Gembloux Agro-Bio Tech
Université de Liège

Hemipteran - host plant interactions: focus on some model insect saliva

Serteyn Laurent*, Moreau Sophie*, Delatour Anaïs*, Francis Frédéric*

*Functional and Evolutionary Entomology - Gembloux Agro-Bio Tech - University of Liege (Belgium)

E-mail : laurent.serteyn@ulg.ac.be

Introduction

The interactions between herbivorous insects and the plants they consume have resulted in the evolution of a fascinating and complex web of chemical signals, behavioral responses, and genetic changes.

Insect salivary components play important roles in plant-insect interactions. A variety of enzymes and organic components in saliva of herbivory insects can induce series of biochemical responses in damaged plants, which could be very specific.

It has been demonstrated that the oral secretions of several chewing insects contain elicitors that either stimulate the plant defense, or promote infestation by manipulating plant metabolism/physiology. The effects of salivary compounds injected by piercing-sucking insects into the plant are much less understood.

Objectives

In our lab, several studies have been screening proteins in different aphid saliva (Harmel et al., 2008, for *Myzus persicae* ; Vandermoten et al., 2013, for *M. persicae*, *Megoura viciae* and *Acyrtosiphon pisum*).

The purpose of our current and future works is to widen that field of study to other piercing-sucking pests and host plant models. We focus on pure saliva and salivary glands extract.

Three models will be compared: the pea aphid (feeds on Fabaceae), the invasive Asian brown marmorated stink bug (tree fruit), and the invasive South America green stink bug (Fabaceae, Solanaceae…).

Brown marmorated stink bug
(*Halyomorpha halys* Stål)

Broad bean
(*Vicia faba* L.)

Bean
(*Phaseolus vulgaris* L.)

Saliva proteome comparison
(gel-free liquid chromatography)

(Experiment in process)

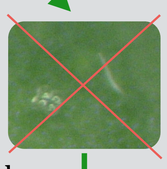
Southern green stink bug
(*Nezara viridula* L.)

Broad bean

Tomato
(*Solanum lycopersicum* L.)

Salivary glands proteome comparison
(2D-DIGE-MALDI-ToF/MS)

(Analysis in process)



Glandular trichomes

2D-DIGE

Pea aphid
(*Acyrtosiphon pisum* Harris)

Different symbiont profiles

Saliva proteome comparison

(Experiment in process)

Impacts of endosymbionts on salivary proteins

Comparison between 2 stink bugs with different feeding preferences (herbaceous plant for *N. viridula* and tree fruits for *H. halys*)

N° spot	Average Normalised Volumes		Fold	Title	Accession	Mascot Score	MS Coverage	PM (Da)	pI	Query coverage	E value	Source organism	Database
	Wildtype	Mutant											
Energy metabolism													
745	1,184	1,086	1,1	ATP synthase subunit alpha	gi|501562949	122	24	55116	5,6			*Rhodospirillum centenum*	Bacteria
747	1,035	0,829	1,2	ATP synthase subunit alpha	gi|501562949	95	22	55116	5,6			*Rhodospirillum centenum*	Bacteria
931	0,799	1,112	1,4	Polyphosphate kinase	gi|506275770	80	26	37938	5,3			*Catenulispora acidiphila*	Bacteria
DNA replication													
995	0,935	0.692	1,4	Primase	gi|497672544	80	23	51135	8,6			*Ruminococcus flavefaciens*	Bacteria
Traduction													
1120	0,930	1,497	1,6	Tyrosyl-tRNA synthetase	gi|488496990	85	11	43891	5,1			*Grimontia* sp. AK16	Bacteria
Protein binding													
1032	1,202	1,043	1,2	Pentatricopeptide repeat-containing protein At1g63130	gi|489572326|WP_003476772.1	71	15	48391	7,7	70%	5E-84	*Xanthomonas translucens*	Bacteria
Protein transport													
1065	1,194	1,052	1,1	Coiled-coil domain-containing protein 132	gi|751455004|XP_011182003.1	62	4	112133	5,6	88%	0	*Bactrocera cucurbitae* Coquillett	Arthropoda
Detoxification													
943	0,709	1,144	1,6	Zn-dependent hydrolase including glyoxylase	gi|557678046|WP_023432353.1	69	16	34119	5,9	99%	4E-166	*Lutibaculum baratangense*	Bacteria
Pathogenicity factor													
843	1,223	1,018	1,2	AvrE	gi|62001344	74	14	185549	6,8			*Pseudomonas viridiflava*	Bacteria
Signal transduction													
1182	1,183	0,890	1,3	Putative large Ala/Glu-rich protein	gi|294327738|EFG09381.1	85	19	151454	4,9	90%	0	*Streptomyces clavuligerus*	Bacteria
Unknown													
1306	0,954	1,323	1,4	Membrane protein	gi|493777496	74	16	32140	5,6			*Agrobacterium albertimagni*	Bacteria
1409	1,285	0,761	1,7	Hypothetical protein	gi|496872292	76	12	29712	5,9			*Acinetobacter baumannii*	Bacteria
1862	0,569	0,964	1,7	Hypothetical protein	gi|488799977	67	22	8419	4,1			Bradyrhizobiaceae	Bacteria

Differential expressions of bacterial proteins in salivary glands when *N. viridula* were exposed to tomato with or without glandular trichomes.

Discussion

This study takes place as a continuation of a first description of *H. halys* salivary proteins (Peiffer & Felton, 2014). Salivary glands and gut of stink bugs may be colonized by a bacterial community, which could explain the presence of bacterial proteins in these glands. This is in concordance with other proteomic studies on aphid saliva (Vandermoten et al., 2013 ; Chaudhary et al., 2014). Then it will be relevant to analyze the impact of aphid secondary symbionts on salivary proteins in order to assess their role in aphid performance on its host plant. Some of the identified proteins might indeed play a role in induction or repression of plant defence mechanisms.

The perspective would be applying saliva, salivary gland extracts and/or purified proteins on plant in order to screen its defensive responses by complementary “omic” approaches. Thanks to this comparative study of these three insect models, we would be able to move forward in the understanding of general and specific interactions between plants and Hemipteran pests.

Chaudhary R. et al., 2014. GroEL from the endosymbiont Buchnera aphidicola betrays the aphid by triggering plant defense. *PNAS*, **111**(24): 8919-8924.
Harmel et al., 2008. Identification of aphid salivary proteins: a proteomic investigation of Myzus persicae. *Insect Molecular Biology* **17**(2): 165-174.
Peiffer M. & Felton G.W., 2014. Insights into the saliva of the brown marmorated stink bug Halyomorpha halys (Hemiptera: Pentatomidae). *PLoS One*, **9**.
Vandermoten et al., 2013. Comparative analysis of salivary proteins from three aphid species. *Insect Molecular Biology*, **32**.

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