Genetic diversity of the melon aphid Aphis gossypii Glover in different melon growing areas of France

Sophie Thomas, Pascale Mistral, Virginie Chareyron, Bastien Barral, Nathalie Boissot, Flavie Vanlerberghe-Masutti

▶ To cite this version:

Sophie Thomas, Pascale Mistral, Virginie Chareyron, Bastien Barral, Nathalie Boissot, et al.. Genetic diversity of the melon aphid Aphis gossypii Glover in different melon growing areas of France. 8. International Symposium on Aphids, Jun 2009, Catania, Italy. hal-02752596

HAL Id: hal-02752596
https://hal.inrae.fr/hal-02752596v1

Version définitive du manuscrit publié dans / Final version of the manuscript published in : 8th International Symposium on Aphids Programme and abstracts 2009, Catania 2009/06/08-12

Genetic diversity of the melon aphid *Aphis gossypii* Glover in different melon growing areas of France

S. Thomas(1), P. Mistral(1), V. Chareyron(1), B. Barral, N. Boissot(1), F. Vanlerberghe-Masutti(2)

(1)*INRA-GAFL, INRA, GAFL UR 1052, BP 94, F-84143 Montfavet*

(2)*INRA - UMR 1301 – Equipe Biologie des Populations en Interaction - 400 Route des Chappes - BP 167 – F-06903 Sophia Antipolis cedex – France*

Aphis gossypii (Glover) is a cosmopolitan pest of crops which population genetic diversity is structured in relation to the host plants (Carletto et al., in press). The genotypes that have been found to colonize Cucurbits are distributed into two genetic clusters, on the basis of eight microsatellite markers. The first one comprises a single genotype called NM1 that has been only observed in South-East of France. The second cluster comprises all the other genotypes observed on Cucurbits, including the C9 genotype found all over the distribution area of *A. gossypii*. In melon, the *Vat* gene confers resistance to the *A. gossypii* colonization (Pitrat and Lecoq, 1982). The resistance appears to be complete for clones having a genotype NM1 and partial for clones having a genotype C9 (Boissot et al, 2008).

In this study, our aim is (i) to describe the genetic structure of *A. gossypii* populations infesting Cucurbits in geographically distant melon producing areas and (ii) to evaluate the selection pressure that the *Vat* gene is exerting on *A. gossypii* populations.

We therefore sampled apterous *A. gossypii* (isolated or in colony) from melon crops either made of susceptible cultivars or made of resistant cultivars and for all the crop cycle. Samples were collected in four fields of three regions located in South-East of France, South West, and in the French West Indies. Every one of the 1409 apterous aphids sampled was genotyped using eight microsatellite markers to assess its multilocus genotype (MLG).

We discriminated 19 frequent MLGs and 35 MLGs present in only one copy. In metropolitan France, 5 MLGs were frequently observed over all the areas: NM1, C11, C9, CUC2 and MTB. The dominant MLGs were C9 (26.6%) and CUC1 (28.0%) in South-East while it was MTB (55.7%) in South-West. In the French West Indies, the Guadeloupe, the most frequent MLGs, were C6 and GWD (83.6%) that had never been observed in metropolitan France. Both MLGs observed in Guadeloupe and 13 of those observed in France were found to belong to the second cluster described by Carletto et al., in press. The 3 other MLGs detected in France were close to NM1 and therefore belong the first cluster. Then, the diversity of *A. gossypii* appeared to be reduced in Guadeloupe, a small island in the Caribbean basin with a tropical climate that could induce a geographical isolation, as compared to France with a temperate climate where sexual reproduction events generating genetic variability may occur.

Moreover, we compared the global MLG frequencies in aphids collected on melon plants with the *Vat* gene and on melon plant without the *Vat* gene. NM1, C9 and MTB were significantly less frequent on melon with the *Vat* gene than on melon without the *Vat* gene ($\chi^2=29.70$, 10.05 and 28.45 respectively, $p<0.01$). This decrease is consistent with the known effects of the *Vat* gene on NM1 and C9. On the contrary, the frequencies of CUC1 and C6 increased significantly on melon plants with the *Vat* gene ($\chi^2=19.69$ and 27.36 respectively, $p<0.0001$). Then, some MLG were identified as able to develop on resistant cultivars. These results should be confirmed with several years' trials to evaluate the selection pressure that the *Vat* gene is exerting on *A. gossypii* populations.

Keywords: *Aphis gossypii,* genetic diversity, microsatellites, *Vat,* resistance gene, *Cucumis melo*

References:

Boissot, N., V. Chareyron, et al. (2008). A new view on Aphid Resistance in melon: The role of Aphis gossypii variability. Cucurbitaceae 2008, IXth Eucarpia meeting on Genetic an Breeding of Curcubitaceae, France, Avignon.

Carletto, J., E. Lombaert, et al. "Ecological specialization of the aphid Aphis gossypii Glover on cultivated host plants." Molecular Ecology, in press.

Pitrat, M. and H. Lecoq (1982). "Relations génétiques entre les résistances par non-acceptation et par antibiose du melon à Aphis gossypii. Recherche de liaisons avec d'autres gènes." Agronomie 2(6): 503-508.