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(71) Applicant: TEXAS TECH UNIVERSITY SYSTEM
[US/US]; Office Of Technology Transfer and Intellectual
Property, P.O. Box 42007, Lubbock, TX 79409-2007
(US).

(72) Inventors: BUGAREL, Marie; 2326 95th Street, Lub-
bock, TX 79423 (US). NIGHTINGALE, Kendra; 16003
CR 1820, Lubbock, TX 79424 (US). LONERAGAN,
Guy; 8903 153rd Street, Wolfforth, TX 79382 (US).
BRASHEARS, Mindy; 8705 149th Street, Wolfforth, TX
79382 (US).

(74) Agents: CHALKER, Daniel J. et al.; Chalker Flores,
LLP, 14951 North Dallas Parkway, Suite 400, Dallas, TX
75254 (US).

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(54) Title: SEROTYPE DISCRIMINATION BIOMARKERS TO DISTINGUISH INFANTIS FROM HEIDELBERG AND NEW-
PORT FROM HADAR

(57) Abstract: The present invention provides a set of oligonucleotides to screen for the presence of targeted Salmonella serotypes
in enrichment or to characterize presumptive colonies. The set of oligonucleotides includes at least one set of primers and probe for
the detection of Salmonella serotype selected from Newport, Heidelberg, Infantis, and Hadar and to discriminate between. These
new markers can be used after the initial screening assay described herein as a discrimination assay to differentiate S. Heidelberg
from S. Infantis and S. Hadar from S. Newport.



SEROTYPE DISCRIMINATION BIOMARKERS TO DISTINGUISH INFANTIS FROM HEIDELBERG AND NEWPORT FROM HADAR

Technical Field of the Invention

The present invention relates generally to methods and compositions used for the
5 detection of bacteria of the genus *Salmonella* and specifically to serotype discrimination
biomarkers to distinguish, e.g., *Infantis* from Heidelberg and Newport from Hadar.

Background of the Invention

Without limiting the scope of the invention, its background is described in connection
with methods and compositions used for the molecular discrimination of *Salmonella* serotypes.
10 *Salmonella* is a genus of bacteria that may cause severe infections leading to bacterial enteric
illness in both humans and animals, e.g., salmonellosis, which include gastro-enteritis, as well as
typhoid and para-typhoid fevers. Millions of human cases are reported every year, and the
diseases result in thousands of deaths worldwide. In recent years, problems related to *Salmonella*
have increased significantly, both in terms of incidence and severity of cases of human
15 salmonellosis.

United States Patent No. 8,268,984, entitled, "Detection of *Salmonella* by Real-Time
Multiplex PCR," discloses the detection of *Salmonella* by nucleic acid amplification and
provides primer and probe oligonucleotides that can be used in multiplex to detect *Salmonella* in
real-time amplification. The oligonucleotides of the invention detect all group I serotypes, and
20 have an increased *Salmonella* detection range and cover seven *Salmonella* groups.

Summary of the Invention

Salmonella is an important cause of human and animal morbidity and mortality.
Furthermore, *Salmonella* can be divided into a variety of different serotypes yet the traditional
approach to serotyping is expensive, slow, and requires considerable expertise. This is important
25 because several serotypes are regulated as adulterants in laying hen and broiler flocks of *Gallus*
chickens in Europe (e.g., *S. Enteritidis*, *S. Typhimurium*, *S. Infantis*, *S. Virchow*, and *S. Hadar*)
and some are likely to be targeted for regulation in raw foods in the United States (e.g., *S.*
Typhimurium, *S. Newport*, *S. Heidelberg*, and *S. Hadar*).

In one embodiment, the present invention includes a pair of oligonucleotides for the
30 identification of a *Salmonella* serotype comprising: at least one oligonucleotide pair selected

from: a first primer set having SEQ ID NOS: 1 and 3 for the amplification of one or more sequences and a first probe having SEQ ID NO: 2 for discrimination with *S. Infantis* and identification of *S. Heidelberg*; a second primer set having SEQ ID NOS: 4 and 6 for the amplification of one or more sequences and a second probe having SEQ ID NO: 5 for discrimination with *S. Heidelberg* and identification of *S. Infantis*; a third primer set having SEQ ID NOS: 7 and 9 for the amplification of one or more sequences and a third probe having SEQ ID NO: 8 for discrimination with *S. Newport* and identification of *S. Hadar*; or a fourth primer set having SEQ ID NOS: 10 and 12 for the amplification of one or more sequences and a fourth probe having SEQ ID NO: 11 for discrimination with *S. Hadar* and identification of *S. Newport*.

In one aspect, the at least one oligonucleotide pair includes the first, second, third and fourth primer sets and the respective first, second, third and fourth probes, for discrimination with *S. Infantis* and identification of *S. Heidelberg*; discrimination with *S. Heidelberg* and identification of *S. Infantis*; discrimination with *S. Newport* and identification of *S. Hadar*; or discrimination with *S. Hadar* and identification of *S. Newport*, respectively. In another aspect, the *Salmonella* serotype is selected from Newport, Heidelberg, Infantis, and Hadar. In another aspect, the oligonucleotides further comprise at least one detection label. In one aspect, the amplification is a multiplex-, or a real-time multiplex-amplification process.

Another embodiment of the present invention includes a kit for the identification of a *Salmonella* serotype comprising: a pair of oligonucleotide primers comprising SEQ ID NOS: 1 and 3, SEQ ID NOS: 4 and 6, SEQ ID NOS: 7 and 9, or SEQ ID NOS: 10 and 12 for the amplification of one or more sequences of one or more *Salmonella* serotypes; one or more probes selected from SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, and SEQ ID NO: 11 for the identification of one or more *Salmonella* serotypes; reagents for PCR amplification; and instructions for determining the *Salmonella* serotype based on the product of amplification using the primers and probes. In one aspect, the kit further comprises at least one selected from a nucleic acid extraction solution; a DNA polymerase; at least one dNTPs; a buffer having a pH adapted to a polymerase activity; a PCR Master Mix; and an instruction set for performing a real-time multiplex amplification to detect a *Salmonella* serotype. In another aspect, the at least one oligonucleotide pair includes the first, second, third and fourth primer sets and the first, second, third and fourth probes, for discrimination with *S. Infantis* and identification of *S. Heidelberg*; discrimination with *S. Heidelberg* and identification of *S. Infantis*; discrimination with *S. Newport* and identification of *S. Hadar*; or discrimination with *S. Hadar* and identification of *S. Newport*, respectively. In one aspect, the amplification is a multiplex-, or a real-time multiplex-amplification process.

Yet another embodiment of the present invention includes a method of detecting *Salmonella* in a sample comprising the steps of: providing a nucleic acid sample suspected of having one or more *Salmonella* serotypes; adding a pair of primers to the nucleic acid sample, wherein the set of primers comprise at least one primer set selected from SEQ ID NOS: 1 and 3; SEQ ID NOS: 4 and 6; SEQ ID NOS: 7 and 9; and SEQ ID NOS: 10 and 12; contacting the amplified nucleic acid sample with one or more *Salmonella* isolate identification probes selected from SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, and SEQ ID NO: 11; amplifying the nucleic acid sample using the set of primers to form an amplified nucleic acid sample; and detecting the presence of the one or more *Salmonella* isolate identification probes, wherein a positive detection is indicative of at least one *Salmonella* being present in the sample. In one aspect, the amplified nucleic acid sample is a double stranded DNA and the one or more *Salmonella* isolate identification probes are destroyed by a 5' to 3' exonuclease activity of a polymerase thereby releasing the positive detection, wherein the positive detection is a free fluorophore. In another aspect, the method further comprises the step of homogenizing a tissue sample to produce a nucleic acid sample. In another embodiment, the method further comprises the step of extracting the nucleic acids from a homogenized sample. In another aspect, the at least one oligonucleotide pair includes the first, second, third and fourth primer sets and the first, second, third and fourth probes, for discrimination with *S. Infantis* and identification of *S. Heidelberg*; discrimination with *S. Heidelberg* and identification of *S. Infantis*; discrimination with *S. Newport* and identification of *S. Hadar*; or discrimination with *S. Hadar* and identification of *S. Newport*, respectively. In another aspect, the process is a real-time amplification process. In one aspect, the amplification is a multiplex-, or a real-time multiplex-amplification process.

Yet another embodiment of the present invention includes a method of checking the safety of a foodstuff for *Salmonella* comprising the steps of: providing a foodstuff suspected of being contaminated with *Salmonella*; homogenizing the foodstuff; extracting a nucleic acid sample from a homogenized foodstuff; adding a set of primers to the nucleic acid sample, wherein the set of primers comprise at least one primer set selected from SEQ ID NOS: 1 and 3; SEQ ID NOS: 4 and 6; SEQ ID NOS: 7 and 9; and SEQ ID NOS: 10 and 12; adding one or more *Salmonella* isolate identification probes to the nucleic acid sample, wherein the one or more *Salmonella* isolate identification probes are selected from SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, and SEQ ID NO: 11; amplifying the nucleic acid sample using the set of primers to form an amplified nucleic acid sample to form a double stranded DNA; destroying the one or more *Salmonella* isolate identification probes as the double stranded DNA is formed; releasing a

fluorophore attached to the one or more *Salmonella* isolate identification probes; and detecting the presence of the fluorophore, wherein a positive detection is indicative of at least one *Salmonella* being present in the sample. In one aspect, the foodstuff is for human consumption, animal consumption or both. In another aspect, the foodstuff is a food or a beverage. In another aspect, the at least one oligonucleotide pair includes the first, second, third and fourth primer sets and the first, second, third and fourth probes, for discrimination with *S. Infantis* and identification of *S. Heidelberg*; discrimination with *S. Heidelberg* and identification of *S. Infantis*; discrimination with *S. Newport* and identification of *S. Hadar*; or discrimination with *S. Hadar* and identification of *S. Newport*, respectively. In one aspect, the amplification is a multiplex-, or a real-time multiplex-amplification process.

Yet another embodiment of the present invention includes a primer-probe set for real-time PCR assays to identify *Salmonella* isolate comprising: at least one oligonucleotide set selected from SEQ ID NOS: 1 and 3, SEQ ID NOS: 4 and 6, SEQ ID NOS: 7 and 9, and SEQ ID NOS: 10 and 12 for the amplification of one or more sequences of one or more *Salmonella* serotype. In one aspect, primer-probe set further comprises one or more probes selected from SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, and SEQ ID NO: 11 for the identification of one or more *Salmonella* isolate. In one aspect, the primers and probes are used in an amplification that is a multiplex-, or a real-time multiplex-amplification process.

Yet another embodiment of the present invention includes a method of checking the safety of a foodstuff for *Salmonella* comprising the steps of: providing a foodstuff suspected of being contaminated with *Salmonella*; homogenizing the foodstuff; extracting a nucleic acid sample from a homogenized foodstuff; determining the presence or absence of one or more of the following: *Salmonella* selected from Newport, Heidelberg, Infantis, and Hadar using primers and probes SEQ ID NO: 13 to 24; and identifying further a *Salmonella* serotype comprising: at least one oligonucleotide pair selected from: a first primer set having SEQ ID NOS: 1 and 3 for the amplification of one or more sequences and a first probe having SEQ ID NO: 2 for discrimination with *S. Infantis* and identification of *S. Heidelberg*; a second primer set having SEQ ID NOS: 4 and 6 for the amplification of one or more sequences and a second probe having SEQ ID NO: 5 for discrimination with *S. Heidelberg* and identification of *S. Infantis*; a third primer set having SEQ ID NOS: 7 and 9 for the amplification of one or more sequences and a third probe having SEQ ID NO: 8 for discrimination with *S. Newport* and identification of *S. Hadar*; or a fourth primer set having SEQ ID NOS: 10 and 12 for the amplification of one or more sequences and a fourth probe having SEQ ID NO: 11 for discrimination with *S. Hadar* and

identification of *S. Newport*. In one aspect, the amplification is a multiplex-, or a real-time multiplex-amplification process.

Description of the Drawings

None.

5 Description of the Invention

While the making and using of various embodiments of the present invention are discussed in detail below, it should be appreciated that the present invention provides many applicable inventive concepts that can be embodied in a wide variety of specific contexts. The specific embodiments discussed herein are merely illustrative of specific ways to make and use
10 the invention and do not delimit the scope of the invention.

To facilitate the understanding of this invention, a number of terms are defined below. Terms defined herein have meanings as commonly understood by a person of ordinary skill in the areas relevant to the present invention. Terms such as “a”, “an” and “the” are not intended to refer to only a singular entity, but include the general class of which a specific example may be
15 used for illustration. The terminology herein is used to describe specific embodiments of the invention, but their usage does not delimit the invention, except as outlined in the claims.

Various *Salmonella* strains are common foodborne microbes that cause disease in humans and animals. For example, some strains can cause intestinal infections, while others can cause typhoid fever. Because of the large variety of *Salmonella* strains present and the different
20 pathogenic effects of these strains, it is important to develop rapid and flexible assays that have the capacity to distinguish between these strains.

Presently, *Salmonella* serotype determination takes a long period of time and can be inaccurate. This technology allows for the rapid characterization of *Salmonella*, and specifically distinguishes between those serotypes in the United States and European Union, allowing
25 government and industry to make a determination of a serotype within hours that would have previously taken days. For the most part *Salmonella* serotyping has been used to characterize isolates from culture confirmed samples. The present invention provides screening enrichments for the presence (or absence) of regulated (and potentially regulated) *Salmonella* serotypes so that the decision can be made to accept or reject a food product. This benefit is especially
30 important with regard to perishable food products.

The invention provides oligonucleotides that enable the detection of *Salmonella* by nucleic acid hybridization, notably by nucleic acid amplification, more particularly, by PCR, advantageously by multiplex amplification (e.g., multiplex PCR), very advantageously, by real-time multiplex amplification (e.g., real-time multiplex PCR).

5 The present invention provides a primer-probe based real-time PCR (RTi PCR) assays to identify whether a *Salmonella* isolate (belongs to the regulated serotypes: 1 assay for Europe and 1 assay for the United States) or if it is outside of that group of serotypes. Specifically, unique primers and probes were developed to detect, e.g., genes SNSL254_A0607 (for Newport and Hadar, Accession number CP001113), , SNSL254_A0607 (for Newport and Hadar, Accession
10 number CP001113), and CFSAN002069_17050 (for Heidelberg and Infantis, Accession number CP005390), for the 4 out of the 5 regulated serotypes in the European Union. With this approach, the invention can be used to accurately determine the presence of a *Salmonella* isolate belonging to the regulated and/or potentially regulated serotypes selected from Newport, Heidelberg, Infantis, and Hadar.

15 The present invention includes a rapid assay to quickly categorize a *Salmonella* isolate in the United States or European Union depending on the gene targets (and identify them as regulated and/or potentially regulated), selected from Newport, Heidelberg, Infantis, and Hadar. This invention allows key stakeholders (i.e., government and industry) to quickly make decision (within hours) that today would take days to determine which is important for perishable
20 products. The present invention provides an assay that can quickly recognize whether or not a sample contains a regulated (or potentially regulated) *Salmonella* serotype. In addition, the assay could be used for downstream applications to characterize suspect colonies on plates.

 Presently *Salmonella* serotype determination takes a long period of time and is invariably inaccurate. The present invention allows for the rapid characterization of *Salmonella* as being
25 regulated or not. Also, if it is regulated, the present invention can be used to further categorize which of the regulated serotypes it is. The present invention includes primers to detect 2 batteries of sequences one specifically for the United States and one for the European Union.

 Serotypes were selected to be tested against the markers in the RT PCR assay based on their prevalence in human and non-human cases of salmonellosis, according to data collected by
30 the CDC. In addition to the five targeted serotypes, 30 serotypes with the highest percentages of reported cases of salmonellosis attribution were included. Also included in the exclusivity panel were serotypes that very rarely caused disease, or only caused disease in animals. To investigate the intra-serotype variability, when it was possible, the present inventors selected at least 25

strains for each targeted serotype and 5 strains for each of the 30 most prevalent serotypes. In total, the exclusivity panel includes 121 serotypes from *S. enterica* subsp. *enterica*, together with few strains of the 5 other *Salmonella* subspecies. Also included outside genus isolates from the Enterobacteriaceae family as well as similar organisms to *Salmonella enterica*. These strains

5 belong to 13 different genera. The inclusivity panel included *S. Typhimurium* (25), *S. Enteritidis* (26), *S. Newport* (30); 4 of which were characterized as clade A and 5 as clade B, *S. Heidelberg* (27) and *S. Hadar* (25). The exclusivity panel included *Salmonella* strains: S.I 4,5,12:b:- (1), S.I 4,5,12:b:- var. L(+) tartrate (1), S.I 1,4,[5],12:i:- (17), S.I 4,5,12:r:- (1), S.I 1,4,[5],12:-:1,2 (1), S.I 6,7:-:1,5 (1), S.I 6,7:k:- (1), S.II (2), S.IIIa 18:z4,z23:- (1), S.IIIa (1),

10 S.IIIb 50:k:z (1), S.IIIb 50:r:z (1), S.IIIb 61:l,v:1,5,7 (1), S.IV 44:z4,z23:- (1), S.IV 48:g,z51:- (1), S.IV 50:g,z51:- (1), S.V (1), Aarhus (1), Aberdeen (1), Abony (1), Adelaide (1), Agbeni (1), Agona (5), Alachua (1), Albany (1), Amager (1), Anatum (4), Anatum variant 15+ (1), Apapa (1), Arechaveleta (1), Baildon (1), Bardo (1), Bareilly (5), Barranquilla (1), Berta (1), Blockley (1), Bovismorbificans (1), Braenderup (5), Brandenburg (3), Bredeney (4), Carrau (1), Cerro (5),

15 Chester (1), Choleraesuis (1), Colindale (1), Concord (1), Copenhagen (1), Corvallis (1), Cotham (1), Cubana (1), Derby (3), Dublin (3), Durban (1), Ealing (1), Florida (1), Gaminara (1), Give (3), Give variant 15+ (1), Glostrup (1), Grumpensis (1), Hartford (1), Havana (2), Hindmarsh (1), Holcomb (1), Hvitthvingfoss (1), Ibadan (1), Indiana (1), Infantis (12), Inverness (1), Istanbul (1), Itami (1), Javiana (5), Johannesburg (1), Kentucky (12), Kiambu (1), Kintambo

20 (1), Kottbus (1), Kuzendorf (1), Lexington (1), Lille (4), Litchfield (1), Liverpool (1), Livingstone (1), London (1), Luciana (1), Madelia (1), Manhattan (2), Mbandaka (6), Meleagridis (5), Miami (1), Mikawasima (1), Minnesota (1), Mississippi (5), Monschau (1), Montevideo (11), Muenchen (9), Muenster (2), Napoli (1), Norwich (1), Ohio (2), Oranienburg (5), Orion (1), Panama (2), ParatyphiB (5), Pomona (1), Poona (1), Potsdam (1), Putten (1),

25 Reading (11), Richmond (1), Rissen (1), Roodeport (1), Rubislaw (1), SaintPaul (5), SanDiego (1), Saphra (1), Schwarzengrund (5), Senftenberg (5), Stanley (1), Sundsvall (2), Telekelbir (1), Tennessee (1), Thompson (5), Typhi (5), Uganda (2), Urbana (1), Virchow (10), Wandsworth (1), Waycross (1), Weltevreden (1), Worthington (4). The non-*Salmonella* strains included *Aeromonas hydrophila/caviae* (1), *Citrobacter freundii* (1), *Cronobacter sakazakii* (1),

30 *Enterobacter aerogenes* (1), *Hafnia paralvei* (1), *Klebsiella oxytoca* (1), *Klebsiella pneumoniae* (1), *Pantoea agglomerans* (1), *Pseudomonas fluorescens* (1), *Pseudomonas fragi* (1), *Pseudomonas aeruginosa* (1), *Proteus vulgaris* (1), *Serratia marcesans* (1), *Shigella flexneri* (1), *Shigella sonnei* (1), *Vibrio mimicus* (1), *Vibrio parahaemolyticus* (1), *Yersinia enterocolitica* (1).

The present invention provided DNA extractions that were either provided or were performed as described herein. In brief, organisms were grown up on a BHI agar plate and one isolated colony was transferred into 50µl of distilled water. The tubes were incubated for 10 minutes at 95-99°C and then centrifuged for 3 minutes at maximum speed. The supernatant containing the DNA was then transferred to a fresh 1.5ml microcentrifuge tube and stored at -20°C until use. DNA extractions provided by ANSES were performed using the Instagene Matrix (BioRad, Berkeley, CA, USA) following the manufacturer's recommendations. The PureLink Genomic DNA Mini Kit (Invitrogen, Carlsbad, CA, USA) was used to extract the genomic DNA following the manufacturer's recommendations, and it was then quantified using the Nanodrop 2000c Spectrophotometer (ThermoScientific, Waltham, MA, USA).

The present invention provided RNA extractions from an overnight culture of each of the 5 serotypes of interest. Cultures were grown in 50mL flasks with an estimated final concentration of roughly 10^9 CFU/ml. The cultures were pelletized and treated with RNA Protect (Qiagen, Venlo, The Netherlands) for overnight storage. Extraction was performed using a modified version of the TRI Reagent protocol (Molecular Research Center, Inc., Cincinnati, OH). Briefly, pelleted cells were resuspended in TRI Reagent to lyse, and then bromochloropropane (BCP) was added to induce phase separation. A supernatant containing RNA was transferred to a new tube, then isopropanol was added to precipitate the RNA, the tubes were spun to pelletize the RNA, and then this supernatant was removed. The pellets were washed with an Ethanol solution, dried, treated with DNase (Promega, Madison, WI), quantified using the Nanodrop 2000c Spectrophotometer (ThermoScientific, Waltham, MA, USA), and stored in -80°C until ready for use in quantitative reverse transcriptase (qRT) realtime (RTi) PCR. The Black Hole Quencher Dye-2 (BHQ-2™) (Sigma-Aldrich), and HEX™ dye (Life Technologies) were used as instructed for inclusion in an oligonucleotide, e.g., as a HEX™ dye or BHQ-2 Phosphoramidite.

The present inventors have previously identified molecular markers to specifically detect the four important serotypes of *Salmonella*: Newport, Heidelberg, Infantis, and Hadar. However, only the serotypes Typhimurium and Enteritidis are specifically identified using their respective markers, STM2 and Ent6. The marker Heid2 detects both *S. Heidelberg* and *S. Infantis* strains. In addition, the marker Newp2 detects both *S. Newport* and *S. Hadar*. In order to clarify the identity of the detected strains with Heid2 and Newp2 markers, the present inventors developed a new set of 4 markers that allow the discrimination between the related serotypes with the previous set of markers.

Table 1. Table of oligonucleotides and sequences (F - Forward Primer, R - Reverse Primer, P - Probe).

Primer ID	Sequence (5'...3')	Comment
Heidspe-F3	TCATGATTATGCCGAAATTATGCG (SEQ ID NO.:1)	Discrimination with <i>S. Infantis</i> and identification of <i>S. Heidelberg</i>
Heidspe-P3	HEX-AATGGTGGTTGGGATTGGGATAGGTCTC-BHQ2 (SEQ ID NO.:2)	
Heidspe-R3	ATCATAAGAGACTAATTGCCCATC (SEQ ID NO.:3)	
Infspe-F2	AAGTTGCCCCCTTGAGTTCC (SEQ ID NO.:4)	Discrimination with <i>S. Heidelberg</i> and identification of <i>S. Infantis</i>
Infspe-P2	FAM-TGTTGCCAGCGGCATGAAGAAAATCCC-BHQ1 (SEQ ID NO.:5)	
Infspe-R2	AATGTGCGCACGTTTGGTGG (SEQ ID NO.:6)	
Hadspe-F1	GAATCAAACCGCTTTATGGTGC (SEQ ID NO.:7)	Discrimination with <i>S. Newport</i> and identification of <i>S. Hadar</i>
Hadspe-P1	FAM-ATCCGGCGCTGCATGGGTATATGACC-BHQ1 (SEQ ID NO.:8)	
Hadspe-R1	TGCTCTTGAGCATCCCGTTG (SEQ ID NO.:9)	
Newpspe-F1	TGATGCTTTCTTATTATGAACAAGG (SEQ ID NO.:10)	Discrimination with <i>S. Hadar</i> and identification of <i>S. Newport</i>
Newpspe-P1	HEX-ATTATTCTGAGCTAACGCCATCGCAGAGG-BHQ2 (SEQ ID NO.:11)	
Newpspe-R1	TCTATAGGCATATGAATACTCGC (SEQ ID NO.:12)	

Table 2. Each marker has been evaluated on a set of DNA extractions of strains belonging to the targeted serotype (inclusivity) and of the non-targeted serotype (exclusivity). Furthermore, the expression of the targeted region was investigated for each marker.

Marker ID	Inclusivity	Exclusivity	Expression
Heidspe3	<u>Heidelberg</u> : Detection of 23/23	<u>Infantis</u> : Detection of 0/11	Yes
Infspe2	<u>Infantis</u> : Detection of 11/11	<u>Heidelberg</u> : Detection of 0/23	Yes
Hadspe1	<u>Hadar</u> : Detection of 22/22	<u>Newport</u> : Detection of 0/28	No
Newspe1	<u>Newport</u> : Detection of 28/28	<u>Hadar</u> : Detection of 0/22	No

Table 3. Discrimination between serotypes.

ID	Serotype	Infspe2	Heidspe3	Newspe1	Hadspe1	Heid2
Expression investigation from samples growth into BHI at 37C		really low level of expression	expressed	not expressed	not expressed	
R1-023	Newport (T+)			1	0	
R1-024	Newport			1	0	
R1-025	Newport			1	0	
R1-026	Newport			1	0	
R1-027	Newport			1	0	

ID	Serotype	InfSpe2	HeidSpe3	NewSpe1	HadSpe1	Heid2
R1-028	Newport			1	*	
R1-029	Newport			1	0	
R1-030	Newport			1	0	
R1-031	Newport			1	0	
R1-032	Newport			1	0	
R1-033	Newport			1	0	
R1-034	Newport			1	0	
R1-035	Newport			1	0	
R1-036	Newport			1	0	
R1-037	Newport			1	0	
R1-038	Newport			1	0	
R1-039	Newport			1	0	
R1-041	Newport			1	0	
R1-042	Newport			1	0	
T1-470	Newport			1	0	
T1-471	Newport			1	0	
T1-472	Newport			1	0	
T1-473	Newport			1	0	
T1-474	Newport			1	0	
T1-475	Newport			1	0	
T1-476	Newport			1	0	
T1-477	Newport			1	0	
T1-478	Newport			1	0	
T1-248	Hadar (not detected with 1st screening)			0	*	
T1-391	Hadar (not detected with 1st screening)			0	0	
T1-213	Hadar (T+)			0	1	
T1-231	Hadar			0	1	
T1-235	Hadar			0	1	
T1-267	Hadar			0	1	
T1-289	Hadar			0	1	
T1-314	Hadar			0	1	
T1-332	Hadar			0	1	
T1-357	Hadar			0	1	
T1-358	Hadar			0	1	
T1-359	Hadar			0	1	
T1-361	Hadar			0	1	
T1-362	Hadar			0	1	
T1-363	Hadar			0	1	
T1-364	Hadar			0	1	

ID	Serotype	InfSpe2	HeidSpe3	Newspe1	Hadspe1	Heid2
T1-366	Hadar			0	1	
T1-373	Hadar			0	1	
T1-374	Hadar			0	1	
T1-378	Hadar			0	1	
T1-379	Hadar			0	1	
T1-382	Hadar			0	1	
T1-387	Hadar			0	1	
T1-391	Hadar			0	1	
12TT	Infantis (T+)	1	0			
21TT	Infantis	1	0			
26TT	Infantis	1	0			
281TT	Infantis	1	0			
282TT	Infantis	1	0			
284TT	Infantis	1	0			
294TT	Infantis	1	0			
29TT	Infantis	1	0			
307TT	Infantis	1	0			
40TT	Infantis	1	0			
C-043	Infantis	1	0			
T1-480	Heidelberg (T+)	0	1			
T1-481	Heidelberg	0	1			
T1-482	Heidelberg	0	1			
T1-483	Heidelberg	*	1			
T1-484	Heidelberg	*	1			
T1-485	Heidelberg	*	1			
T1-486	Heidelberg	*	1			
T1-487	Heidelberg (not detected with 1st screening)	*	0			
T1-488	Heidelberg	*	1			
T1-489	Heidelberg	*	1			
T1-490	Heidelberg	*	1			
T1-491	Heidelberg	*	1			
T1-492	Heidelberg	*	1			
T1-510	Heidelberg	0	1			
T1-511	Heidelberg	*	1			
T1-512	Heidelberg	*	1			
T1-513	Heidelberg	*	1			
T1-514	Heidelberg	*	1			
T1-515	Heidelberg	0	1			
T1-516	Heidelberg	*	1			
T1-518	Heidelberg	*	1			

ID	Serotype	InfSpe2	HeidSpe3	Newspe1	Hadspe1	Heid2
T1-519	Heidelberg	*	1			
T1-520	Heidelberg	*	1			
T1-521	Heidelberg	*	1			
T1-522	Heidelberg	*	1			
T1-293	Aarhus	*				0
T1-273	Aberdeen	0				0
T1-456	Abony	0				0
T1-204	Agona	0				0
T1-340	Amager	0				0
C-001	Anatum	0				0
T1-421	Apapa	*				0
T1-458	Arechavaleta	0				0
T1-263	Baildon	0				0
T1-228	Bareilly	1				0
T1-316	Barranquilla	*				0
T1-216	Berta	0				0
T1-347	Braenderup	1				0
1838	Brandenburg	*				0
25RV	Cerro	0				0
T1-448	Cholerasuis	1				0
T1-439	Colindale	1				0
T1-304	Concord	1				0
T1-202	Copenhagen	0				0
T1-310	Cotham	0				0
T1-281	Dublin	0				0
T1-405	Durban	0				0
C2-060	Enteritidis	0				0
T1-452	Florida	0				0
T1-210	Gaminara	0				0
1833	Give	0				0
T1-355	Glostrup	0				0
T1-213	Hadar	0				0
T1-377	Hindmarsh	0				0
T1-224	Holcomb	0				0
T1-388	Inverness	0				0
T1-432	Istanbul	0				0
T1-211	Javiana	0				0
1780	Kentucky	0				0
T1-455	Kintambo	0				1
T1-375	Lexington	0				0
14TT	Lille	*				0
T1-440	Liverpool	0				0
T1-392	Livingstone	1				0

ID	Serotype	InfSpe2	HeidSpe3	Newspe1	Hadspe1	Heid2
T1-381	Luciana	0				0
75TT	Manhattan	0				0
1811	Mbandaka	*				0
471	Meleagridis	0				0
T1-265	Mikawasima	1				0
T1-218	Mississippi	0				0
272	Montevideo	1				0
1011TT	Muenchen	0				0
T1-470	Newport-A	0				0
T1-474	Newport-B	1				0
T1-422	Norwich	0				0
1890	Ohio	*				0
T1-275	Oranienburg	1				0
1853	Panama	0				0
T1-321	ParatyphiB	*				0
T1-271	Pomona	0				0
T1-214	Putten	0				0
680	Reading	0				0
T1-215	Richmond	0				0
T1-424	Roodeport	0				0
T1-396	S.I 1,4,[5],12:- :1,2	*				0
R1-142	S.I 1,4,[5],12:i:-	0				0
T1-429	S.I 1,4,5,12:b:- var. L(+) tartrate +	0				0
T1-354	S.I 4,5,12:b:-	*				0
T1-416	S.I 4,5,12:r:-	0				1
T1-259	S.I 6,7:-:1,5	1				0
T1-370	S.I 6,7:k:-	1				0
T1-305	S.II salamae	*				0
T1-401	S.IIIb 50:k:z	0				0
T1-451	S.IIIb 50:r:z	0				0
T1-436	S.IIIb 61:l,v:1,5,7	0				0
T1-390	S.IV 44:z4,z23:- (a4,a23)	0				0
T1-272	S.IV 48:g,z51:-	0				0
T1-446	S.IV 50:g,z51:-	1				0
T1-209	S.V	*				0

ID	Serotype	InfSpe2	HeidSpe3	NewSpe1	HadSpe1	Heid2
T1-246	SaintPaul	0				0
T1-450	Saphra	0				0
T1-203	Schwarzengr und	0				0
T1-208	Senftenberg	0				0
T1-441	Sundsvall	1				0
T1-319	Telekelbir	*				0
T1-221	Thompson	1				0
T1-317	Typhi	0				0
R1-089	Typhimurium	0				0
1842	Uganda	*				0
T1-447	Virchow	*				*
T1-212	Wandsworth	0				0
T1-404	Waycross	0				0
T1-302	Worthington	0				0

Raw data, * means delayed signal (above 32 cycle for the Ct)

Thus, the present invention can be used to identify the following serotypes of *Salmonella*, Newport, Heidelberg, Infantis, and Hadar.

It will be understood that the present invention includes sequences similar to the primer and probe sequences listed herein. The included sequences have a homology of between 85 and 100% homology to the sequences listed herein. For example, the homology may be 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent to the primers and sequences listed herein.

The methods of the invention can be applied to detection of *Salmonella* in a variety of samples, including foodstuff samples. Such foodstuff samples can be derived from, e.g., beef (e.g., frozen or raw), chicken (e.g., cooked deli or raw), cod, cookie dough, eggs, lettuce, tomatoes, turkey (e.g., cooked deli or raw), black pepper, cheese (e.g., string cheese), chocolate (e.g., milk), cocoa, eggs (e.g., pasteurized, dried, or whole), milk (e.g., instant, nonfat, or dry), nacho cheese seasoning, pasta, pet food, peanut butter (e.g., non-organic and/or creamy), or soy flour. Other samples include environmental samples (e.g., plastic, sealed concrete, and stainless steel). The methods can be performed at the farm or processing facility prior to initial packaging, after packaging (e.g., prior to or after export from one country to another), or at the point of sale.

The present invention can be used alone, or in combination with additional probes to more fully characterize the different *Salmonella*. Additional primers for use with the present

invention also include those listed in Table 4. These primers can be used prior to the screen of the present invention to determine *Salmonella* serotypes selected from *S. Newport*, *S. Heidelberg* and *S. Hadar* depending on the primer set and the corresponding probe. As such, the present invention also includes the method of determining which of the following *Salmonella* serotypes are present in a sample selected from *S. Newport*, *S. Heidelberg*, *S. Infantis*, and *S. Hadar*.

Table 4. The primer and probe sequences are shown in the table below:

Name	Sequence (5'... 3')	
Ent6 Forward Primer (FPrimer)	TCGTACCTGCTGATGCTGGG	SEQ ID NO:13
Ent6 Probe	HEX-TATGCGCTGGTTCCGTTCCGTTTCTGG-BHQ2	SEQ ID NO:14
Ent6 Reverse Primer (RPrimer)	AGGATGAAGACGGGTAATGTCC	SEQ ID NO:15
Newp2 FPrimer	AATGGCTGGTAGCCTGTTCG	SEQ ID NO:16
Newp2 Probe	Cy5-TCATGCTATGCACTGGGAACAATTTCTGGC-Iowa BRQ	SEQ ID NO:17
Newp2 RPrimer	AGGGAAAGCAAGGAACAGTAG	SEQ ID NO:18
STM2 FPrimer	AGATATTCCGTAGCAATTGAGTTG	SEQ ID NO:19
STM2 Probe	FAM-TGTGTTCAAGCAATGGTGAACAAACATAATCCC- BHQ2	SEQ ID NO:20
STM2 RPrimer	AATAGCTAAAAATGACTGGGACTC	SEQ ID NO:21
Heid2 FPrimer	CCTGCAGAAAGATATGTTTGGC	SEQ ID NO:22
Heid2 Probe	HEX-TTAATCTGTGCGACGAATTGGGCAGCC-BHQ2	SEQ ID NO:23
Heid2 RPrimer	TGCGATGAAGATTGATGATGCC	SEQ ID NO:24

Using the primers hereinabove, it was previously found by the present inventors that *S. Typhimurium* marker (STM2) detects 100% of *S. Typhimurium* and its somatic and flagellar variant (1,4,[5],12:i:-, 1,4,[5],12:-:1,2 and *S. Copenhagen*) strains tested, as well as one strain that had been serotyped as Heidelberg. This strain of *S. Heidelberg*, however, did not amplify with the Heidelberg marker (Heid2), and is likely to have been mis-serotyped.

The Heidelberg marker (Heid2) detected all the other *S. Heidelberg* isolates tested, but also amplified all 12 of the *S. Infantis* strains that were tested against this marker. This marker detects also one *S. Kintambo* strain and one *S. I 4,5,12:r:-* strain. Together these 3 cross-reacting serotypes represent less than 2% of human and non-human cases in the United States between 1999 and 2009 (National *Salmonella* Surveillance Annual Summary 2009).

The Newport marker (Newp2) detected all *S. Newport* strains tested, including isolates from both clades A and B, as well as 23 of 25 *S. Hadar* strains that were tested in the study. Furthermore, this marker also detects few strains belonging to other serotypes, such as Bardo, Blockley, Bovismorbificans, Glostrup, Istanbul, Kottbus, Litchfield, Manhattan, Muenchen, and Virchow.

The Enteritidis marker (Ent6) detects 24 out of the 26 *S. Enteritidis* strains tested. This marker does not strongly cross-react with non-targeted serotypes, but present several weak cross-reactions with diverse serotypes.

Furthermore, the inventors investigated the expression of these 4 targeted regions. The inventors were able to highlight the expression of the targeted regions for *S. Typhimurium*, *S. Heidelberg* and *S. Newport* markers. Only the Enteritidis marker seems to be located on a non-coding region.

Marker	Targeted serotypes	Inclusivity panel	Cross-reacted serotypes	% cross-reactivity ^a	Diagnostic sensitivity ^b	Diagnostic specificity ^c
STM2	Typhimurium and its variants	44/44	/	0%	1	1
Ent6	Enteritidis	24/26	/	0%	0.96	1
Heid2	Heidelberg	26/27	Infantis, Kintambo, S.I 4,5,12:r:-	1.526%	0.96	0.97
Newp2	Newport and Hadar	53/55	Bardo, Blockley, Glostrup, Bovismorbificans, Istanbul, Kottbus, Litchfield, Muenchen, Manhattan, Virchow	3.582%	0.96	0.97

^a in human cases in the US between 1999 and 2009 according to the CDC report titled National *Salmonella* Surveillance Annual Summary 2009. Only the strong cross-reactions with a Ct< 32 were considered. ^b Diagnostic sensitivity: number of true positive/ number of expected positive (Saah and Hoover, 1997). ^c Diagnostic specificity: number of true negative/ number of expected negative (Saah and Hoover, 1997).

It is contemplated that any embodiment discussed in this specification can be implemented with respect to any method, kit, reagent, or composition of the invention, and vice versa. Furthermore, compositions of the invention can be used to achieve methods of the invention.

It will be understood that particular embodiments described herein are shown by way of illustration and not as limitations of the invention. The principal features of this invention can be employed in various embodiments without departing from the scope of the invention. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, numerous equivalents to the specific procedures described herein. Such equivalents are considered to be within the scope of this invention and are covered by the claims.

All publications and patent applications mentioned in the specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

The use of the word “a” or “an” when used in conjunction with the term “comprising” in the claims and/or the specification may mean “one,” but it is also consistent with the meaning of “one or more,” “at least one,” and “one or more than one.” The use of the term “or” in the claims is used to mean “and/or” unless explicitly indicated to refer to alternatives only or the alternatives are mutually exclusive, although the disclosure supports a definition that refers to only alternatives and “and/or.” Throughout this application, the term “about” is used to indicate that a value includes the inherent variation of error for the device, the method being employed to determine the value, or the variation that exists among the study subjects.

As used in this specification and claim(s), the words “comprising” (and any form of comprising, such as “comprise” and “comprises”), “having” (and any form of having, such as “have” and “has”), “including” (and any form of including, such as “includes” and “include”) or “containing” (and any form of containing, such as “contains” and “contain”) are inclusive or open-ended and do not exclude additional, unrecited elements or method steps.

The term “or combinations thereof” as used herein refers to all permutations and combinations of the listed items preceding the term. For example, “A, B, C, or combinations thereof” is intended to include at least one of: A, B, C, AB, AC, BC, or ABC, and if order is important in a particular context, also BA, CA, CB, CBA, BCA, ACB, BAC, or CAB. Continuing with this example, expressly included are combinations that contain repeats of one or more item or term, such as BB, AAA, AB, BBC, AAABCCCC, CBBAAA, CABABB, and so forth. The skilled artisan will understand that typically there is no limit on the number of items or terms in any combination, unless otherwise apparent from the context.

All of the compositions and/or methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the compositions and/or methods and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

Claims:

1. A pair of oligonucleotides for the identification of a *Salmonella* serotype comprising:
at least one oligonucleotide pair selected from:

a first primer set having SEQ ID NOS: 1 and 3 for the amplification of one or more
5 sequences and a first probe having SEQ ID NO: 2 for discrimination with *S. Infantis* and
identification of *S. Heidelberg*;

a second primer set having SEQ ID NOS: 4 and 6 for the amplification of one or more
sequences and a second probe having SEQ ID NO: 5 for discrimination with *S. Heidelberg* and
identification of *S. Infantis*;

10 a third primer set having SEQ ID NOS: 7 and 9 for the amplification of one or more
sequences and a third probe having SEQ ID NO: 8 for discrimination with *S. Newport* and
identification of *S. Hadar*; or

a fourth primer set having SEQ ID NOS: 10 and 12 for the amplification of one or more
sequences and a fourth probe having SEQ ID NO: 11 for discrimination with *S. Hadar* and
15 identification of *S. Newport*.

2. The oligonucleotides of claim 1, wherein the at least one oligonucleotide pair includes
the first, second, third and fourth primer sets and the first, second, third and fourth probes, for
discrimination with *S. Infantis* and identification of *S. Heidelberg*; discrimination with *S.*
Heidelberg and identification of *S. Infantis*; discrimination with *S. Newport* and identification of
20 *S. Hadar*; or discrimination with *S. Hadar* and identification of *S. Newport*, respectively.

3. The oligonucleotides of claim 1, wherein the *Salmonella* serotype is selected from
Newport, *Heidelberg*, *Infantis*, and *Hadar*.

4. The oligonucleotides of claim 1, further comprising at least one detection label.

5. A kit for the identification of a *Salmonella* serotype comprising:

25 a pair of oligonucleotide primers comprising SEQ ID NOS: 1 and 3, SEQ ID NOS: 4 and
6, SEQ ID NOS: 7 and 9, or SEQ ID NOS: 10 and 12 for the amplification of one or more
sequences of one or more *Salmonella* serotypes;

one or more probes selected from SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, and
SEQ ID NO: 11 for the identification of one or more *Salmonella* serotypes;

30 reagents for PCR amplification; and

instructions for determining the *Salmonella* serotype based on the product of amplification using the primers and probes.

6. The kit of claim 5, further comprising at least one selected from a nucleic acid extraction solution; a DNA polymerase; at least one dNTPs; a buffer having a pH adapted to a polymerase activity; a PCR Master Mix; and an instruction set for performing a real-time multiplex amplification to detect a *Salmonella* serotype.

7. The kit of claim 5, wherein the at least one oligonucleotide pair includes the first, second, third and fourth primer sets and the first, second, third and fourth probes, for discrimination with *S. Infantis* and identification of *S. Heidelberg*; discrimination with *S. Heidelberg* and identification of *S. Infantis*; discrimination with *S. Newport* and identification of *S. Hadar*; or discrimination with *S. Hadar* and identification of *S. Newport*, respectively.

8. A method of detecting *Salmonella* serotypes in a sample comprising the steps of:
providing a nucleic acid sample suspected of having one or more *Salmonella* serotypes;
adding a pair of primers to the nucleic acid sample, wherein the set of primers comprise at least one primer set selected from SEQ ID NOS: 1 and 3; SEQ ID NOS: 4 and 6; SEQ ID NOS: 7 and 9; and SEQ ID NOS: 10 and 12;

contacting the amplified nucleic acid sample with one or more *Salmonella* isolate identification probes selected from SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, and SEQ ID NO: 11;
amplifying the nucleic acid sample using the set of primers to form an amplified nucleic acid sample; and

detecting the presence of the one or more *Salmonella* isolate identification probes, wherein a positive detection is indicative of at least one *Salmonella* being present in the sample.

9. The method of claim 8, wherein the amplified nucleic acid sample is a double stranded DNA and the one or more *Salmonella* isolate identification probes are destroyed by a 5' to 3' exonuclease activity of a polymerase thereby releasing the positive detection, wherein the positive detection is a free fluorophore.

10. The method of claim 8, further comprising the step of homogenizing a tissue sample to produce a nucleic acid sample.

11. The method of claim 8, further comprising the step of extracting the nucleic acids from a homogenized sample.

12. The method of claim 8, wherein the at least one oligonucleotide pair includes the first, second, third and fourth primer sets and the first, second, third and fourth probes, for discrimination with *S. Infantis* and identification of *S. Heidelberg*; discrimination with *S. Heidelberg* and identification of *S. Infantis*; discrimination with *S. Newport* and identification of *S. Hadar*; or discrimination with *S. Hadar* and identification of *S. Newport*, respectively.
14. The method of claim 8, which is a multiplex-, or a real-time multiplex-amplification process.
15. A method of checking the safety of a foodstuff for *Salmonella* serotypes comprising the steps of:
- 10 providing a foodstuff suspected of being contaminated with *Salmonella*;
homogenizing the foodstuff;
extracting a nucleic acid sample from a homogenized foodstuff;
adding a set of primers to the nucleic acid sample, wherein the set of primers comprise at least one primer set selected from SEQ ID NOS: 1 and 3; SEQ ID NOS: 4 and 6; SEQ ID NOS: 15 7 and 9; and SEQ ID NOS: 10 and 12;
adding one or more *Salmonella* isolate identification probes to the nucleic acid sample, wherein the one or more *Salmonella* isolate identification probes are selected from SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, and SEQ ID NO: 11;
amplifying the nucleic acid sample using the set of primers to form an amplified nucleic acid sample to form a double stranded DNA;
20 destroying the one or more *Salmonella* isolate identification probes as the double stranded DNA is formed;
releasing a fluorophore attached to the one or more *Salmonella* isolate identification probes; and
25 detecting the presence of the fluorophore, wherein a positive detection is indicative of at least one *Salmonella* being present in the sample.
16. The method of claim 15, wherein the foodstuff is for human consumption, animal consumption or both.
17. The method of claim 15, wherein the foodstuff is a food or a beverage.

18. The method of claim 15, wherein the at least one oligonucleotide pair includes the first, second, third and fourth primer sets and the first, second, third and fourth probes, for discrimination with *S. Infantis* and identification of *S. Heidelberg*; discrimination with *S. Heidelberg* and identification of *S. Infantis*; discrimination with *S. Newport* and identification of *S. Hadar*; or discrimination with *S. Hadar* and identification of *S. Newport*, respectively.

19. A primer-probe set for real-time PCR assays to identify *Salmonella* isolate comprising:
at least one oligonucleotide set selected from SEQ ID NOS: 1 and 3, SEQ ID NOS: 4 and 6, SEQ ID NOS: 7 and 9, and SEQ ID NOS: 10 and 12 for the amplification of one or more sequences of one or more *Salmonella* serotype.

20. The primer-probe set of claim 19, further comprising one or more probes selected from SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, and SEQ ID NO: 11 for the identification of one or more *Salmonella* isolate.

21. A method of checking the safety of a foodstuff for *Salmonella* comprising the steps of:
providing a foodstuff suspected of being contaminated with *Salmonella*;
homogenizing the foodstuff;
extracting a nucleic acid sample from a homogenized foodstuff;
determining the presence or absence of one or more of the following: *Salmonella* selected from Newport, Heidelberg, Infantis, and Hadar using primers and probes SEQ ID NO: 13 to 24; and

identifying further a *Salmonella* serotype by a multiplex-, or a real-time multiplex-amplification process using:

at least one oligonucleotide pair selected from:
a first primer set having SEQ ID NOS: 1 and 3 for the amplification of one or more sequences and a first probe having SEQ ID NO: 2 for discrimination with *S. Infantis* and identification of *S. Heidelberg*;

a second primer set having SEQ ID NOS: 4 and 6 for the amplification of one or more sequences and a second probe having SEQ ID NO: 5 for discrimination with *S. Heidelberg* and identification of *S. Infantis*;

a third primer set having SEQ ID NOS: 7 and 9 for the amplification of one or more sequences and a third probe having SEQ ID NO: 8 for discrimination with *S. Newport* and identification of *S. Hadar*; or

5 a fourth primer set having SEQ ID NOS: 10 and 12 for the amplification of one or more sequences and a fourth probe having SEQ ID NO: 11 for discrimination with *S. Hadar* and identification of *S. Newport*.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2016/024990

A. CLASSIFICATION OF SUBJECT MATTER

C12Q 1/68 (2006.01)

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)

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)

WPIAP, EPODOC, TXTE, MEDLINE, CAPLUS, BIOSIS, EMBASE & keywords: Salmonella, Heidelberg, Infantis, Hadar, Newport, primer, PCR and like terms.

GENOMEQUEST: SEQ ID NOs: 1-12

ESPACENET, PUBMED, Internal databases: Inventor names

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	Documents are listed in the continuation of Box C	



Further documents are listed in the continuation of Box C



See patent family annex

* "A"	Special categories of cited documents: document defining the general state of the art which is not considered to be of particular relevance	"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
"E"	earlier application or patent but published on or after the international filing date	"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
"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)	"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
"O"	document referring to an oral disclosure, use, exhibition or other means	"&"	document member of the same patent family
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 3 June 2016	Date of mailing of the international search report 03 June 2016
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA Email address: pct@ipaustalia.gov.au	Authorised officer Richard Filmer AUSTRALIAN PATENT OFFICE (ISO 9001 Quality Certified Service) Telephone No. +61 2 6283 2735

INTERNATIONAL SEARCH REPORT		International application No.
C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		PCT/US2016/024990
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 2012/145557 A1 (LIFE TECHNOLOGIES CORPORATION) 26 October 2012 [0007]-[00027]; SEQ ID NO: 53	1-21
A	GenBank Accession No: CP006053.1, "Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000189, complete genome", 16 July 2013	1-21
A	GenBank Accession No: CP001120.1, "Salmonella enterica subsp. enterica serovar Heidelberg str. SL476, complete genome", 31 January 2014	1-21
A	MAJCHRZAK, M. et al., "TRS-based PCR as a potential tool for inter-serovar discrimination of Salmonella Enteritidis, S. Typhimurium, S. Infantis, S. Virchow, S. Hadar, S. Newport and S. Anatum", Molecular Biology Reports, 2014, vol. 41, pages 7121-7132 Abstract, Materials and Methods	1-21
A	SALEM, I. B. et al., "Two five-plex PCRs methods for identification of common Salmonella spp. serotypes", Annals of Microbiology, 2010, vol. 60, pages 135-141 Abstract, Materials and Methods	1-21
A	LIU, B. et al., "PCR identification of Salmonella serogroups based on specific targets obtained by comparative genomics", International Journal of Food Microbiology, 2011, vol. 144, pages 511-518 Abstract, Materials and Methods	1-21
A	US 2014/0080130 A1 (LIFE TECHNOLOGIES CORPORATION) 20 March 2014 Abstract, [0011]-[0034]	1-21
P,A	WO 2015/148785 A1 (TEXAS TECH UNIVERSITY SYSTEM) 01 October 2015	

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing filed or furnished:
 - a. (means)
☐ on paper
☒ in electronic form
 - b. (time)
☐ in the international application as filed
☒ together with the international application in electronic form
☐ subsequently to this Authority for the purposes of search
2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.
3. Additional comments:

INTERNATIONAL SEARCH REPORT		International application No.	
Information on patent family members		PCT/US2016/024990	
This Annex lists known patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.			
Patent Document/s Cited in Search Report		Patent Family Member/s	
Publication Number	Publication Date	Publication Number	Publication Date
WO 2012/145557 A1	26 October 2012	WO 2012145557 A1	26 Oct 2012
		EP 2699694 A1	26 Feb 2014
		US 2012270216 A1	25 Oct 2012
		US 2015191778 A1	09 Jul 2015
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		US 2015203901 A1	23 Jul 2015
WO 2015/148785 A1	01 October 2015	WO 2015148785 A1	01 Oct 2015
End of Annex			
Due to data integration issues this family listing may not include 10 digit Australian applications filed since May 2001.			