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(54) **Titre : BAG3 EN TANT QUE MARQUEUR SERIQUE ET TISSULAIRE BIOCHIMIQUE**
 (54) **Title: BAG3 AS BIOCHEMICAL SERUM AND TISSUE MARKER**

Figure 10

bag3 score	Sample number	PCA3 score	bag3 score	Sample number	PCA3 score
1.09	1	low	4.92	11	high
2.00	2	low	3.78	12	high
0.62	3	low	2.23	13	high
2.17	4	low	3.48	14	high
1.07	5	low	2.85	15	high
1.39	6	low	1.01	16	high
0.78	7	low	0.79	17	high
1.00	8	low	3.44	18	high
0.66	9	low	2.64	19	high
1.29	10	low	3.71	20	high
bag3 score mean	1.20		2.88		

(57) **Abrégé/Abstract:**

The present disclosure concerns the field of diagnostic biological markers. Specifically the invention relates to BAG3 RNA or a fragment thereof for use as biological markers for the diagnosis of a pathological state. Furthermore, the disclosure involves specific kits and methods, for detecting and/or evaluating the levels of BAG3 RNA or a fragment thereof in a biological sample.

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(57) Abstract: The present disclosure concerns the field of diagnostic biological markers. Specifically the invention relates to BAG3 RNA or a fragment thereof for use as biological markers for the diagnosis of a pathological state. Furthermore, the disclosure involves specific kits and methods, for detecting and/or evaluating the levels of BAG3 RNA or a fragment thereof in a biological sample.

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BAG3 AS BIOCHEMICAL SERUM AND TISSUE MARKER

DESCRIPTION

The present invention concerns BAG3 RNA or a fragment thereof for use as biochemical markers in the diagnosis of a pathological state.

STATE OF THE ART

BAG3 (RefSeq: NP_004272; Gene ID 9531) is a 74 kDa cytoplasmic protein particularly concentrated in the rough endoplasmic reticulum. BAG3 protein belongs to the family of co-chaperones that interact with the ATPase domain of the heat shock protein HSP70 through the structural domain known as BAG domain (110-124 amino acids). In addition to the BAG domain, BAG3 contains a WW domain and a proline-rich repeat (PXXP), that can mediate binding to other proteins. Furthermore, two conserved IPV (Ile-Pro-Val) motifs are located between the WW and the PXXP regions and mediate BAG3 binding to HspB8, a member of the HspB family of molecular chaperones. Therefore BAG3, due to the adaptor nature of its multidomain structure, can interact with different partner proteins. *bag3* gene expression is constitutive in a few normal cell types, including myocytes, and in several primary tumours or tumour cell lines. Moreover it can be induced by a variety of stressors: indeed stressful stimuli activate the heat shock transcription factor (HSF) 1, that is responsible for the expression of stress-activated genes, including *bag3* (Rosati A, Graziano V, De Laurenzi V, Pascale M, Turco MC. BAG3: a multifaceted protein that

regulates major cell pathways. Cell Death Dis. 2011; 2: e141). Evidence indicates that BAG3 has a role in sustaining cell survival, by modulating, in either Hsp70-dependent or -independent fashion, the levels or localisation of apoptosis-regulating proteins, such as IKK γ , Bax or BRAF, depending on cell context.

BAG3 protein appears to be expressed during cardiomyoblasts differentiation and to sustain myogenin expression. These findings indicate an involvement of BAG3 in late heart development (De Marco M, Turco MC, Rosati A. BAG3 protein is induced during cardiomyoblast differentiation and modulates myogenin expression. Cell Cycle. 2011; 10: 850-852). Moreover, in cardiomyocytes BAG3 has been shown to localize at Z-disc and interact with the actin capping protein, CapZ β 1, stabilizing myofibril structure and possibly preserving myofibrillar integrity during mechanical stress. BAG3 mutations can impair the Z-disc assembly and increase the sensitivity to stress-induced apoptosis. In keeping with the role of BAG3 in the survival and myofibrillar integrity in cardiocytes and, in general, in muscle cells, mutations in *bag3* gene have been associated with some forms of myofibrillar myopathy and dilated cardiomyopathy.

Up to now both a cytoplasmic BAG3 and soluble serical form of BAG3 have been detected and found associated with different pathologies, as well as more generally to cell survival.

The need and importance is increasingly felt for the identification of a biological marker which

allows the rapid identification of such pathologies, without having the disadvantages of being associated with invasive diagnostics in a surprisingly specific and sensitive manner, and/or that can allow to early detect the pathology, monitor the effect of therapy, predict the risk of complication, perform an informative follow-up.

SUMMARY OF THE INVENTION

The present invention concerns BAG3 RNA or a fragment thereof for use as biochemical markers in the diagnosis of a pathological state.

Preferably, said BAG3 RNA is a BAG3 mRNA.

According to a preferred embodiment of the present invention said diagnosis is *in vitro* or *ex vivo*.

A further aspect of the present invention is that the recipient of said diagnosis is a mammalian, preferably a human.

As will be further described in the detailed description of the invention, the use of BAG-3 RNA or a fragment thereof of the present invention has the advantages of being specific for a pathological state selected from the group consisting of a heart disease, cancer, diabetes, inflammation and inflammatory related diseases of the skin, nerves, bones, blood vessels and connective tissues.

According to a preferred embodiment of the invention, said heart disease is selected from: angina pectoris, pre-infarction angina, myocardial infarction, heart failure, ischemia, acute coronary disease, acute heart failure, chronic heart failure and iatrogenic heart disease.

According to another preferred embodiment of the

invention, the cancer is selected from: pancreatic cancer, bladder cancer and prostate cancer.

A further embodiment of the present invention is a kit for the detection and/or quantification of BAG3 gene expression in a biological sample characterized by comprising a couple of single-stranded oligonucleotide primers encompassed by the bag3 nucleotide sequence (SEQ ID NO 18).

Preferably said kit comprise a couple of primers selected from those having a nucleotide sequence included in one of the region from nucleotide 1 to nucleotide 360, from nucleotide 466 to nucleotide 1570 or from nucleotide 1801 to nucleotide 2533 of the bag3 nucleotide sequence.

A further preferred embodiment of the present invention is that the kit comprises a couple of primers selected from those having the following sequences: SEQ ID NO. 1 and SEQ ID NO. 2; SEQ ID NO. 3 and SEQ ID NO. 4; SEQ ID NO. 5 and SEQ ID NO. 6; SEQ ID NO. 7 and SEQ ID NO. 8; SEQ ID NO. 9 and SEQ ID NO. 10.

Preferably, said primers have an annealing temperature between 60 and 75° C, preferably of 72° C.

Preferably, said set of primers is suitable for the detection and/or quantification of BAG3 RNA or a fragment thereof by quantitative real-time RT-PCR.

In a preferred embodiment of the present invention, said biological sample is a serum, plasma, urine, saliva or tissue sample.

Preferably, said serum, plasma, urine, saliva or tissue sample is from a mammalian, preferably a human.

According to a further embodiment of the present invention, said kit is specific for the diagnosis of a pathological state selected from the group consisting of a heart disease, cancer, diabetes, inflammation and inflammatory related diseases of the skin, nerves, bones, blood vessels and connective tissues.

According to a preferred embodiment of the invention, said heart disease is selected from: angina pectoris, pre-infarction angina, myocardial infarction, heart failure, ischemia, acute coronary disease, acute heart failure, chronic heart failure and iatrogenic heart disease.

According to another preferred embodiment of the invention, the cancer is selected from: pancreatic cancer, bladder cancer and prostate cancer.

A further embodiment of the present invention is a method for detecting and quantify the levels of BAG3 RNA or a fragment thereof in a biological sample, comprising the steps of:

- a. obtaining a biological sample, consisting of serum, plasma, urine, saliva or tissue sample.
- b. extracting the total RNA from the biological sample.
- c. quantifying the BAG3 RNA or a fragment thereof by quantitative real-time RT-PCR.

According to a preferred embodiment, the method of the present invention further comprises the additional step of:

c. comparing the values obtained from biological sample with reference values or with the values obtained from healthy donors.

According to another preferred embodiment of the present invention said serum, plasma, urine, saliva or tissue sample is from a mammalian, preferably a human.

According to a preferred embodiment in the method of the present invention the presence of said BAG3 RNA or of a fragment thereof is associated with a pathological condition.

Preferably, said pathological condition is selected from the group consisting of a heart disease, cancer, diabetes, inflammation and inflammatory related diseases of the skin, nerves, bones, blood vessels and connective tissues.

Preferably said heart disease is selected from: angina pectoris, pre-infarction angina, myocardial infarction, heart failure, ischemia, acute coronary disease, acute heart failure, chronic heart failure and iatrogenic heart disease.

Preferably said cancer disease is selected from: pancreatic cancer, bladder cancer and prostate cancer.

The invention still further relates to a immunohistochemistry (IHC) kit for the detection of BAG3 protein in a biological sample, wherein said biological sample is preferably a tissue sample, comprising BAG3-specific antibodies and reagents

including probes needed for the staining.

BRIEF DESCRIPTION OF THE DRAWINGS

The characteristics and advantages of the present invention will be apparent from the detailed description reported below, from the Examples given for illustrative and non-limiting purposes, and from the annexed Figures 1-9, wherein:

Figure 1.

Figure 1A: detection of BAG3 protein in supernatants from cultured cardiomyocytes. Human (HCMa) and rat (H9c2) cardiomyocytes at 80% confluency were incubated with or without 10% FBS for 16 hours at 37°C in a 5% CO₂ atmosphere. Supernatants were dialyzed in a buffer containing 50 mM NaCl and 0.05% IGEPAL, lyophilized, resuspended in 1 ml of RIPA buffer (50 mM Tris HCl pH 7.6, 150 mM sodium chloride, 2 mM sodium orthovanadate, 4 mM EDTA, 10mM sodium pyrophosphate, 1% NP-40, 0.1% sodium deoxycholate), and analyzed with anti-BAG3 or anti-GAPDH antibodies by western blotting.

Figure 1B: detection of BAG3 protein in exocytic vesicles. Supernatants obtained from H9c2 cells were subjected to sequential centrifugations: (i) 2'000×g for 15 min, to remove cells; (ii) 10'000×g for 30 min, to remove cellular debris; (iii) 150'000×g for 90 min, to pellet exocytic vesicles. The pellet was washed once in PBS at 150'000×g for 90 min and analyzed with the anti-BAG3 TOS-2 polyclonal antibody in comparison with a whole-cell lysate by western blot. Rab-4 was analyzed as a marker for exocytic vesicles. GAPDH, a cytosolic

protein, was analyzed as a control.

Figure 1C: Sera from two healthy donors and from two patients affected by chronic heart failure were analyzed with the anti-BAG3 antibody TOS-2 polyclonal antibody in western blotting.

Figure 1D: Bands obtained in two patients affected by chronic heart failure were excised from the gel and its identity analyzed by mass spectrometry using the program MASCOT.

Figure 2.

Figure 2A: detection of BAG3 protein in sera from CHF patients. BAG3 recombinant protein and whole-cell lysate from HCMA cells were analyzed by western blotting with serum (1:40) obtained from a patient with heart failure. Analysis with serum from a healthy donor was performed as negative control.

Figure 2B: detection of anti-BAG3 antibodies by ELISA test. Sera from 50 CHF patients (with ejection fraction < 60%) were compared with sera from 50 healthy donor for the presence of anti-BAG3 antibodies in a specific ELISA test. Results are plotted as arbitrary units.

Figure 2C: ROC analysis of ELISA test results. Cut-off on 0.083 A.U. results in 74% sensitivity and 68% specificity.

Figure 3.

Figure 3A: Confocal microscopy analysis of direct fluorescence performed for detection of rBAG3-FITC binding to HCMA cells (a, b, c) and J774 A1 cells (d, e, f, g, h, i). BAG3 recombinant protein and purified BSA (albumin from bovine serum purchased

from SIGMA) were conjugated to FITC using the FluoroTag FITC Conjugation Kit purchased from SIGMA following the manufacturer instructions. Equal amount of rBAG3-FITC (b, e) and BSA-FITC (h) proteins, calculated following the manufacturer instructions, were added in HCM and J774 A1 culture media with 0.1 % NaN₃ for 1 h. β -integrin was analyzed as control (a, d, g). Cells were analyzed by a Zeiss LSM confocal microscope. Merged images are shown in c, f and i.

Figure 3B: BAG3 binds macrophages. J774 A1 macrophages (1×10^6 cells/ml) were incubated with different concentration of Fitc-BAG3 protein (7, 14 and 70 nM). FITC-BSA (70 nM) was used as a negative control (grey). Cells fluorescence was analyzed by flow cytometry.

Figure 3C: panel a - Analysis of Cox-2 and iNOS levels in J774 A1 macrophages incubated with BAG3. J774 A1 cells at 80% confluency were incubated with control medium, BSA, LPS or rBAG3, for 20 hours. Polymixin was added where indicated to verify that the effects of E. coli- derived rBAG3 were independent from the presence of contaminating endotoxin. Cox-2 and iNOS expression were analyzed in cell lysates by Western blotting.

Figure 3C panel b - Analysis of nitrite release from J774 A1 macrophages incubated with BAG3. J774 A1 cells at 80% confluency were incubated with control medium, BSA, LPS or rBAG3 for 24 hours. 100 μ l of supernatants from each sample were incubated with 100 μ l of Griess reagent; the optical density at 550 nm (OD₅₅₀) was measured with a Beckman DU62

spectrophotometer. Nitrite concentration was evaluated by comparing the OD550 of the sample with that of a standard curve of sodium nitrite.

Figure 3C panel c - Analysis of IL-6 release from J774 A1 macrophages incubated with BAG3. J774 A1 cells at 80% confluency macrophages were incubated with control medium, BSA, LPS or recombinant BAG3 for 5 hours. BAG3 peptides (peptide 1, peptide 2, peptide 3, peptide 4 or scrambled peptide) 625 nM were added where indicated to verify their ability to block BAG3 activity. IL-6 production was measured in cell culture medium using an ELISA test. IL-6 concentration was evaluated by comparing the OD of the sample with that of a standard curve of recombinant IL-6.

Figure 4.

Figure 4A.

Representative images of BAG3 staining using the monoclonal anti-BAG3 antibody AC-1 in normal pancreas tissue. Sections were counterstained with hematoxylin. Staining revealed a moderate positivity of Langerhans islets, while normal pancreatic ducts and pancreatic acinar cells had no BAG3 expression.

Figure 4B.

Representative images of BAG3 low positive and BAG3 high positive tumour samples stained using a monoclonal anti-BAG3 antibody revealed with a biotinylated secondary antibody. Sections were counterstained with hematoxylin. Two different magnifications are shown: 100X (left panels) and 400X (right panels). We assigned a score based on

the proportion of positive cancer cells in the sample by counting the number of positive cells over the total cancer cells in 10 non-overlapping fields using a 400x magnification. The median percentage of BAG3 positive cells, calculated as described, was 40% and this value was used as a cut-off to separate low and high positive samples.

Figure 4C.

Survival curves were made comparing 39 patients with low BAG3 staining ($\leq 40\%$ of positive cells) and 27 patients with high BAG3 staining ($> 40\%$ of positive cells). All patients analyzed underwent R0 resection of the pancreatic adenocarcinoma. Median survival increases from 12 months in the high positive group to 23 months in the low positive group. Log-rank test p-value=0.0013.

Figure 5.

Representative image of BAG3 staining in synovial tissues from several rheumatoid arthritis. BAG3 positivity is observed in synovial fibroblasts and inflammatory infiltrates. Sections were counterstained with hematoxylin.

Figure 6.

Representative image of BAG3 staining in normal urocytis that resulted negative and in transitional cell bladder carcinoma that resulted highly positive for BAG3 in cytoplasm of tumor cells. Sections were counterstained with hematoxylin.

Figure 7.

Figure 7A.

bag3 mRNA relative expression evaluated by qRT-PCR

is shown in a graph where values are reported as mean + S.D. The blue line represents the median value calculated.

Figure 7B.

Survival analysis was made for all patients analyzed with qRT-PCR. 13 patients with high *bag3* expression had shorter survival (median survival =19.0 months) as compared to 12 patients with low *bag3* expression (median survival = 32.0 months). Log-rank test p-value = 0.0198.

Figure 8.

Figure 8A.

Pancreatic cancer cell lines (PSN1, Capan-1, AsPC-1, PANC-1 and MIA PaCa-2) were treated with different concentrations of gemcitabine as indicated in the graph. After 48 hours, apoptotic cell death was analyzed. Graph depicts mean percentage of Sub G0/G1 cells (\pm S.D.). Data are representative of three independent experiments.

Figure 8B.

Western blot analysis of BAG3 in pancreatic cancer cell lines; GAPDH housekeeping protein contents were used to monitor equal loading conditions.

Figure 8C.

MIA PaCa-2 and PANC-1 cell lines were treated with 2 μ M gemcitabine (GEM) for the indicated times BAG3 protein expression levels were monitored by western blot.

Figure 8D.

bag3 mRNA levels were analyzed by RT-PCR; graph depicts relative *bag3* mRNA levels (\pm S.D.) and data are representative of three independent

experiments.

Figure 8E.

MIA PaCa-2 and PANC-1 cell lines were transfected with BAG3 siRNA or a non-targeted siRNA (NTsiRNA) for 72 hours and then treated with 2 μ M gemcitabine (GEM) for 24h. BAG3 levels were analyzed by western blot and GAPDH levels were detected to monitor equal loading conditions.

Figure 8F.

MIA PaCa-2 and PANC-1 cells were transfected as described above and treated with 2 μ M gemcitabine (GEM) for 24h or 48h. Apoptotic cell death was analyzed as described. Graph depicts mean percentage of Sub G0/G1 cells (\pm S.D.). Data are representative of three independent experiments.

Figure 9.

Figure 9A: Detection of BAG3 specific immune-complexes by ELISA test. Sera from 55 pancreatic adenocarcinoma patients were compared with sera from 51 healthy donors for the presence of BAG3 specific immune-complexes in a specific ELISA test. Results are plotted as arbitrary units \pm S. E.

Figure 9B: ROC analysis of ELISA test results. Cut-off on 0.183 A.U. results in 65% sensitivity and 78% specificity.

Figure 10.

Bag3 score was calculated in each sample, as relative expression levels using the comparative method, after normalizing for the expression of the endogenous GAPDH. The mean of bag3 score was evaluated in two groups of patients: low PCA3 score patients and high PCA3 score patients. Difference

between the two groups was measured by student t test and resulted significant: $P = 0.001$.

DETAILED DESCRIPTION OF THE INVENTION

The present invention concerns BAG3 RNA or a fragment thereof for use as biochemical markers in the diagnosis of a pathological state.

With the term "BAG3 RNA fragment" in the present invention we refer to fragments of 150-300 nucleotides.

With the term "diagnosis" in the present invention we refer to medical diagnosis (often simply termed diagnosis) that refers to the process of attempting to determine or identify a possible disease or disorder. The diagnosis of the present invention encompasses also the early diagnosis. With the term "early diagnosis" we refer to the capacity of the test to discriminate a pathological state before specific or aspecific symptoms.

Anti-BAG3 antibodies have now been advantageously detected in serum. Until now such antibodies had never been found in serum either in physiological or pathological condition. The detection of anti-BAG3 antibodies in serum has the advantage of being a rapid and non-invasive technique be exploited for diagnostic, early diagnosis and prognostic purposes, risk stratification, as a tool for the identification and for monitoring therapies.

A further advantage of the detection of antibodies

is that a very small amount of serum is required for the detection. In fact, soluble BAG3 protein can also be detected in the serum of patients suffering from some pathologies, but the amount of serum requested for the detection of the soluble protein is much higher than that required for the detection of antibodies. Furthermore, it is possible that soluble BAG3 protein levels can be much lower than those of antibodies and/or that, respect to soluble BAG3 protein, antibodies can be detectable in earlier phases of specific pathologies and/or can more efficiently predict risk of complications or monitor the effects of therapies.

In the present invention, by serum is intended the component of blood that is neither a blood cell nor a clotting factor; it is the blood plasma with the fibrinogens removed. Serum includes all proteins not used in blood clotting (coagulation) and all the electrolytes, antibodies, antigens, hormones, and any exogenous substances.

In the present invention, by plasma is intended the straw-colored/pale-yellow liquid component of blood that normally holds the blood cells in whole blood in suspension. It contains clotting factors, such as fibrinogens.

In a further embodiment, the invention provides the use of anti-BAG3 antibodies as biochemical markers, wherein said anti-BAG3 antibodies are bound to soluble BAG3 to form immune complexes.

Anti-BAG3 antibodies, either free or bound to soluble BAG3 to form immune complexes have

advantageously been now detected in a biological and may be used as a marker in the diagnosis of a pathological condition. The detection of such antibodies and/or immune complexes in a biological sample also has the advantage of being a rapid and non-invasive technique for diagnostic and/or prognostic purposes.

In the present invention, by immune complex or protein/antibody complex is intended the integral binding of an antibody to a soluble antigen, the bound antigen acting as a specific epitope, bound to an antibody is referred to as a singular immune complex.

Such immune complexes have the same advantages seen as for the detection of antibodies, since a very small amount of serum is required also for the detection of the immune complex. The amount of serum required for the detection of soluble BAG3 is much higher also than that required for the detection of the protein/antibody (immune) complexes. Immune complexes as well as free antibodies can be detectable in earlier phases of specific pathologies and can more efficiently predict risk of complications or monitor the effects of therapies.

A still further embodiment of the invention is the use of anti-BAG3 antibodies or said immune complexes (formed by anti-BAG3 antibodies bound to soluble BAG3) as biological markers of a pathological state, wherein said pathological state is a heart disease, cancer, diabetes, inflammation and inflammatory related diseases of the skin,

nerves, bones, blood vessels and connective tissues.

Preferably said heart disease is selected from the group consisting of: angina pectoris, pre-infarction angina, ischemia, myocardial infarction, heart failure, acute coronary disease, acute heart failure, chronic heart failure and iatrogenic heart disease.

A further embodiment of the present invention is method for detecting the presence of an anti-BAG3 antibody or an anti-BAG3 antibody bound to soluble BAG3 to form an immune complex in a biological sample, comprising the steps of:

- a. obtaining a biological sample, consisting of serum, plasma,
- b. determining the presence of anti-BAG3 or BAG3 associated antibodies in the biological sample.

The method according to the present invention has the advantage of allowing to detect significant differences between anti-BAG3 antibodies and/or BAG3/antibodies complexes between healthy individuals and patients affected by BAG3-involving pathologies. The proposed assay method allows a statistically significant separation of the group of cardiac patients from the group of healthy people. It can also stratify such patients with heart disease in subgroups of patients at increased risk (heart failure, HF).

In a still further aspect the invention relates to a method for detecting the presence of an anti-BAG3 antibody in a biological sample or an anti-BAG3

antibody bound to soluble BAG3 to form an immune complex, further comprising the step of:

- c. comparing the values obtained from the biological sample with reference values or with the values obtained from healthy donors.

In a preferred aspect the method according to the present invention is a method wherein said determination step b. is performed by an ELISA test.

The method according to the present invention has the advantage of allowing the rapid and non-invasive detection of the biological markers allowing the evaluation of pathologies, risks for diseases and/or their complications, and monitoring of therapies.

According to a further aspect the invention relates to a detection method wherein the presence of said anti-BAG3 antibody or said anti-BAG3 antibody bound to soluble BAG3 to form an immune complex is associated with a pathological condition.

In a preferred embodiment said pathological condition is chosen from the group consisting of heart disease, cancer, diabetes, inflammation and inflammatory related diseases of the skin, nerves, bones, blood vessels and connective tissues. In particular said heart disease is selected from the group consisting of: angina pectoris, pre-infarction angina, myocardial infarction, ischemia, heart failure, acute coronary disease, acute heart failure, chronic heart failure or iatrogenic heart disease.

The invention further relates to an ELISA kit for

the detection of anti-BAG3 antibodies or anti-BAG3 antibodies bound to soluble BAG3 to form an immune complexes in a biological sample.

The ELISA kit according to the present invention comprises a BAG3 recombinant protein for capturing anti-BAG3 antibodies or BAG3-specific mouse monoclonal antibodies AC-1, AC-2, AC-3, AC-4 and AC-5, for capturing soluble BAG3 and antibodies able to recognize human immunoglobulins.

Such antibodies can be enzyme-linked antibodies able to recognize human immunoglobulins.

The invention also relates to a kit for the detection of BAG3-associated antibodies in a biological sample and is performed by ELISA with BAG3-specific mouse monoclonal antibodies AC-1, AC-2, AC-3, AC-4 and AC-5, capturing soluble BAG3 and enzyme-linked antibodies for the detection able to recognize human immunoglobulins.

The invention still further relates to a immunohistochemistry (IHC) kit for the detection of BAG3 protein in a biological sample, wherein said biological sample is preferably a tissue sample. Tissue samples can be biopsies, frozen tissues, paraffin embedded tissues.

The IHC kit according to the present invention comprises BAG3-specific antibodies and reagents including probes needed for the staining.

Said BAG3-specific antibodies can be mouse monoclonal antibodies AC-1, AC-2 and AC-3 and/or enzyme-linked antibodies for the detection able to recognize mouse immunoglobulins.

In particular, the IHC kit advantageously allows to

reveal BAG3 protein in 100% of pancreatic carcinoma tissue samples from patients that undergo pancreas resection and is expressed in most bladder carcinoma samples. Furthermore, BAG3 protein can be revealed with the kit for BAG3 detection by IHC also in normal pancreas tissue in Langerhans islets while other normal tissues result negative (such for example normal urocyctis). BAG3 positivity can be also observed in synovial fibroblasts and inflammatory infiltrates in rheumatoid arthritis tissue samples.

Long-term survival of patients affected by PDAC is very poor: only about 4% of patients will live 5 years after diagnosis. Indeed, surgical resection is presently the only chance of cure, but only approximately 20% of patients are diagnosed with resectable disease; furthermore, in a large proportion (about 80%) of such subset of patients the metastatization process is already occurring at diagnosis, and indeed distant metastases appear after surgical resection. Hence we need to better understand early stages in the development of pancreatic cancer and identify molecules that can allow detecting them. Also, markers that can allow a better prognosis and help the choice of therapies are highly required.

Advantageously the BAG3 IHC kit allows the identification of the prognosis of PDAC patients. It was seen that the intensity of BAG3 expression identified by IHC, correlates with patients' survival. Therefore it can be used for both prognosis and for making a choice of therapy.

A further embodiment of the present invention is BAG3 RNA or a fragment thereof for use as biochemical markers in the diagnosis of a pathological state.

Preferably, said BAG3 RNA is a BAG3 mRNA.

The BAG3 RNA corresponds to the BAG3 nucleotide sequence of SEQ ID N. 18 (Reference: NCBI PubMed, XM 055575.1 Homo sapiens BCL2-associated athanogene 3 (BAG3) mRNA).

SEQ ID NO: 18.

1gcggagctcc	gcatccaacc	ccgggccgcg	gccaactttt
ttggactgga	ccagaagttt	ctagccggcc	agttgctacc
tccctttatc	tcctccttcc	cctctggcag	cgaggaggct
atttccagac	acttccaccc	ctctctggcc	acgtcacccc
cgctttaat	tcataaaggt	gcccggcgcc	ggcttcccgg
acacgtcggc	ggcggagagg	ggcccacggc	ggcggcccgg
ccagagactc	ggcgcccgga	gccagcgccc	cgcacccgcg
ccccagcggg	cagaccccaa	cccagcatga	gcgcccgcac
ccactcgccc	atgatgcagg	tggcgtccgg	caacggtgac
cgcgaccctt	tgccccccgg	atgggagatc	aagatcgacc
cgcagaccgg	ctggcccttc	ttcgtggacc	acaacagccg
caccactacg	tggaacgacc	cgcgcggtgcc	ctctgagggc
ccaaggaga	ctccatcctc	tgccaatggc	ccttcccggg
agggctctag	gctgcccgcct	gctaggggaag	gccaccctgt
gtacccccag	ctccgaccag	gctacattcc	cattcctgtg
ctccatgaag	gcgctgagaa	ccggcaggtg	caccctttcc
atgtctatcc	ccagcctggg	atgcagcgat	tccgaactga
ggcggcagca	gcggtcctc	agaggtccca	gtcacctctg
cggggcatgc	cagaaaccac	tcagccagat	aaacagtgtg
gacaggtggc	agcggcggcg	gcagcccagc	cccagcctc
ccacggacct	gagcgggtccc	agtctccagc	tgctctgac

tgctcatcct	catectcctc	ggccagcctg	ccttcctccg
gcaggagcag	cctgggcagt	caccagctcc	cgcgggggta
catctccatt	ccggtgatac	acgagcagaa	cgttaccggg
ccagcagccc	agccctcctt	ccaccaagcc	cagaagacgc
actaccagc	gcagcagggg	gagtaccaga	cccaccagcc
tgtgtaccac	aagatccagg	gggatgactg	ggagccccgg
ccctgcggg	cggcatcccc	gttcaggtca	tctgtccagg
gtgcatcgag	ccgggagggc	tcaccagcca	ggagcagcac
gccactccac	tccccctcgc	ccatccgtgt	gcacaccgtg
gtcgacaggc	ctcagcagcc	catgaccat	cgagaaactg
cacctgtttc	ccagcctgaa	aacaaaccag	aaagtaagcc
aggcccagtt	ggaccagaac	tcctcctgg	acacatccca
attcaagtga	tccgcaaaga	ggtggattct	aacctgttt
cccagaagcc	cccacctccc	tctgagaagg	tagaggtgaa
agttccccct	gctccagttc	cttgtcctcc	tcccagccct
ggcccttctg	ctgtcccctc	ttcccccaag	agtgtggcta
cagaagagag	ggcagccccc	agcactgccc	ctgcagaagc
tacacctcca	aaaccaggag	aagccgaggc	tcccccaaaa
catccaggag	tgctgaaagt	ggaagccatc	ctggagaagg
tgcaggggct	ggagcaggct	gtagacaact	ttgaaggcaa
gaagactgac	aaaaagtacc	tgatgatcga	agagtatttg
accaaagagc	tgctggccct	ggattcagtg	gaccccgagg
gacgagccga	tgtgcgtcag	gccaggagag	acggtgtcag
gaagggtcag	accatcttgg	aaaaacttga	acagaaagcc
attgatgtcc	caggtcaagt	ccaggtctat	gaactccagc
ccagcaacct	tgaagcagat	cagccactgc	aggcaatcat
ggagatgggt	gccgtggcag	cagacaaggg	caagaaaaat
gctggaaatg	cagaagatcc	ccacacagaa	accagcagc
cagaagccac	agcagcagcg	acttcaaacc	ccagcagcat
gacagacacc	cctggtaacc	cagcagcacc	gtagcctctg

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ccctgtaaaa   atcagactcg   gaaccgatgt   gtgctttagg
gaattttaag   ttgcatgcat   ttcagagact   ttaagtcagt
tggtttttat   tagctgcttg   gtatgcagta   acttgggtgg
aggcaaaaaca  ctaataaaaag  ggctaaaaaag  gaaaatgatg
cttttcttct   atattcttac   tctgtacaaa   taaagaagtt
gcttgttggt   tcagaagttt   aaccccgttg   cttgttctgc
agccctgtct   acttgggcac   cccaccacc    tgtagctgt
ggttgtgcac   tgtcttttgt   agctctggac   tggaggggta
gatggggagt   caattacca   tcacataaat   atgaaacatt
tatcagaaat   gttgccattt   taatgagatg   attttcttca
tctcataatt   aaaataacctg  actttagaga   gagtaaatg
tgccaggagc   cataggaata   tctgtatggt   ggatgacttt
aatgctacat   ttt

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BAG3 RNA or a fragment thereof has now been advantageously detected in serum, plasma, urine, saliva or tissue sample. Until now such BAG3 RNA had never been found in the above mentioned biological sample either in physiological or pathological condition. The detection of BAG3 RNA or a fragment thereof in serum, and in different biological sample, such as plasma, urine, saliva or tissue has the advantage of being a rapid and non-invasive technique be exploited for diagnostic, early diagnosis and prognostic purposes, risk stratification, as a tool for the identification and for monitoring therapies.

A further advantage of the detection and the quantification of BAG3 RNA or a fragment thereof is that a very small amount of sample is required for the detection.

According to a preferred embodiment of the present invention said diagnosis is *in vitro* or *ex vivo*.

A further aspect of the present invention is that the recipient of said diagnosis is a mammalian, preferably a human.

As will be further described in the detailed description, the use of BAG-3 RNA or of a fragment thereof of the present invention has the advantages of being specific for a pathological state selected from the group consisting of a heart disease, cancer, diabetes, inflammation and inflammatory related diseases of the skin, nerves, bones, blood vessels and connective tissues.

According to a preferred embodiment of the invention, said heart disease is selected from: angina pectoris, pre-infarction angina, myocardial infarction, heart failure, ischemia, acute coronary disease, acute heart failure, chronic heart failure and iatrogenic heart disease.

According to another preferred embodiment of the invention, the cancer is selected from: pancreatic cancer, bladder cancer and prostate cancer.

A further embodiment of the present invention is a kit for the detection and/or quantification of BAG3 gene expression in a biological sample characterized by comprising a couple of single-stranded oligonucleotide primers encompassed by the bag3 nucleotide sequence (SEQ ID NO 18).

Preferably said kit comprise a couple of primers selected from those having a nucleotide sequence included in one of the region from nucleotide 1 to nucleotide 360, from nucleotide 466 to nucleotide 1570 or from nucleotide 1801 to nucleotide 2533 of the bag3 nucleotide sequence.

A further preferred embodiment of the present invention is that the kit comprises a couple of primers selected from those having the following sequences: SEQ ID NO. 1 and SEQ ID NO. 2; SEQ ID NO. 3 and SEQ ID NO. 4; SEQ ID NO. 5 and SEQ ID NO. 6; SEQ ID NO. 7 and SEQ ID NO. 8; SEQ ID NO. 9 and SEQ ID NO. 10.

Specific primers *bag3* primers according to primer sets 1 to 5, which are described below and identified by the SEQ ID NO. 1 to SEQ ID NO. 10, allow the detection and quantification of BAG3 expression by quantitative real-time PCR.

Primer set 1

fw: SEQ ID NO. 1: AACGGTGACCGCGACCCTTT;

rev: SEQ ID NO. 2: CCTTCCCTAGCAGGCGGCAG

Primer set 2

fw: SEQ ID NO. 3: CCGGCTGGCCCTTCTTCGTG;

rev: SEQ ID NO. 4: CAGCCTAGAGCCCTCCCGGG

Primer set 3

fw: SEQ ID NO. 5: GTCACCTCTGCGGGGCATGC;

rev: SEQ ID NO. 6: GGTGACTGCCCAGGCTGCTC

Primer set 4

fw: SEQ ID NO. 7: CCAGCCTCCCACGGACCTGA;

rev: SEQ ID NO. 8: CTGGTACTGCCCAGGCTGC

Primer set 5

fw: SEQ ID NO. 9: CAGGAGCAGCACGCCACTCC;

rev: SEQ ID NO. 10: TGGTCCA ACTGGGCCTGGCT.

The RT-PCR kit for *bag3* mRNA detection in a biological sample allows to correlate the levels of *bag3* gene expression with patients' survival and can be used for prognosis and for choice of therapy. Preferably said biological sample is a

serum, plasma, saliva, urine and tissue sample.

Preferably, said primers have an annealing temperature between 60 and 75° C, more preferably of 72° C.

Preferably, said set of primers is suitable for the detection and/or quantification of BAG3 RNA or a fragment thereof by quantitative real-time RT-PCR.

In a preferred embodiment of the present invention, said biological sample is a serum, plasma, urine, saliva or tissue sample.

Preferably, said serum, plasma, urine, saliva or tissue sample is from a mammalian, preferably a human.

According to a further embodiment of the present invention, said kit is specific for the diagnosis of a pathological state selected from the group consisting of a heart disease, cancer, diabetes, inflammation and inflammatory related diseases of the skin, nerves, bones, blood vessels and connective tissues.

According to a preferred embodiment of the invention, said heart disease is selected from: angina pectoris, pre-infarction angina, myocardial infarction, heart failure, ischemia, acute coronary disease, acute heart failure, chronic heart failure and iatrogenic heart disease.

According to another preferred embodiment of the invention, the cancer is selected from: pancreatic cancer, bladder cancer and prostate cancer.

A further embodiment of the present invention is a method for detecting and quantify the levels of BAG3 RNA or a fragment thereof in a biological

sample, comprising the steps of:

- a. obtaining a biological sample, consisting of serum, plasma, urine, saliva or tissue.
- b. extracting the total RNA from the biological sample.
- c. quantifying the BAG3 RNA or a fragment thereof by quantitative real-time RT-PCR.

In molecular biology there are different methods for detecting or quantify the RNA levels in a biological sample: Northern blot, RT-PCR, qRT-PCR, DNA-microarray.

A real-time polymerase chain reaction, also called quantitative real time polymerase chain reaction (qPCR) or kinetic polymerase chain reaction is a laboratory technique based on the polymerase chain reaction (PCR), which is used to amplify and simultaneously quantify a targeted DNA molecule. For one or more specific sequences in a DNA sample, Real Time-PCR enables both detection and quantification. The quantity can be either an absolute number of copies or a relative amount when normalized to DNA input or additional normalizing genes.

The procedure follows the general principle of polymerase chain reaction; its key feature is that the amplified DNA is detected as the reaction progresses in real time. This is a new approach compared to standard PCR, where the product of the reaction is detected at its end. Two common methods for the detection of products in real-time PCR are: (1) non-specific fluorescent dyes that intercalate with any double-stranded DNA, and (2) sequence-

specific DNA probes consisting of oligonucleotides that are labelled with a fluorescent reporter which permits detection only after hybridization of the probe with its complementary DNA target.

Frequently, real-time PCR is combined with reverse transcription to quantify messenger RNA (mRNA) and non-coding RNA in cells, tissues or biological samples.

Real-time reverse-transcription PCR is often denoted as: qRT-PCR. The acronym "RT-PCR" commonly denotes reverse transcription polymerase chain reaction.

According to a preferred embodiment, the method of the present invention further comprises the additional step of:

d. comparing the values obtained from biological sample with reference values or with the values obtained from healthy donors.

According to another preferred embodiment of the present invention said serum, plasma, urine, saliva or tissue sample is from a mammalian, preferably a human.

According to a preferred embodiment in the method of the present invention the presence of said BAG3 RNA or a fragment thereof is associated with a pathological condition.

Preferably, said pathological condition is selected from the group consisting of a heart disease, cancer, diabetes, inflammation and inflammatory related diseases of the skin, nerves, bones, blood vessels and connective tissues.

Preferably said heart disease is selected from:

angina pectoris, pre-infarction angina, myocardial infarction, heart failure, ischemia, acute coronary disease, acute heart failure, chronic heart failure and iatrogenic heart disease.

Preferably said cancer disease is selected from: pancreatic cancer, bladder cancer and prostate cancer.

A still further aspect of the invention is represented by anti-BAG3 monoclonal antibodies, their fragments, and peptides corresponding to specific aminoacidic sequences of BAG3 protein that are able to block macrophage activation and can therefore be used for therapy of inflammatory, oncologic or other diseases involving macrophage activation. See in particular Figure 3 and Table I. This invention relates to the use of BAG3- specific mouse monoclonal antibodies AC-1, AC-2 and AC-3 or same modified as F(ab), F(ab')₂, F(ab) or humanized; or peptides comprising sequences as follows:

PEP 1: DRDPLPPGWEIKIDPQ (SEQ ID NO. 11)

PEP2: SSPKSVATEERAAPS (SEQ ID NO. 12)

PEP3: DKGKKNAGNAEDPHT (SEQ ID NO. 13)

PEP4: NPSSMTDTPGNPAAP (SEQ ID NO. 14)

as molecules able to bind and/or block soluble BAG3 effects.

EXAMPLES

Example 1.

Serum deprivation-induced stress in cultured human primary cardiomyocytes and the rat cardiomyocyte cell line H9c2

Cardiomyocytes are known to release protective

factors in mounting a response against stressful agents. Since stress-induced proteins, such as Hsp70, Hp27, Hsp90 and others, although exerting an intracellular activity, can also be secreted in response to stress, BAG3 release by cardiomyocytes was analyzed in stressful conditions. For this purpose, we analyzed the effect of serum deprivation-induced stress in cultured human primary cardiomyocytes or the rat cardiomyocyte cell line H9c2. As shown in Figure 1, we could detect BAG3 protein in the supernatants of cardiomyocytes exposed to serum deprivation for 16 h (Figure 1A). Since at that time point cell survival was not affected by serum deprivation (results not shown), we discarded the hypothesis that BAG3 release was due to cell necrosis. Therefore we verified whether BAG3 was present in exocytic vesicles. Indeed, by isolating extracellular vesicles through a differential centrifugation procedure (16), we found that they contained BAG3 protein (Figure 1B).

To further verify the existence of a soluble form of BAG3, we investigated its presence in two blood sera from patients affected by chronic heart failure (CHF). Through western blot analysis, we could identify a band recognized by anti-BAG3 antibody. We excised the band and subjected it to mass spectrometry, confirming its identity (Figure 1C). This evidence confirmed that the protein could be detected in an extracellular form. We could not detect the protein in sera from healthy donors (Figure 1C).

Peptides recognized and matched by mass spectrometry on the entire BAG3 protein sequence are indicated in bold:

MSAATHSPMM QVASGNGDRD PLPPGWEIKI DPQTGWPFV
 DHNSRTTWN DPRVPSEGPK ETPSSANGPS REGSRLPPAR
EGHPVYPQLR PGYIPIVLH EGAENRQVHP FHVYPQGMQ
RFRTAAAAA PQRSQSPLRG MPETTQPKQ CGQVAAAAA
 QPPASHGPER SQSPAASDCS SSSSSASLPS SGRSSLGSHQ
 LPRGYISIPV IHEQNVTRPA AQPSFHQAQK **THYPAQQGEY**
QTHQPVYHKI QGDDWEPRPL RAASPFSSV QGASSREGSP
 ARSSTPLHSP SPIRVHTVVD RPQQPMTHRE TAPVSQPENK
 PESKPGPVGP ELPPGHIPIQ VIRKEVDSKP VSQKPPPSE
 KVEVKVPPAP VPCPPSPGP SAVPSSPKSV ATEERAAPST
 APAEATPPKP GEAEAPPKHP GVLKVEAILE KVQGLEQAVD
 NFEGKKTDKK YLMIEEYLTK ELLALDSVDP EGRADVRQAR
 RDGVRKVQTI LEK**LEQKAID VPGQVQVYEL QPSNLEADQP**
LQAIMEMGAV AADKGKKNAG NAEDPHTETQ QPEATAAATS
NPSSMTDTPG NPAAP (SEQ ID NO: 15).

The human BAG 3 protein has the amino acid sequence according to SEQ ID NO:15.

Example 2.

anti-BAG3 antibodies in CHF patients' sera

We found that sera from CHF patients recognized BAG3 protein in western blotting, using an anti-human IgG as secondary antibody (results representative of experiments with sera from three different patients are shown in Figure 2A). This result indicated the presence of anti-BAG3 antibodies in CHF patients' sera. To confirm this finding, we analyzed sera from 50 CHF patients (with ejection fraction < 60%) compared with sera from 50 healthy donors, for the presence of anti-

BAG3 antibodies in a specific ELISA test. As shown in Figure 2B, we detected significantly higher values of anti-BAG3 antibodies in patients' compared to controls' sera. ROC analysis of ELISA test results, using as cut-off 0.083 A.U., in 74% sensitivity and 68% specificity (Figure 2C).

Example 3.

BAG3 binding to macrophages

We addressed the functional significance of BAG3 release by cardiomyocytes. We excluded that the protein could be involved in an autocrine pathway, because it did not apparently bind to the cardiomyocyte surface, as we assessed in experiments using fluorescein isothiocyanate (FITC)-conjugated BAG3 (Figure 3A). Therefore we investigated whether BAG3 could interact with blood cells. Indeed, we found that FITC-BAG3 bound to macrophages of the cell line J774 (Figure 3B). BAG3 binding to macrophages was specifically impaired by competing BAG3 peptides or by BAG3-sequestering F(ab')₂ fragments from anti-BAG3 monoclonal antibodies (Table I).

Table I

	FITC-rBAG3	FITC-BSA	Competiton assays	
	% of positive cells (± S.D.)	% of positive cells (± S.D.)	% of positive cells (± S.D.)	% inhibition
FITC-rBAG3	15.7 (±0.45)			
FITC-BSA		4.04 (±0.06)		
(FITC-rBAG3)-(FITC-BSA)	11.06 (±0.45)			
FITC-rBAG3 + Pep1			0.18 (±0.05)	98.4
FITC-rBAG3 + Pep2			1.21(±0.63)	89.1
FITC-rBAG3 + Pep3			5.86 (±0.43)	47.2
FITC-rBAG3 + Pep4			0.68 (±0.20)	93.8
FITC-rBAG3 + Pep Scr			12.1 (±0.21)	0.0
FITC-rBAG3 + Mouse IgG F(ab')₂			12.3 (±0.40)	0.0
FITC-rBAG3 + Rabbit IgG F(ab')₂			14.7 (±0.20)	0.0
FITC-rBAG3 + AC1 IgG F(ab')₂			4.11 (±0.26)	62.8
FITC-rBAG3 + AC2 IgG F(ab')₂			3.76 (±0.43)	66.0
FITC-rBAG3 + TOS2 IgG F(ab')₂			3.19 (±0.21)	71.1

In particular J774 cells were incubated with 14 nM FITC-BAG3 protein and with 625 nM of BAG3 peptides (peptide 1, peptide 2, peptide 3, peptide 4 or scrambled peptide) or with 420 nM of F(ab')₂ fragments from anti-BAG3 monoclonal and polyclonal antibodies (mouse monoclonal AC1, AC2 and rabbit polyclonal TOS2). F(ab')₂ fragments from mouse IgG or F(ab')₂ fragments from rabbit IgG were used as a negative control.

To explore functional consequences of BAG3 binding to macrophages, we tested the effect of recombinant BAG3 on the expression of inducible nitric oxide synthase (iNOS) and cyclooxygenase (Cox)-2 in the cells. As shown in Figure 3C panel a the levels of those enzymes were enhanced in BAG3-treated macrophages. Furthermore, BAG3 induced the release of nitrite and interleukin (IL)-6 (Figure 3C panels b and c) confirming that macrophages were activated in response to their binding to the protein.

In sera from CHF patients we could detect significant amounts of anti-BAG3 antibodies (Figure 2A,B). Autoantibodies production is likely related to the extracellular release of a normally intracellular protein, as happens, for example, in chronic ischaemia patients who produce anti-troponin autoantibodies. ELISA values of anti-BAG3 antibodies in CHF patients' sera are significantly higher than those detected in healthy controls'

sera.

Therefore, production of anti-BAG3 antibodies, detected by ELISA, appears a biomarker of chronic heart failure. Its utility for risk stratification and therapy monitoring is worthy of investigation. BAG3 release by stressed cardiomyocytes and subsequent activation of macrophages, leading to local release of NO, might constitute a protective circuit in heart ischemia. Indeed, vasodilation, neoangiogenesis and remodelling might be targeted. BAG3 release and its transient or chronic effects deserve investigation and could contribute to our understanding of ischemia and other heart stress states.

Furthermore, BAG3-specific mouse monoclonal antibodies AC-1, AC-2 and AC-3 and/or others or same modified as F(ab), F(ab')₂, F(ab) or humanized; or peptides comprising sequences PEP 1 to 4 and/or others are molecules able to bind and/or block soluble BAG3 effects to be used for therapy of inflammatory, oncologic or other diseases involving macrophage activation.

Example 4.

BAG3 expression in PDAC by immunohistochemistry.

We have developed an immunohistochemistry (IHC) kit, including our anti-BAG3 monoclonal antibodies and able to detect BAG3 protein by immunohistochemistry (IHC). This kit revealed BAG3 expression in all the 346 (100%) PDAC biopsies that we analyzed. BAG3 staining revealed a moderate positivity of Langerhans islets, while normal pancreatic ducts and pancreatic acinar cells had no

BAG3 expression. This was true in both normal pancreas and non-neoplastic pancreatic tissue adjacent to the tumour mass. BAG3 staining was observed predominantly in the cytoplasm of tumor cells. The intensity of staining of BAG3 was variable as was the number of positive cancer cells. Furthermore, Langerhans insulae were positive and constituted a good internal control of IHC (Figure 4A). Therefore our kit allows the detection of BAG3 protein in PDAC by IHC. Furthermore, it allows detecting BAG3 protein by IHC also in other tumor or normal tissues.

We investigated also the expression of BAG3 in correlation with patients' survival and in response to therapy. We analyzed a cohort of 346 PDAC samples from the same number of patients (Table II) describing data of all tumor samples analyzed by immunohistochemistry and data of the subgroup of R0 patients analyzed with survival data; We assigned a score based on the proportion of positive cancer cells in the sample by counting the number of positive cells over the total cancer cells in 10 non-overlapping fields using a 400x magnification.

TABLE II

	No. Tot	age average \pm S.D.	sex		Local tumor stage T (%)				Nodal stage N (%)		Tumor grade G (%)		
			M	F	T1	T2	T3	T4	N0	N1	G1	G2	G3
PDAC patients data	346	63.0 \pm 10.5	181	165	5 (1.4)	59 (17.1)	264 (76.3)	18 (5.2)	130 (37.6)	216 (62.4)	16 (4.6)	177 (51.2)	153 (44.2)
PDAC patients with survival data	66	61.9 \pm 11.3	36	30	0 (0.0)	1 (1.5)	65 (98.5)	0 (0.0)	13 (19.7)	53 (80.3)	3 (4.5)	37 (56.1)	26 (39.4)

The median percentage of BAG3 positive cells, calculated as described, was 40% and this value was

used as a cut-off to separate low and high positive samples. Based on this classification 190 patient samples (55%) were classified as low positive ($\leq 40\%$ of positive cells), and 156 (45%) were classified as high positive ($>40\%$ of positive cells) (Figure 4, panel B). The survival analysis was performed in a cohort of 66 patients of which all the lesions examined were with resection margins free from tumor cells (R0) and only the 3.7% showed the presence of metastases to distant organs (Table II). Obtained data showed that patients with high BAG3 expression had a significantly shorter survival (median survival = 12.0 months) than those with low BAG3 expression (median survival = 23.0 months), ($p = 0.0013$) (Figure 4, panel C). Based on Cox proportional analysis high BAG3 expression was associated with a more than two-fold higher risk of death (Table III).

Table III

Parameter	HR	95% CI	p-value
Age (years)	0.99	0.97-1.02	0.601
Sex (M vs. F)	0.86	0.48-1.55	0.617
Tumor grade (G2 vs. G1)	0.84	0.24-2.98	0.789
Tumor grade (G3 vs. G1)	1.55	0.45-5.37	0.486
Local tumor stage (T3 vs. T2)	2.5	0.30-21.17	0.400
Nodal stage (N1 vs. N0)	1.17	0.58-2.37	0.668
BAG3 Positivity (High vs. Low)	2.7	1.53-4.78	<0.001
events=66 n=66			

Example 5.

BAG3 protein in response to therapy

The first-line chemotherapy for treatment of

pancreatic cancer is gemcitabine. In order to investigate the role of BAG3 protein in response to therapy, we analyzed the effect of BAG3 down-modulation in human PDAC cells. We transfected the cells with a specific siRNA targeting *bag3* mRNA or with a non specific (NT) siRNA, and treated cells with gemcitabine for the indicated times. Silencing of BAG3 enhanced cell apoptosis in response to the drug (Figure 8).

These results demonstrate the over expression of BAG3 protein and mRNA in pancreatic adenocarcinoma and the association of high expression levels with a higher risk of death, assigning to BAG3 a role of marker useful for prognosis and therapy choice. Furthermore they show that BAG3 down-modulation enhances apoptosis in PDAC cells. Due to its wide expression in all the lesions tested and to its involvement in sustaining pancreatic cancer cell survival, BAG3 represents a valuable target for innovative therapies in PDAC.

Example 6.

BAG3 protein in sera of pancreatic cancer patients

Because of its wide expression in pancreatic cancer patients, we investigated whether BAG3 was present in sera of pancreatic cancer patients. We found that indeed BAG3 was detectable. Also anti-BAG3 antibodies were detectable, although in prevalence complexed with BAG3. We therefore developed an ELISA test for detecting BAG3/antibody complexes. We analyzed sera from 51 healthy donors and 55 patients affected by PDAC (Table IV).

Table IV

	N (TOT)	AGE (median + s.e.)	M	F
healthy donors	51	58.7 + 1.6	35	16
PDAC patients	55	64.0 + 1.3	30	25

As shown in Figure 9A, immunocomplexes (measured in arbitrary units) were significantly higher in sera from patients than in those from healthy donors. Furthermore ROC analysis of ELISA test results, using as cut-off 0.183 A.U., in 65% sensitivity and 78% specificity (Figure 9B).

Example 7.

BAG3 expression by quantitative real-time PCR

The immunohistochemical data on BAG3 expression was also confirmed measuring *bag3* mRNA levels in 25 PDAC tissue samples (Table V).

Table V

No. Tot	age average + S.D.	sex		Local tumor stage T (%)				Nodal stage N (%)		Tumor grade G (%)		
		M	F	T1	T2	T3	T4	N0	N1	G1	G2	G3
25*	65.4 ± 11.9	21	4	2 (8.0)	3 (12.0)	20 (80.0)	-	6 (24.0)	19 (76.0)	3 (12.5)	13 (54.2)	8 (33.3)

In particular, there were 16 survivors out of the 25 patients, while 9 patients died of pancreatic cancer progression, at the time of the analysis. The median of expression of *bag3* mRNA in tumors

analyzed was set at 0.0068 (Q1=0.004; Q3=0.010) (Figure 7, panel A). All the considered demographics and clinical features of PDAC patients were unrelated to bag3 mRNA levels. Thus, correlation with survival was evaluated and the median of bag3 expression levels in PDAC samples was used as a cut-off to separate patients with low from those with high bag3 expression. Thirteen samples (52%) were thus classified as high bag3 positive and 12 samples (48%) as low bag3 positive. Patients with high bag3 expression had shorter survival (median survival =19.0 months) than those with low bag3 expression (median survival = 32.0 months), p-value=0.0198 (Fig 7, panel B). Based on Cox proportional analysis high bag3 expression was associated with over six fold higher risk of death (univariate: HR=6.094; 95% CI=1.105-33.597, p=0.038).

bag3 primers that detect BAG3 expression by quantitative real-time RT-PCR. We developed a RT-PCR kit containing specific primers for bag3 mRNA detection and quantification.

Example 8

1 ml of urine, after prostatic massage was collected from male patients screened for prostate cancer. Total RNA was obtained from urine and bag3 RNA levels were measured by RT-PCR. Bag3 score was calculated in each sample, as relative expression levels using the comparative method, after normalizing for the expression of the endogenous GAPDH. In the reported table bag3 was compared

between two groups having displaying different PCA3 score.

PCA3 is a prostate specific non-coding mRNA that is significantly overexpressed in prostate cancer tissue.

Urinary PCA3 RNA levels have been associated with prostate cancer grade suggesting a significant role in the diagnosis of prostate cancer. PCA3 score is calculated using quantitative polymerase chain reaction (qPCR) technology; in particular PCA3 and PSA (Prostate Specific Antigen) mRNA molecules are amplified and the PCA3 Score is calculated as equal to $1000 \times [\text{mRNA PCA3}]/[\text{mRNA PSA}]$. (ref: Bussemakers MJ, van Bokhoven A, Verhaegh GW, Smit FP, Karthaus HF, Schalken JA et al. DD3: a new prostate-specific gene, highly overexpressed in prostate cancer. *Cancer Res* 1999;59: 5975-9).

A patient with a PCA3 Score ≥ 35 has a high probability of having PCA and repeat biopsy is advisable. If the outcome is negative (PCA3 Score < 35), the patient has a lower probability of having PCA and repeat biopsy might be delayed with active surveillance/follow-up of the patient. BAG3 score analysis in these two groups of samples showed a similar trend between bag3 score and PCA3 score, indeed, patients having a low PCA3 score were associated with a BAG3 score mean of 1.20 while high PCA3 score patients were associated with a BAG3 score mean of 2.88. Difference between the two groups was measured by student t test and resulted significant: $P = 0.001$.

This result suggests the possibility that bag3 RNA determination in urine samples can represent a novel tool for risk assessment to develop prostate cancer.

Methods

Cell cultures

HCMA (Human Cardiac Myocytes–adult) were purchased from Sciencell Research Laboratories (San Diego, CA) and grown in Cardiac Myocyte Medium (CMM, FBS 5%, Cardiac Myocyte Growth Supplement 1%, penicillin/streptomycin solution 1%) (Sciencell Research Laboratories, San Diego, CA). All experiments were performed on low-passage cell cultures. Embryonic rat cardiomyoblasts (line H9c2) was purchased from the American Type Culture Collection (ATCC, Manassas, VA, USA) and grown in Dulbecco's Modified Eagle's Medium (DMEM) supplemented with 10 % fetal bovine serum (FBS), 100 U/mL penicillin and 100 µg/mL streptomycin. J774A.1, murine monocyte macrophage cell line (ATCC, Manassas, VA, USA), was grown in DMEM supplemented with 10% fetal bovine serum (FBS), 25 mM HEPES, 2 mM glutamine, 100 u/mL penicillin and 100 µg/mL streptomycin.

The pancreatic cancer cell lines (MIA PaCa-2, AsPC-1, PSN1, Capan-1 and PANC-1) were received from the American Type Culture Collection (ATCC; Manassas, VA) cell bank. MIA PaCa-2 cells were cultured in Dulbecco's Modified Eagle's Medium (DMEM) and supplemented with 10% FBS and 2.5% horse serum. AsPC-1 and PSN1 cells were grown in RPMI-1640 Medium supplemented with 10% FBS. Capan-1 were

cultured in RPMI-1640 containing 20% FBS while PANC-1 were cultured in DMEM supplemented with 10% FBS. All media for the above cell lines were purchased from BioWhittaker-Lonza (Bergamo, Italy) MediaTech (Manassas, VA) and were supplemented with 100 units of penicillin/mL and 2 µg streptomycin/mL (Sigma-Aldrich, St. Louis, MO). The cells were incubated at 37°C in a 5% CO₂ environment. Cells were treated with Gemcitabine (2',2'-difluorodeoxycytidine; GEM, Gemzar®) provided by Eli Lilly (Sesto Fiorentino, Italy) at the indicated concentrations.

Dissociation of BAG3 antibodies in human sera

Sera were diluted 1:40 with dissociation buffer (PBS with 1.5% BSA and 0.2 M glycine-acetate pH 2.5) to a 500 µl final volume and incubated for 20 min at room temperature. The sera were then pipetted into the sample reservoir of Microcon centrifugal filter device, YM-100 (100,000 MW cut-off; Millipore, Billerica, MA, USA) and centrifuged at 14,100 rpm for 20 min at room temperature. The sample reservoir was then separated from the flow through, placed inverted into a second tube and centrifuged at 5,000 rpm for 3 min at room temperature. The collected solution containing the antibody dissociated was adjusted to pH 7.0 with 1 M Tris buffer, pH 9.0. The retentate volume was reconstituted to the initial volume (500 µl) with dilution buffer (PBS with 1.5% BSA and 0.1% Tween-20).¹⁴ For detection of BAG3 protein by immunoblotting, the dissociated antibodies were diluted 1:200 in TBST containing 5% bovine serum

albumin overnight at 4°C.

Western blot analysis

Cells were harvested and lysed in a buffer containing 20 mM HEPES (pH 7.5), 150 mM NaCl, 0.1% Triton (TNN buffer) supplemented with a protease inhibitors cocktail (1 mM phenylmethylsulfonyl fluoride, 1 mg/ml pepstatin A, 2 mg/ml aprotinin) by 3 cycles of freezing and thawing. Soluble proteins were collected after a centrifugation at 10,000 g for 15 min and their amount was determined by Bradford assay (Bio-Rad, Hercules, CA). 25 µg of total protein and serum samples (1:2 in PBS-T 0.05%) were run on 8% or 10% SDS-PAGE gels and electrophoretically transferred to nitrocellulose membrane. Nitrocellulose blots were blocked with 10% non-fat dry milk in TBST buffer (20 mM Tris-HCl pH 7.4, 500 mM NaCl, and 0.1% Tween 20) and incubated with primary antibodies in TBST containing 5% bovine serum albumin or 5% non-fat dry milk, overnight at 4°C. Immunoreactivity was detected by sequential incubation with horseradish peroxidase-conjugated secondary antibodies purchased from Pierce (Rockford, IL) and ECL detection reagents purchased from Amersham Life Sciences Inc. (Arlington Heights, IL, USA).

Scanning densitometry of the bands was performed with an Image Scan (SnapScan 1212; Agfa-Gevaert NV). The area under the curve related to each band was determined using Gimp2 software. Background was subtracted from the calculated values.

Mass spectrometry

Protein bands were excised and gel pieces were

subsequently washed with MilliQ Water and Acetonitrile and the proteins were digested in situ as described in Shevchenko protocol. Briefly, gel slices were reduced in 1,4-dithiothreitol (10 mM) and alkylated with iodoacetamide (50 mM), then washed and rehydrated in trypsin solution (12 ng/ μ L) on ice for 1h. After the addition of 30 μ L ammonium bicarbonate (10 mM, pH 7.5), samples were digested overnight at 25 °C. 5 μ L of the obtained peptide mixture were injected onto a nano Acquity LC system (Waters Corp. Manchester, United Kingdom). The peptides were separated on a 1.7 μ m BEH C-18 column (Waters Corp. Manchester, United Kingdom) at a flow rate of 200 nl/min. The gradient (Solution A: 0.1% formic acid, solution B: 0.1% formic acid, 100% ACN) started at 5% and ended at 50% B after 55 min. MS and MS/MS data were acquired using a Q-TOF Premier mass spectrometer (Waters Corp., Micromass, Manchester, United Kingdom). Doubly and triply charged peptide-ions were automatically chosen by the MassLynx software and fragmented. MS data were automatically processed and peak lists for protein identifications by database searches were generated by the ProteinLynx software. Database searches were carried out with MASCOT server using the SwissProt protein database. The SwissProt human database (405506 sequences; 146166984 residues) was searched allowing 1 missed cleavage, carbamidomethyl(C) as fixed modification. The peptide tolerance was set to 60 ppm and the MS/MS tolerance to 0.8 Da.

Purification of exocytic vesicles by differential

ultracentrifugation

Serum-free medium of H9c2 was cleared of cells and large debris by serial centrifugation at 4°C (2000xg for 15 min, 10,000xg for 30 min). After each of the first two centrifugations, pellets are discarded, and the supernatant is kept for the next step. The final supernatant is then ultracentrifuged at 150,000xg for 90 min at 4°C (with a SW50.1 rotor, and an Optima L-90K Ultracentrifuge, Beckman Coulter) to pellet exosomes. The pellet is washed in PBS to eliminate contaminating proteins and centrifuged one last time at 150,000xg for 90 min at 4°C.¹⁶ After washing, the pellet (exosomes) was resuspended in 20 µl of PBS and analyzed with the anti-BAG3 TOS-2 polyclonal antibody in comparison with a whole-cell lysate by western blot. Rab-4 was analyzed as a marker for exocytic vesicles.

FACS analysis

rBAG3 binding - J774 A.1 cells were blocked with 2 % FBS + 0.1 % NaN₃ in PBS for 15 min on ice and incubated (2.5 x 10⁵/100 µl) with different concentration of FITC-rBAG3 protein (7, 14 and 70 nm) or FITC-BSA (70 nM) in PBS containing 2% FBS+ 0.1 % NaN₃ for 30 min at 4 °C in the dark. After washing with PBS, the cells were resuspended in PBS + 2% FBS+ 0.1 % NaN₃ and analyzed with a FACScan (BD Biosciences) flow cytometer.

Competition - J774 A.1 cells (2.5x10⁵/100 µl) were incubated with 625 nM of BAG3 peptides (peptide 1, peptide 2, peptide 3, peptide 4 or scrambled peptide) or with 420 nM of F(ab')₂ fragments from

anti-BAG3 monoclonal and polyclonal antibodies (mouse monoclonal AC1, AC2 and rabbit polyclonal TOS2) or F(ab')₂ fragments from mouse IgG or F(ab')₂ fragments from rabbit IgG in PBS containing 2% FBS+ 0.1 % NaN₃ for 30 min on ice. After incubation the cells were washing with PBS and then were incubated with of FITC-rBAG3 protein (14 nM), in PBS containing 2% FBS+ 0.1 % NaN₃ for 30 min at 4 °C in the dark. After washing with PBS, the cells were resuspended in PBS + 2% FBS + 0.1 % NaN₃ and analyzed by flow cytometer (BD Biosciences).

IL6 detection by ELISA

IL6 was measured in supernatant of J774 A.1 cells (5x10⁴/ in 96-well microplates) treated with LPS (10 ng/ml) or with rBAG3 (14 nM) or BSA (14 nM) for 10 or 20 hours in absence or presence of polymyxin B sulfate (5 µg/ml). After treatment 50 µL of cell culture medium were collected and analyzed in triplicate with a mouse IL6 Kit (eBioscience).

Fluorescence

Cells were cultured on coverslips in six-well plates to 60-70% confluence and equal amount of rBAG3-FITC and BSA-FITC proteins were added in HCMA and J774 A1 culture media with 0.1 % NaN₃ for 1 h. Coverslips were washed in 1x PBS and fixed in 3.7% formaldehyde in 1x PBS for 30 min at room temperature, and then incubated for 5 min with 1x PBS 0.1M glycine. Following incubation with a 1:100 dilution of anti-β-integrin monoclonal antibody at 4 °C, coverslips were washed three times with 1x PBS. After incubation with a 1:500 dilution of goat anti-mouse IgG DyLight 594-conjugated antibodies

(Jackson ImmunoResearch, West Grove, PA, USA) at room temperature for 45 min, coverslips were again washed for three times in 1x PBS. Once incubation with Hoechst 33342 (Sigma Aldrich, 2 µg/ml) at room temperature for 10 min, coverslips were again washed for 3 times in PBS and then in distilled water. The coverslips were then mounted on a slide with interspaces containing 47% (v/v) glycerol. Samples were analyzed using a confocal laser scanning microscope (Zeiss LSM confocal microscope, Germany). Images were acquired in sequential scan mode by using the same acquisitions parameters (laser intensities, gain photomultipliers, pinhole aperture, objective 63X, zoom 2) when comparing experimental and control material. For production of figures, brightness and contrast of images were adjusted by taking care to leave a light cellular fluorescence background for visual appreciation of the lowest fluorescence intensity features and to help comparison among the different experimental groups. Final figures were assembled using Adobe Photoshop 7 and Adobe Illustrator 10. Leica Q9 Confocal Software and ImageJ were used for data analysis.

Measurement of antibody titers by ELISA

NUNC Maxisorp 96 well ELISA plates were coated with recombinant BAG3 protein 1µg/ml (50µl/well) in PBS, pH 7 and incubated overnight at 4°C. Plates were washed 2 times with washing buffer (PBS + 0.05% Tween-20), and then blocked (150 µl/well) for one hour at room temperature with 0.5% fish gelatin in PBS. Following blocking, the plates were washed 2

times with washing buffer and sera were diluted 1:70 with 0.5% fish gelatin in washing buffer and then applied (50 μ l/well) in triplicate and incubated at room temperature for two hour. The plates were then washed 6 times with washing buffer. Anti-human IgG (H+L) antibody (Sigma Aldrich) was diluted 1:20,000 with 0.5% fish gelatin in washing buffer, added at 50 μ l/well and incubated at 4°C for 30 minutes. After incubation, the plates were washed 6 times, developed with TMB (50 μ l/well) (eBioscience), the reaction stopped with 4.5 M sulfuric acid (25 μ l/well) and the plates were analyzed spectrophotometrically at 450 nm.

NO₂⁻ assay

Nitrite content (NO₂⁻), a stable metabolite of NO released by cells in the culture supernatant, was measured¹⁸ in J774 A.1 cells (5x10⁴/ in 96-well microplates) treated with LPS (10 ng/ml) or with rBAG3 (7, 14 and 28 nM) or BSA (28 nM) for 24 hours in absence or presence of polymyxin B sulfate (Sigma-Aldrich, St. Louis, MO, USA) 5 μ g/ml. NO₂⁻ amounts were measured by Griess reaction. Briefly, 100 μ L of cell culture medium were mixed with 100 μ L of Griess reagent - equal volumes of 1% (w:v) sulphanilamide in 5% (v:v) phosphoric acid and 0.1% (w:v) naphthylethylenediamine-HCl - and incubated at room temperature for 10 min, and then the absorbance was measured at 550 nm in a microplate reader Titertek (Dasit, Cornaredo, Milan, Italy). The amount of NO₂⁻ (as μ M) in the samples was calculated from a sodium nitrite standard curve.

Measurement of BAG3/antibody immunocomplexes by ELISA

NUNC Maxisorp 96 well ELISA plates were coated with anti-BAG3 monoclonal antibody AC-1, AC-2 or AC-3 in PBS, pH 7 and incubated overnight at 4°C. Plates were washed 2 times with washing buffer (PBS + 0.05% Tween-20), and then blocked (150 µl/well) for one hour at room temperature with 0.5% fish gelatin in PBS. Following blocking, the plates were washed 2 times with washing buffer and sera were diluted 1:70 with 0.5% fish gelatin in washing buffer and then applied (50 µl/well) in triplicate and incubated at room temperature for two hour. The plates were then washed 6 times with washing buffer. Anti-human IgG (H+L) antibody (Sigma Aldrich) was diluted 1:20,000 with 0.5% fish gelatin in washing buffer, added at 50 µl/well and incubated at 4°C for 30 minutes. After incubation, the plates were washed 6 times, developed with TMB (50 µl/well) (eBioscience), the reaction stopped with 4.5 M sulfuric acid (25 µl/well) and the plates were analyzed spectrophotometrically at 450 nm.

Immunohistochemistry

Immunohistochemistry protocol included: deparaffination in xylene, re-hydration through descending concentrations of alcohol up to pure water, non-enzymatic antigen retrieval in citrate buffer, pH 6.0, for 30 minutes at 95°C, and endogenous peroxidase quenching with H₂O₂ in methanol for 20 minutes. After rinsing with PBS, the samples were blocked with 5% normal horse serum

in 0.1% PBS/BSA. To detect BAG3, samples were incubated for 1 hour at room temperature with BAG3 monoclonal antibody AC-1, AC-2 or AC-3 at the concentration of 3 microg/ml. After washing thoroughly with PBS, sections were incubated with a biotinylated secondary anti-mouse IgG for 20 minutes, then rinsed, incubated with avidin-biotin-complexes peroxidase (purchased from Novocastra-Leica Microsystems, Milano, IT) and developed with diaminobenzidine (Sigma-Aldrich, St. Louis, MO). Finally, the sections were counterstained with hematoxylin, dehydrated in alcohol, cleared in xylene, and mounted with Permount (Fisher Scientific, Milan, IT).

Quantitative Real-time RT-PCR

Tissue specimens of resected pancreatic cancer were taken, immediately frozen in liquid nitrogen, and stored at -80°C until RNA extraction. Total RNA was isolated from frozen tissues and from pancreatic cancer cell lines by means of phenol extraction (TRIzol Reagent, Invitrogen Corporation, Carlsbad, CA, USA). In tissue samples Cancer cellularity was enriched by cryostat sectioning and dissection of most cellular areas. RNA concentration and purity ($\text{A}_{260}:\text{A}_{280}>2.0$; $\text{A}_{260}/\text{A}_{230}>1.8$) were validated by NanoDrop Spectrophotometer (Thermo Fisher, Waltham, MA, USA). 1.0 μg of total RNA was reverse-transcribed using the High-Capacity cDNA Reverse Transcription Kit according to the manufacturer's instructions (Applied Biosystems, Applied, Foster City, CA, USA). Quantitative real-time PCR assay was used to assess the differential expression of

BAG3 in tumor tissue samples. Primers for the human bag3 gene were synthesized by Primm srl (Milano, Italy) (forward primer: (SEQ ID NO:16) CCT GTT AGC TGT GGT TG; reverse primer: (SEQ ID NO:17) AAC ATA CAG ATA TTC CTA TGG C).

For urine samples, 1 ml of urine collected after prostatic massage and stabilized with RNA protector buffer were transferred in 15 ml falcon tube, and mixed with 2ml of Trizol Reagent ® and 1ml of chloroform. Samples were centrifuged for 15 minutes at 4°C, 8000 rpm. Aqueous phase was transferred in a new falcon tube and 1 ml of pure ethanol was added. Sample was mixed and transferred (in 4 steps) on RNAeasy qiagen column, then supplier protocol suitable for RNA purification was followed. RNA was eluted in 15 µl of elution buffer. 12 µl of eluted RNA were used for the Reverse transcription reaction performed in a final volume of 20 µl. (Quantitect reverse transcription kit, Qiagen). 2 µl of synthesized cDNA were used for Real Time PCR screening, on Light Cycler 480 Roche instrument.

Bag3 primers were: fw 5'-CAGGAGCAGCAGCCACTCC-3' (SEQ ID NO:16); rev 5'-TGGTCCAACCTGGGCCTGGCT-3' (SEQ ID NO:17).

GAPDH mRNA was measured to normalize measured bag3 RNA values with primers: fw 5'-AGCTCCCGCTTCGCTCTCT-3'; rev 5'-CCAGGCGCCCAATACGACCA-3'.

All qPCRs were performed in a 25-µl final volume, in three replicates per sample, by using QuantiFast SYBR Green PCR kit (QIAGEN, Hamburg, Germany) and

run in an ABI PRISM® 7700 Sequence Detection System (Applied Biosystems, Applied Biosystems, Foster City, CA, USA) or in a Light Cycler 480 Roche instrument, according to the following conditions: 95° C for 5 min, 40 cycles at 95° C for 10 s and at 60° C for 30 sec. Data were acquired as threshold cycle (Ct) value using the S.D.S software v 2.1. In each sample, bag3 mRNA relative expression levels was obtained using the comparative method, after normalizing for the expression of the endogenous GAPDH.

From the above description and the above-noted examples, the advantage obtained by the biological markers described and obtained according to the present invention are apparent.

CLAIMS

1. BAG3 RNA or a fragment thereof for use in the diagnosis of a pathological state.
2. BAG3 RNA or a fragment thereof for use according to claim 1, characterized in that said BAG3 RNA is a BAG3 mRNA.
3. BAG3 RNA or a fragment thereof for use according to claim 1, wherein said diagnosis is *in vitro* or *ex vivo*.
4. BAG3 RNA or a fragment thereof for use according to anyone of claims 1 to 3, wherein the recipient of said diagnosis is a mammalian, preferably a human.
5. BAG3 RNA or a fragment thereof for use according to anyone of claims 1 to 4, wherein said pathological state is selected from: heart disease, cancer, diabetes, inflammation and inflammatory related diseases of the skin, nerves, bones, blood vessels and connective tissues.
6. BAG3 RNA or a fragment thereof for use according to claim 5 wherein said heart disease is selected from: angina pectoris, pre-infarction angina, myocardial infarction, heart failure, ischemia, acute coronary disease, acute heart failure, chronic heart failure and iatrogenic heart disease.
7. BAG3 RNA or a fragment thereof for use according to claim 5 wherein said cancer is selected from: pancreatic cancer, bladder cancer and prostate cancer.
8. Kit for the detection and/or quantification of BAG3 gene expression in a biological sample characterized by comprising a couple of single-

stranded oligonucleotide primers encompassed by the bag3 nucleotide sequence (SEQ ID NO 18).

9. Kit according to claim 8, characterized by comprising a couple of primers selected from those having a nucleotide sequence included in one of the region from nucleotide 1 to nucleotide 360, from nucleotide 466 to nucleotide 1570 or from nucleotide 1801 to nucleotide 2533 of the bag3 nucleotide sequence.

10. Kit according to anyone of claims 8 or 9, characterized by comprising a couple of primers selected from those having the following sequences: SEQ ID NO. 1 and SEQ ID NO. 2; SEQ ID NO. 3 and SEQ ID NO. 4; SEQ ID NO. 5 and SEQ ID NO. 6; SEQ ID NO. 7 and SEQ ID NO. 8; SEQ ID NO. 9 and SEQ ID NO. 10.

11. Kit according to anyone of claims 8 to 10, characterized in that said primers have an annealing temperature between 60 and 75° C, preferably of 72° C.

12. Kit according to anyone of claims 8 to 11, wherein said set of primers is suitable for the detection and/or quantification of BAG3 RNA or a fragment thereof by quantitative real-time RT-PCR.

13. Kit according to claim 8 wherein said biological sample is serum, plasma, urine, saliva or tissue sample.

14. Kit according to claim 13, wherein said serum, plasma, urine, saliva or tissue sample is from a mammalian, preferably a human.

15. Kit according to anyone of the previous claims, for use in the diagnosis of a pathological state.

16. Kit according to claim 15, wherein said pathological state is selected from: heart disease, cancer, diabetes, inflammation and inflammatory related diseases of the skin, nerves, bones, blood vessels and connective tissues.

17. Kit according to claim 16 wherein said heart disease is selected from: angina pectoris, pre-infarction angina, myocardial infarction, heart failure, ischemia, acute coronary disease, acute heart failure, chronic heart failure and iatrogenic heart disease.

18. Kit according to claim 16 wherein said cancer is selected from: pancreatic cancer, bladder cancer and prostate cancer.

19. Method for detecting and/or quantify the levels of BAG3 RNA or a fragment thereof in a biological sample, comprising the step of:

a. obtaining a biological sample, consisting of serum, plasma, urine, saliva or tissue.

b. extracting the total RNA from the biological sample.

c. quantifying the BAG3 RNA or a fragment thereof by quantitative real-time RT-PCR.

20. Method according to claim 19, further comprising the step of:

d. comparing the values obtained from biological sample with reference values or with the values obtained from healthy donors.

21. Method according to anyone of claims 19 or 20, wherein said serum, plasma, urine, saliva or tissue sample is from a mammalian, preferably a human.

22. Method according to anyone of claims 19 to 21, wherein the presence of said BAG3 RNA or a fragment thereof is associated with a pathological condition.

23. Method according to claim 22, wherein said pathological state is selected from: heart disease, cancer, diabetes, inflammation and inflammatory related diseases of the skin, nerves, bones, blood vessels and connective tissues.

24. Method according to claim 23, wherein said heart disease is selected from: angina pectoris, pre-infarction angina, myocardial infarction, heart failure, acute coronary disease, ischemia, acute heart failure, chronic heart failure or iatrogenic heart disease.

25. Method according to claim 23, wherein said cancer is selected from: pancreatic cancer, bladder cancer and prostate cancer.

Figure 10

bag3 score	Sample number	PCA3 score	bag3 score	Sample number	PCA3 score
1.09	1	low	4.92	11	high
2.00	2	low	3.78	12	high
0.62	3	low	2.23	13	high
2.17	4	low	3.48	14	high
1.07	5	low	2.85	15	high
1.39	6	low	1.01	16	high
0.78	7	low	0.79	17	high
1.00	8	low	3.44	18	high
0.66	9	low	2.64	19	high
1.29	10	low	3.71	20	high
bag3 score mean			2.88		