Salivary Gland Proteome Analysis Reveals Modulation of Anopheline Unique Proteins in Insensitive Acetylcholinesterase Resistant Anopheles gambiae Mosquitoes

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Abstract

Insensitive acetylcholinesterase resistance due to a mutation in the acetylcholinesterase (ace) encoding ace-1 gene confers cross-resistance to organophosphate and carbamate insecticides in Anopheles gambiae populations from Central and West Africa. This mutation is associated with a strong genetic cost revealed through alterations of some life history traits but little is known about the physiological and behavioural changes in insects bearing the ace-1R allele. Comparative analysis of the salivary gland contents between An. gambiae susceptible and ace-1R resistant strains was carried out to characterize factors that could be involved in modifications of blood meal process, trophic behaviour or pathogen interaction in the insecticide-resistant mosquitoes. Differential analysis of the salivary gland protein profiles revealed differences in abundance for several proteins, two of them showing major differences between the two strains. These two proteins identified as saglin and TRIO are salivary gland-related proteins, a family unique to anopheline mosquitoes, one of them playing a crucial role in salivary gland invasion by Plasmodium falciparum sporozoites. Differential expression of two other proteins previously identified in the Anopheles sialome was also observed. The differentially regulated proteins are involved in pathogen invasion, blood feeding process, and protection against oxidation, relevant steps in the outcome of malaria infection. Further functional studies and insect behaviour experiments would confirm the impact of the modification of the sialome composition on blood feeding and pathogen transmission abilities of the resistant mosquitoes. The data supports the hypothesis of alterations linked to insecticde resistance in the biology of the primary vector of human malaria in Africa.


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Introduction

Malaria remains one of the most important public health problems worldwide. Due to its high anthropophily Anopheles gambiae s.l. constitutes the main vector of malaria and the target of vector control programmes in Africa [1]. As a result, anopheline mosquito has developed resistance to the different classes of insecticides used in vector control strategies through two major mechanisms. The first mechanism is metabolic resistance, which is due to the increase of expression level or activity of detoxifying enzymes, belonging to three families: the cytochrome P450 monooxygenases, the glutathione S-transferases and the carboxyesterases [2]. The second and most studied mechanism is the target site resistance, such as the insensitive acetylcholinesterase resistance conferring a cross-resistance to carbamates and organophosphates by reducing the ability of these compounds to inhibit acetylcholinesterase in nerve synapses [3]. Two amino acid substitutions in the protein have been shown to play a role in resistance but the resistant allele encoding the G119S mutation, namely ace-1R, was reported several times in field An. gambiae populations [4,5,6]. In Culex pipiens quinquefasciatus, life history traits, reproductive capacity and physiology are strongly impacted by the ace-1 resistance because of the interference between ace-1R allele and the general functioning of the central nervous system [7,8,9,10]. Little information is available so far on the impact of insecticide resistance alleles affecting other traits such as host seeking, blood feeding behaviour and pathogen transmission. A regulation of some salivary proteins was reported in ace-1 resistant C. p. quinquefasciatus mosquito [12]. In this study, D7 long form protein which is known to favor the blood intake was down-regulated in resistant Culex mosquitoes whereas some metabolic components were up-regulated in the resistant strain [13]. For
Anopheles mosquitoes a large fitness cost entailed by the ace-1R mutation has also been hypothesized [14]. Though reports on these fitness costs are rare, they tend to confirm this hypothesis [15]. Experimental infections of ace-1R resistant An. gambiae with Plasmodium falciparum gametocytes revealed a slight variation in parasite prevalence suggesting an impact of this mutation on the parasite development [16].

In this work we focused on the effect of ace-1 resistance on the salivary gland protein composition in An. gambiae. The main function of arthropod saliva is to help blood meal intake by releasing components with anti-coagulation, vasodilatation and platelet aggregation properties [17]. In addition, this saliva at the interface with the host could strongly influence both the human immune response and the pathogen transmission. Mosquito salivary proteins play a major role in host-vector interaction and it has been suggested that salivary content could be influenced by age, or infection status of the Anopheles vector [18]. Other studies have reported that salivary components could intervene in pathogen transmission [19,20]. Using a proteomic approach based on two-dimensional gel electrophoresis followed by mass spectrometry identification, we investigated whether the expression of salivary proteins would be modified in the resistant malaria vector. We performed a differential analysis of the sialome of ace-1R homozygous An. gambiae mosquito and its susceptible counterpart, having a similar genetic background. We therefore, describe and discuss the differential expression of the proteins identified as down- or up-regulated in the insecticide-resistant mosquito. We report for the first time differences in the composition of the insecticide-resistant anophelines sialome with differential expression of proteins belonging to a family exclusively expressed in anophelines. The known or putative functions of the regulated proteins in the invasion of salivary glands by the parasite or in blood meal intake by females are discussed in regards to how they could impact the vectorial capacity.

Materials and Methods

Mosquitoes

Two strains of Anopheles gambiae S molecular form were used in this study. The insecticide-susceptible strain Kisumu (Kis) originating from Kenya [21] is homozygous for the ace-1S allele at the ace-1 locus, while the ace-1R Kisumu strain (AceRKis) is homozygous for the resistant allele ace-1R, bearing the G119S mutation. This strain was obtained through 19 generations of back-crossing and selection, allowing introgression into the genome of the Kis strain [5]. Female mosquitoes aged 2-3 days were fed on rabbits, then maintained on a diet of glucose until they could impact the vectorial capacity.

Salivary gland extract preparation

Salivary glands were pooled (15 to 20 pairs) in 30 μl of rehydration buffer containing 7 M urea, 2 M thiourea, 4% CHAPS (3-[3-Cholamidopropyl]dimethylammonio]-1-propanesulfonate), 0.2% tergitol, 20 mM Dithiothreitol, 1% octyl glucoside, 0.8% IPG (Immobilized pH gradient) buffer (PlusOne reagents, GE Healthcare Bio-Sciences, Uppsala, Sweden) and stored at -80°C. After several cycles of freezing-digesting on liquid nitrogen, samples were centrifuged at 30,000 g for 15 min at 14°C. Soluble salivary proteins in the supernatant were quantified as the matrix). The mixture was deposited on a 384-well MALDI target using the dry-droplet procedure [23], then air dried at room temperature.

Two-dimensional gel electrophoresis (2-DE)

SGE (15 μg) were diluted to 180 μl by adding rehydration buffer and 2% final DeStreak reagent (GE Healthcare) and loaded onto 11 cm Immobiline DryStrap gel pH 3-11 non linear (NL) (GE Healthcare). Strips were rehydrated at 20°C overnight (16 hours) and run using the following conditions: temperature 20°C; current 50 μA per strip; 60 V for 1 hour, 500 V (gradient) for 1 hour, 1000 V (gradient) for 1 hour, 6000 V (gradient) for 2 hours, and a 6000 V step up to 30000 Vhrs. Reduction and alkylation steps were performed under standard conditions [12]. The second dimension was carried out on 10-20% SDS-PAGE gels (Bio-Rad) at 30 V for 16 min followed by one hour at 200 V. After fixation, the gels were stained with LavaPurple Protein Gel & Blot Stain Kit (Fluorotechnics, Australia) according to manufacturer’s instructions. Gel scanning was performed using a Typhoon 9400 imager (GE Healthcare). Preparative 2-DE gels for spot picking were carried out in the same conditions, using 30 μg of SGE. Preparative gels were stained overnight with colloidal coomassie blue (Fermentas, Saint-Remy les Chevreuse, France) and scanned using a Perfection V750 Pro scanner (EPSON). Four analytical gels and one preparative gel were run for each strain.

2-DE gel analysis

Progenesis SameSpots 4.1 software (Nonlinear Dynamics, Newcastle upon Tyne, United Kingdom) was used for 2-DE gel comparative analysis. Statistical tests were performed as recommended by the software provider including a Principal Component Analysis (PCA) and an ANOVA test adjusted by a False Discovery Rate (FDR) approach for all spots in both groups (Kis and AceRKis) assigning to each spot a p-value and a q-value. The statistical power of the analysis was greater than 0.8. Spots under the ANOVA test p-value of 0.01 and above the 1.5-fold minimal difference in expression levels in either direction (up and down-expression) between the two strains were selected and manually excised from the preparative gels.

Mass spectrometry and protein identification

Tryptic digestion of in-gel proteins was performed according to the Shevchenko modified protocol [22]. Digested proteins were dehydrated in a vacuum centrifuge, solubilised in 10 μl of formic acid (2%), desalted using Zip Tips C18 (Millipore, Bedford, MA), eluted with 10 μl of 0.1% trithioacetic acid in 50% acetonitrile and concentrated to 3 μl volume. 0.4 μl of analyse solutions was mixed with the same volume of alpha-cyano-4-hydroxy-trans-cinnamic acid (saturated solution was prepared in 0.1% trithioacetic acid in 50% acetonitrile, vortexed, sonicated 30 s and microfuged 30 s, then a 1/3 dilution of the supernatant was used as the matrix). The mixture was deposited on a 384-well MALDI target using the dry-droplet procedure [23], then air dried at room temperature.
Samples were dehydrated in a vacuum centrifuge, solubilized in MS analysis were subjected to nanoLC ESI MS/MS analysis. Interrogations. For 2 peptides or more/protein).

For 2 peptides or more/protein).

2 peptides or more/protein).

Peptides were excised from the preparative Ks and AceRKis gels, whereas the other two spots were too faint for excision (spots 572 and 658). Statistical results for the 8 spots are summarized in Table 1.

Identification of the differentially expressed salivary proteins in the resistant AceRKis mosquitoes

The eight spot samples excised from the preparative gels were analysed by MALDI-TOF MS. A unique protein identification in the UniProtKB/Swiss-Prot or UniProtKB/TremBL database was assigned to four spots (Table 1), three of which were identified as isoforms of saglin [Q2TLV8_ANOGA] and one as a long form D7 salivary protein [Q7P76j_ANOGA]. A fifth spot was assigned to two proteins, the salivary gland 1-like 3 (SGL-1-like 3) [Q8WR9j_ANOGA] and the TRIO protein [Q7PU5j_ANOGA]. The three remaining spot samples were subjected to nanoLC ESI MS/MS analysis. This analysis allowed for the identification of the TRIO protein [Q7PU5j_ANOGA] and an isoform of the Glutathione S-transferase 1 (GST1) [Q93113_ANOGA]. On the other hand, the remaining spot sample (ID 578) could not be assigned to a single protein. Results of protein identification using mass spectrometry are summarized in Table 1. The peptide sequences and the number of peptides detected by nanoLC ESI MS/MS and used for protein assignment are provided as supporting information (Table S1).

Saglin, D7 long form and Glutathione S-transferase D1 (GST1) proteins were identified as down-regulated in the salivary glands of the resistant AceRKis strain, while the TRIO protein was up-regulated in the resistant strain (Figure 1, B and C). Figure 2 illustrates the differential expression of the identified proteins between the two strains. The graph distinguishes saglin and TRIO proteins, which displayed high expression level differences and the lowest q-values. Saglin, TRIO and D7 long form are secreted proteins as evidenced by the presence of a signal peptide which is indicative of secretion through the classical ER-golgi pathway, as predicted by SignalP 4.0 [26].

Results

Differential analysis between SGE samples from resistant and susceptible mosquitoes

Four independent biological repeats corresponding to four SGE samples of each An. gambiae strain, AceRKis and Ks, were used for the comparative analysis. Principal component analysis (PCA) separated eight gels according to expression variation into two distinct groups corresponding to the SGE samples of the two An. gambiae strains (PCA values of 56% and 12% for the two first components). A significant differential expression between the two strains was observed in 10 of the 708 spots according to ANOVA test, (p < 0.01) and a display of 1.5-fold minimal difference in expression levels. Figure 1A shows the localization of the 10 spots identified as differentially expressed by SameSpots analysis. Of these spots eight were excised from the preparative Ks and AceRKis gels, whereas the other two spots were too faint for excision (spots 572 and 658). Statistical results for the 8 spots are summarized in Table 1.
This 100 kDa-salivary protein was described as a disulphide bond-linked homodimer of ~50 kDa subunits, and then reported as the receptor for sporozoites in salivary gland, binding to the thrombospondin-related anonymous protein (TRAP) expressed in sporozoites and conserved in all *Plasmodium* species [28]. TRAP was shown to be essential for sporozoite gliding, cell invasion and in vivo infectivity, thus candidate target protein for malaria transmission-blocking vaccine [29,30]. Previous sialome studies showed an over-expression of saglin in *An. gambiae* females versus males [31].

Blast analysis identified the closest homologous and orthologous sequences in *An. stephensi*, *An. cracens* and *An. gambiae* (49, 47, and 32% identity, respectively), and confirmed saglin as being a member of the salivary gland-1 (SG1) protein family, described as unique to anophelines [32,33]. Sequence analysis of saglin did not reveal any functional domain, but an N-terminal signal peptide for
Table 1. Differentially expressed salivary gland proteins between the susceptible Kis and resistant AceRKis strains.

<table>
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<tr>
<th>Spot #</th>
<th>Protein ID</th>
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<th>q-value</th>
<th>Fold</th>
<th>Accession</th>
<th>MW (kDa)</th>
<th>pI</th>
<th>Cover</th>
<th>Score*</th>
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<td>6.03</td>
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<td></td>
<td></td>
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<td></td>
<td></td>
<td>Q8WR22</td>
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Protein identification was performed using MALDI-TOF MS or nanoLC ESI MS/MS (underlined spot #) analysis. Insecta entries of Swiss-Prot and TrEMBL databases were searched by using the MASCOT algorithm, or the Proteome Discoverer software for nanoLC ESI MS/MS spectra. All spots displayed a power $>0.9$. Spot # refers to the SameSpots analysis spot number (see Figure 1A); $^*$ indicates the presence of a signal peptide for secretion as predicted by SignalP 4.0 ($^u$: SP in the N-terminal homolog Q5TV62_ANOGA); Fold: fold difference in expression levels between the two strains; Accession: accession number in UniProtKB/Swiss-Prot or UniProtKB/TrEMBL databases (_ANOGA); pI: isoelectric point; Cover: indicates the amino acid coverage (%); *Mascot Score is provided for MALDI-TOF protein identification; for nanoLC ESI MS/MS based identification the peptide sequences and the number of peptides are provided as supporting information (Table S1). Translation IF: Translation Initiation Factor.

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of sporozoite load in this compartment. Further studies targeting gland invasion could thus be one factor contributing to the control stage in the head and thorax [16]. The role of saglin in salivary increase in prevalence of infection in the resistant mosquito An. gambiae considered. With salivary gland invasion being an essential step resistant AceRKis strain might be less susceptible to forms of the protein observed in the resistant strain is low, this protein deserves some comment. Indeed, its ortholog in Plasmodium falciparum reported a low in prevalence of infection in the resistant mosquito regarding the oocyst stage in the midgut but not the sporozoite stage in the head and thorax [16]. The role of saglin in salivary gland invasion could thus be one factor contributing to the control of sporozoite load in this compartment. Further studies targeting both the parasite quantification in the salivary glands and the characterization of saglin partners likely to participate in salivary gland invasion by the pathogen would shed some light on the relevance of the differential expression of saglin in the susceptibility to parasite infection of An. gambiae.

In contrast with saglin, the TRIO protein presents a significant up-regulation in the insecticide resistant AceRKis strain. cDNA encoding this protein was identified among the salivary gland transcripts of An. gambiae adult females [35]. Expression data showed an over-expression of An. gambiae TRIO in adult female versus male, in salivary gland versus whole body extract, and in non-blood-fed versus blood-fed female [31,36]. This female-enriched salivary gland gene product is thus likely to play a role in blood feeding, but not in the digestion of the blood meal. Rather it could be involved in the blood feeding process in relation either with anti-hemostatic/imunomodulation properties or with the different steps preceding the blood meal i.e. probing and blood uptake. Thus up-regulation observed in the resistant strain could testify for some differences in blood meal uptake between the sensitive and resistant mosquitoes. Sequence alignments and similarity searches performed in the present study indicate that this secreted protein is another member of the SG1 family sharing only 16% identity with saglin. Biochemical studies targeting secretion properties, localization, and function of TRIO could shed light on its role in the salivary glands of Anopheles, and on the significance of its up-regulation in the biology of the insecticide-resistant An. gambiae strain.

Surprisingly a Glutathione S-transferase was found as down-regulated in the resistant AceRKis strain. Glutathione S-transferases (GSTs) are a diverse family of enzymes, playing a central role in detoxification of both endogenous and xenobiotic compounds [37]. An. gambiae GSTs have been studied for their implication in resistance to the organochlorine insecticide DDT. Expression profiling experiments identified members of the epsilon-class of GSTs but none of the delta-class GSTs as upregulated in DDT resistant strains, and functional studies confirmed the high DDT-metabolizing ability of one GST member of the epsilon-class [38,39]. The GST identified in the present study is a member of the delta class, named GSTD1 or agGSTd1-6 [39,40]. Structural studies revealed differences in the substrate-binding site conformation that explained the very low DDT-detoxifying activity of this GST [41,42]. Thus, the down-regulation of the protein in the resistant strain might not be linked to a decreased insecticide detoxifying activity, but the relevance of this difference in expression observed between the two strains is unclear. Besides their detoxifying function GSTs are involved in a wide range of biological processes including protection against oxidative stress [43]. Their contribution to the removal of toxic oxygen free radicals and maintenance of the redox status of the cell represents a function that deserves further attention to better understand the role of this enzyme family, particularly in relation to parasite infection and vector competence.

Although the down-regulation of the secreted D7 long form protein observed in the resistant strain is low, this protein deserves some comment. Indeed, its ortholog in Culex pipiens quinquefasciatus, named long form D7 cluster12 salivary protein, was named ace1.R insecticide-resistant and the susceptible strains [12]. D7 protein family is widely conserved in blood sucking diptera, and its expression is restricted to female salivary glands suggesting a potential role in the blood meal process [44]. This family is ancestrally related to Odorant Binding Protein family, but is a separate branch as supported by the structural analysis of Anopheles D7 proteins members [13,45]. The Anopheles D7 family is composed by three long form proteins [27-30 kDa] and
five short form proteins, named D7r1-D7r5. The short forms (D7r1-D7r4) have been demonstrated binding biogenic amines, like serotonin, norepinephrin and histamine, highlighting functions in the inhibition of itching, burning and vasocostriction induced by the bite [13]. D7r1 possess also anticoagulation activity, as its ortholog in An. stephensi, hamadarin. Function of the Anopheles species D7 long form recently became elucidated. A structure/function study on the long form D7 L1 from An. stephensi has shown that this protein binds cysteinyl-leukotrienes and analogues of tromboxane A2. These molecules are released during early inflammatory response following injury, contributing to pain, increase of vascular permeability and platelet activation in the host [46]. The high similarity observed between the D7L1 and the An. gambiae ortholog (60%), especially for amino acid residues involved in ligand binding pocket (80% identity), strongly suggests that the An. gambiae D7 long form could have similar functions in blood feeding. The down regulation of this D7 long form protein may thus alter the efficacy of the blood feeding process, with less inhibition of platelet activation and anticoagulation activity of the host. The blood feeding might be interrupted hence leading the mosquito to bite several hosts/times to achieve a complete blood meal. Biting behavioural studies comparing resistant and susceptible strains of An. gambiae as well as RNAi studies would help to determine the implication of this D7 long form protein in the blood feeding success.

The resistant AceRKis strain was obtained by introgression of the ace-1 G119S allele (ace-1R allele) from a resistant population into the Kisumu genome. After 19 generations of introgression, the two An. gambiae strains should share the same genetic background for most of their genome, mainly differing in their genotype at the ace-1 locus: the Kis strain is homozygous for the ace-1S allele and the AceRKis strain is homozygous for the ace-1R allele. Comparative studies of the two strains should thus reveal changes in characters or phenotypes that could be essentially attributed to the G119S mutation. Nevertheless, the genetic differences between the two strains might not be totally negligible: the presence of inversions, founder effects, and the genes closely linked to ace-1 could have prevented part of the expected recombination. Regarding chromosomal inversions, differences in the parental strains could hamper recombination and limit introgression [47]. Indeed, loci inside a polymorphic inversion and in linkage disequilibrium with the resistant allele may be selected with this allele. The origin of the Kisumu strain is East Africa, where An. gambiae is polymorphic for the chromosomal inversions 2Rb and 2La [48]. The insecticide resistant parental strain was colonized from wild mosquitoes from Bobo-Dioulasso (Burkina Faso) where the S form of An. gambiae has been shown to also possess the 2Rb and 2La inversions at high frequency [49]. Thus, as the two parental populations share the same inversions, they should not prevent recombination between the two strains, except if a founder effect randomly fixed different inversions before or during the introgression process. Moreover, as the ace-1 gene is located in the telomeric region of the chromosome 2R (region 7C), thus far from the closest inversion (2Rb, between sections 11C and 13A), these inversions are not expected to affect recombination near this gene, so that the inversions present in Kis should have been introgressed in AceRKis. If Kis was polymorphic at the beginning of the backcrosses, a unique variant of some genes could have been fixed in AceRKis, due to founder effect, while remaining polymorphic in Kis, thus inducing differences between the two strains. However, as each generation required a new backcross on Kis, this effect would be relatively limited, as most of the Kis polymorphism would have passed in AceRKis. We cannot however rule out the possibility that other genes, such as regulatory regions and loci physically linked to ace-1R could have hitch-hiked with it during the introgression process. Indeed, at the risk level of 0.05, a genetic distance of 13 cM around ace1R would not have been replaced during the successive backcrosses [5,50]. According to the average relationship between genetic distance and physical distance on the chromosome X [5,50], that would correspond to approximately 11 Mb of DNA that could differ between the two strains, depending on the initial polymorphism. In conclusion, we cannot exclude that part of the differences in salivary protein expression observed in the present work between Kis and AceRKis could be due to cis-regulatory elements or other loci from the genome in which the ace-1R mutation originally occurred, rather than to the mutation itself. The analysis of the non-synonymous polymorphism between the two strains, particularly in the flanking regions of the ace-1 locus, could help in quantifying the real impact of the introgression process. Finally, additional crossing experiments between the two strains followed by the analysis of the co-segregation of salivary protein expression and the resistance gene are required to formally establish the causal relationship between the regulation of the salivary protein genes and the resistance allele.

Conclusion

The present work is the first attempt to determine whether insecticide-resistance in An. gambiae mosquitoes could induce a modulation of protein expression in the salivary glands and have some consequences on blood feeding, trophic behaviour and on Plasmodium transmission. We describe for the first time modifications in the salivome composition of insecticide-resistant An. gambiae. The known or putative functions inferred from sequence similarity analyses revealed that the differentially regulated proteins identified in this study are involved in pathogen invasion, blood feeding process, or protection against oxidation. These proteins deserve functional studies to understand the relevance of the differences in expression recorded in the insensitive acetylcholinesterase resistant mosquitoes. This data confirms the profound alterations linked to the resistance in the anopheline mosquito biology but additional genetic studies on the polymorphism between the two strains are needed to confirm whether ace-1R allele is responsible for the variation in protein expression and to determine whether the expression levels influence phenotypes relevant for transmission. Experiments on field mosquitoes bearing the ace-1R allele or the ace-1 gene duplication [6] could also help to specify the link between ace-1 alleles and phenotypes. Further experiments on the behaviour of these mosquitoes during blood feeding will contribute to the understanding of the impact of resistance on blood meal intake and on the transmission of the pathogen. This work opens the way for studying the profound biological alterations in the mosquito linked to the different insecticide resistance mechanisms, alone or in combination.

Supporting Information

Table S1 Details of the nanoLC ESI MS/MS based identification of the differentially expressed salivary gland proteins in insecticide-resistant AcerKis strain.

| Protein Identification | NanoLC ESI MS/MS Based Identification | Details of the nanoLC ESI MS/MS Based Identification | Supporting Information | Table S1 Details of the nanoLC ESI MS/MS based identification of the differentially expressed salivary gland proteins in insecticide-resistant AcerKis strain. | Protein identification was performed using nanoLC ESI MS/MS analysis. Insecta entries of Swiss-Prot and TrEMBL databases (release 2010_11) were searched by using the Proteome Discoverer software. Spot # refers to the sameSpots Analysis spot number (see Figure 1A); Accession number: accession number or entry name in UniProtKB/Swiss-Prot or UniProtKB/TrEMBL; In the peptide sequence column, m means methionine oxidation. (XLSX) |
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References


Author Contributions

Conceived and designed the experiments: SC VC FR FMD. Performed the experiments: SC MR MS FM FMD. Analyzed the data: SC MS ED FMD. Contributed reagents/materials/analysis tools: MS ED ID PM FC FR. Wrote the paper: SC FMD.