Identification by a RNAseq approach of virulence gene candidates in the non-model species Aphis Gossypii

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IDENTIFICATION BY A RNASEQ APPROACH OF VIRULENCE GENE CANDIDATES IN THE NON-MODEL SPECIES *APHIS GOSSYPII*

Aphids, as piercing-sucking insects, are agronomical pests responsible for yield reduction in the field. The damages they induce on the plants are direct through feeding into the phloem but also indirect by transmitting viruses. A major gene in melon, *Vat*, a member of the NBS-LRR gene family, confers resistance to both *A. gossypii* and non-persistent viruses when transmitted by this aphid. The gene was introduced in many commercial melon varieties. Some clones of *A. gossypii* were collected on *Vat*-resistant melons and biotests proved that some of these clones were able to bypass the resistance.

We suppose that an avirulence factor, present in the aphid saliva, allows the establishment of the plant resistance. In fact, during the first seconds of the interaction, the aphid injects its saliva into the plant, leading to the release of proteins into the plant cells. One of the protein ejected by the aphid interacts probably directly with the VAT protein, triggering the plant resistance. Our hypothesis is that the virulence character of some *A. gossypii* clones is mediated by (some) differential gene expression(s) or change(s) at the amino acid level of a (some) protein(s).

We took advantage of the availability of different *A. gossypii* clones, virulent and avirulent, to conduct a global transcriptomic approach to identify potential candidates involved in the virulence character of the aphid on *Vat*-melon. Four genetically-close clones were chosen, with one virulent, and RNA extracted from their heads. One to two millions reads per clone were obtained by a RNASeq approach on an HiSeq2000 (MGX, Montpellier, France). We concatenated the data to generate a head-reference transcriptome of more than 33000 contigs (*de novo* assembly). This reference was used to search for genes differentially expressed and/or presenting sequence polymorphisms between virulent and avirulent clones. We identified 62 down-regulated and 26 up-regulated genes in the virulent clone compared to the three other clones. 1530 contigs exhibited specific polymorphisms in the virulent clone, with only 42 potentially excreted in the aphid saliva.