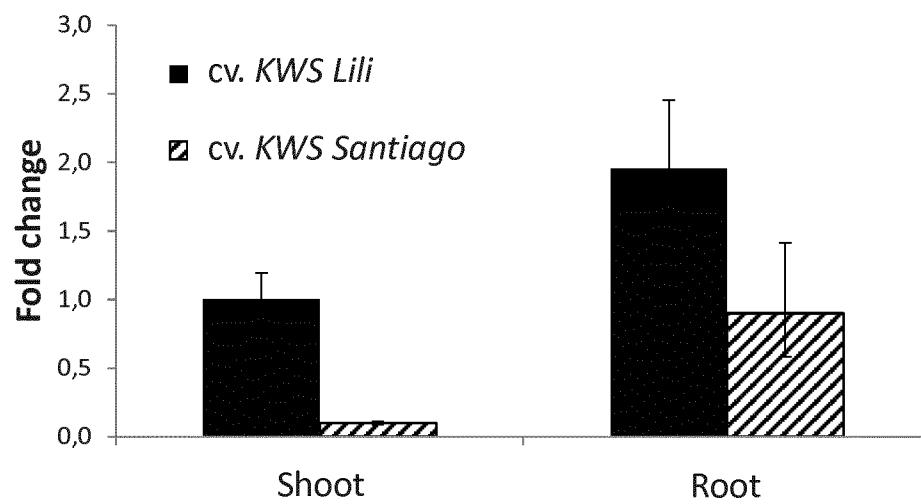


FIGURE 29

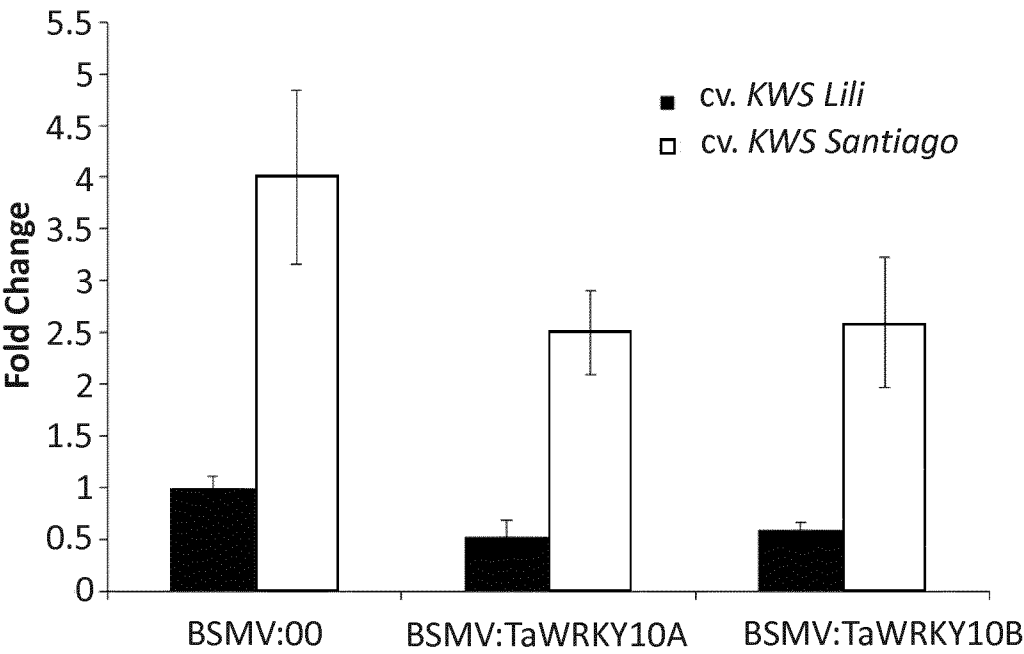
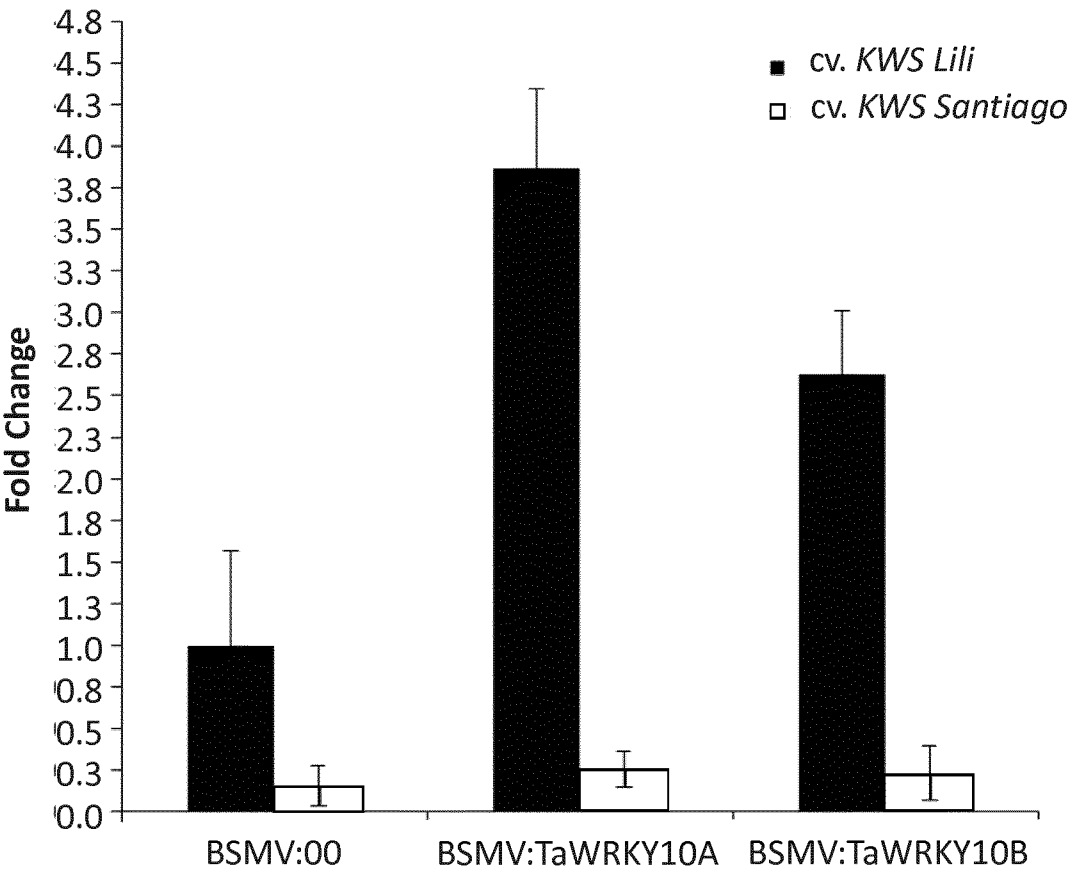


FIGURE 30



INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2017/057333

A. CLASSIFICATION OF SUBJECT MATTER
INV. A01H5/10 C07K14/415 C12N15/82
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12N A01H C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, Sequence Search, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	LEON VAN ECK ET AL: "Virus-induced gene silencing of WRKY53 and an inducible phenylalanine ammonia-lyase in wheat reduces aphid resistance", PLANT BIOTECHNOLOGY JOURNAL, vol. 8, no. 9, 3 November 2010 (2010-11-03), pages 1023-1032, XP055289783, GB ISSN: 1467-7644, DOI: 10.1111/j.1467-7652.2010.00539.x abstract; pages 1024-1026, 1029 -----	1-14, 16-21
X	US 2012/096584 A1 (ALEXANDROV NICKOLAI [US] ET AL) 19 April 2012 (2012-04-19) pages 5, 6 and 8; claims 1, 4-8, 13-16; Seq. ID No. 3584 ----- -/-	1-10,14, 16,17, 20,21



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

12 July 2017

Date of mailing of the international search report

26/07/2017

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Kurz, Birgit

INTERNATIONAL SEARCH REPORT

International application No

PCT/EP2017/057333

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2008/057093 A1 (WAN JINRONG [US] ET AL) 6 March 2008 (2008-03-06) claims 1, 9, 11-13, 15, 21-31; pages 5, 7, 10, 11; figures 8, 15, 17 -----	1-14, 16-21
A	HUALING WU ET AL: "Cloning and expression profiles of 15 genes encoding WRKY transcription factor in wheat (<i>Triticum aestivum</i> L.)", PROGRESS IN NATURAL SCIENCE, vol. 18, no. 6, 10 June 2008 (2008-06-10), pages 697-705, XP055289864, CN ISSN: 1002-0071, DOI: 10.1016/j.pnsc.2007.12.006 abstract; pages 697-699, 703; Figures 1 and 2 -----	1-14, 16-21
A	RUSHTON PAUL J ET AL: "WRKY transcription factors", TRENDS IN PLANT SCIENCE, ELSEVIER SCIENCE, OXFORD, GB, vol. 15, no. 5, 1 May 2010 (2010-05-01), pages 247-258, XP002663962, ISSN: 1360-1385, DOI: 10.1016/J.TPLANTS.2010.02.006 [retrieved on 2010-03-19] abstract; pages 247-251, 254, 255 -----	1-14, 16-21
A	F. YANG ET AL: "Battle through Signaling between Wheat and the Fungal Pathogen <i>Septoria tritici</i> Revealed by Proteomics and Phosphoproteomics", MOLECULAR & CELLULAR PROTEOMICS, vol. 12, no. 9, 29 May 2013 (2013-05-29), pages 2497-2508, XP055289987, US ISSN: 1535-9476, DOI: 10.1074/mcp.M113.027532 abstract; pages 2498, 2500, 2501, 2505; supplementary Tables 4 and 5 -& Fen Yang ET AL: "Supplemental data: Table S4", 29 May 2013 (2013-05-29), pages 1-2, XP055289993, Retrieved from the Internet: URL: http://www.mcponline.org/content/suppl/2013/05/29/M113.027532.DC1/mcp.M113.027532-7.pdf [retrieved on 2016-07-20] the whole document -/--	1-14, 16-21

INTERNATIONAL SEARCH REPORT

International application No

PCT/EP2017/057333

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	-& Fen Yang ET AL: "Table S5: Supplemental data", 29 May 2013 (2013-05-29), XP055289995, Retrieved from the Internet: URL: http://www.mcponline.org/content/suppl/2013/05/29/M113.027532.DC1/mcp.M113.027532-8.pdf [retrieved on 2016-07-20] the whole document -----	
X	WO 00/68406 A2 (DU PONT [US]; CAIMI PERRY G [US]; FAMODU OMOLAYO O [US]; LEE JIANG MIN) 16 November 2000 (2000-11-16) Pages 1-4, 14-17; Table 1; Example 5; claims 1-8, 10-12, 23; Seq. ID Nos 19 and 20 -----	1,4-12, 15,17-19
X	US 2012/159672 A1 (ALEXANDROV NICKOLAI [US] ET AL) 21 June 2012 (2012-06-21) claims 1, 2, 6-11, 13-20; paragraphs [0556] and [0744]; Seq. ID Nos 13024 and 13025 -----	1,4-9, 15,17,19
A	KAZUNORI OKADA ET AL: "Jasmonates Induce Both Defense Responses and Communication in Monocotyledonous and Dicotyledonous Plants", PLANT AND CELL PHYSIOLOGY, vol. 56, no. 1, 4 November 2014 (2014-11-04), pages 16-27, XP055390130, UK ISSN: 0032-0781, DOI: 10.1093/pcp/pcu158 Pages 16-18, 20-22, 24; Figures 2 and 3 -----	1,3-13, 15,17-21
A	CHUN YAN ET AL: "Jasmonate in plant defence: sentinel or double agent?", PLANT BIOTECHNOLOGY JOURNAL, vol. 13, no. 9, 11 June 2015 (2015-06-11), pages 1233-1240, XP055390136, GB ISSN: 1467-7644, DOI: 10.1111/pbi.12417 Summary; pages 1233-1235 -----	1,3-13, 15,17-21

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2017/057333

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 2, 14, 16(completely); 1, 3-13, 17-21(partially)

Cereal plant cells and plants in which expression or activity of at least one WRKY protein which is (i) fertilizer-responsive and or (ii) comprises the motif D-G/E-X1-X2-W-R-K-Y-G-K/E/Q-K/E is inhibited and methods and use thereof

1.1. claims: 1-14, 16-21(all partially)

Cereal plant cells and plants in which expression or activity of the transcription factor TaWRKY10 is inhibited, as well as methods and uses thereof.

1.2. claims: 1-14, 16-21(all partially)

Cereal plant cells and plants in which expression or activity of the transcription factor TaWRKY13 is inhibited, as well as methods and uses thereof.

1.3. claims: 1-14, 16-21(all partially)

Cereal plant cells and plants in which expression or activity of the transcription factor TaWRKY19 is inhibited, as well as methods and uses thereof.

1.4. claims: 1-14, 16-21(all partially)

Cereal plant cells and plants in which expression or activity of the transcription factor TaWRKY29 is inhibited, as well as methods and uses thereof.

1.5. claims: 1-14, 16-21(all partially)

Cereal plant cells and plants in which expression or activity of the transcription factor TaWRKY39 is inhibited, as well as methods and uses thereof.

1.6. claims: 1-14, 16-21(all partially)

Cereal plant cells and plants in which expression or activity of the transcription factor TaWRKY53B is inhibited, as well as methods and uses thereof.

1.7. claims: 1-14, 16-21(all partially)

Cereal plant cells and plants in which expression or activity of the transcription factor TaWRKY68A is inhibited, as well as methods and uses thereof.

2. claims: 15(completely); 1, 3-13, 17-21(partially)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Cereal plant cells and plants in which expression or
activity of the jasmonate receptor protein is increased and
methods and use thereof

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/EP2017/057333

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