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What do spring migrants reveal about sex and host selection in the melon aphid

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Host plants exert considerable selective pressure on aphids because the plants constitute their feeding, mating and oviposition sites. Therefore, host specialisation in aphids evolves through selection of the behavioural and chemical mechanisms of host-plant location and recognition, and through metabolic adaptation to the phloem content of the host plant. How these adaptive traits evolve in an aphid species depends on the complexity of the annual life cycle of that species. The purpose of this field study was to determine how winged spring-migrant populations contribute to the evolution and maintenance of host specialisation in *Aphis gossypii* through host-plant choice and acceptance. We also assessed whether host-specialised genotypes corresponded exclusively to anholocyclic lineages regardless of the environmental conditions.

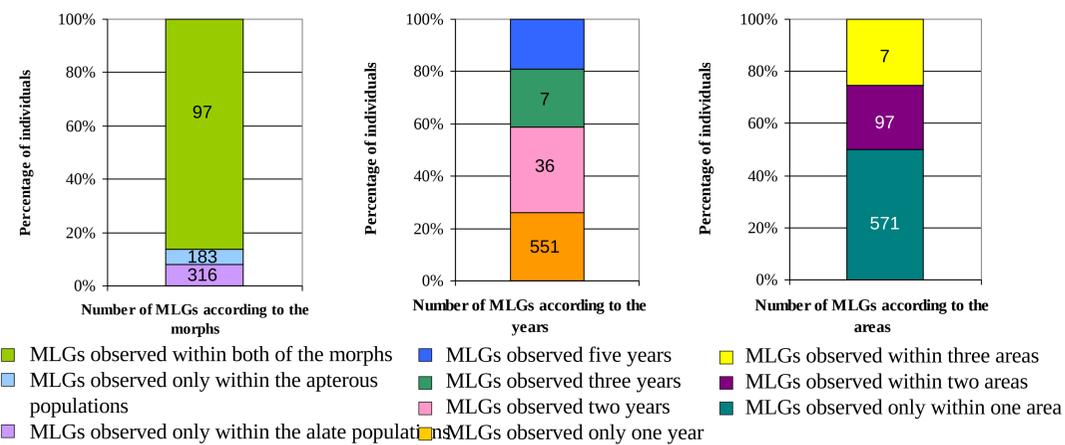
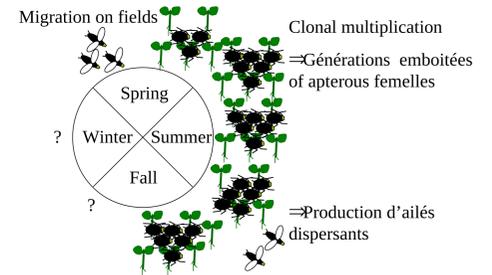


Figure 2 Occurrence of the 596 multilocus genotypes in the *A. gossypii* populations sampled in France and Lesser Antilles. The numbers of multilocus genotypes are shown in the bars and the percentages of individuals exhibiting those multilocus genotypes are shown in the axis y according to a. morphs, b. years and c. areas.

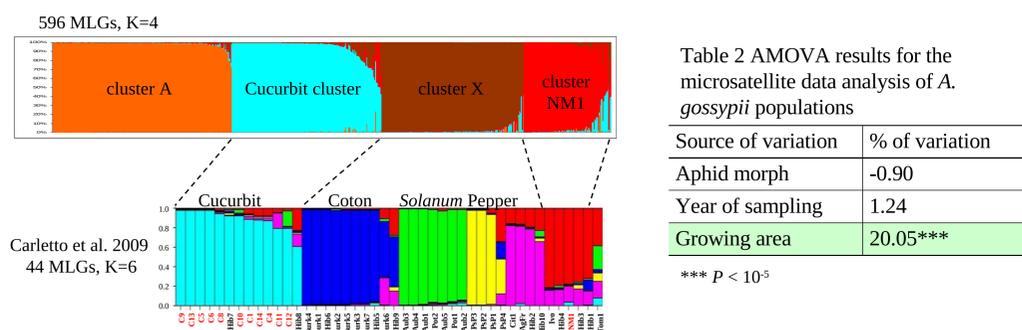


Table 2 AMOVA results for the microsatellite data analysis of *A. gossypii* populations

Source of variation	% of variation
Aphid morph	-0.90
Year of sampling	1.24
Growing area	20.05***

*** $P < 10^{-5}$

Figure 3 Results from the Structure program showing the estimated proportion of assignment of the multilocus genotypes. Assignment of the 596 MLGs with the 44 MLGs previously described and assigned to host races (Carletto et al. 2009).

Host-plant selection

Because the genetic diversity of the populations on the melon crops was geographically structured, as revealed by the AMOVA (Tab. 1), we considered the distribution of the alate and apterous individuals according to the existence of the four genetic clusters A, X, Y and Z, within each of the four geographic areas (Fig. 5). We observed alate individuals that were obviously not specialised on Cucurbitaceae on melon crops, i.e., individuals belonging to the clusters A and X. This finding suggests that olfactory cues are unlikely to be decisive in natura for host recognition, which probably occurs only after landing and plant probing. In all of the areas, the number of individuals with an MLG assigned to the cucurbit cluster or to the NM1 cluster (known for its ability to colonise Cucurbitaceae) was significantly higher in the apterous populations than in the alate populations (Chi-square test, $P < 0.0001$). This tendency was mainly due to a loss of the MLGs belonging to the clusters X and A. This finding argues in favour of host-plant recognition by alate aphids after probing. The clones that were not adapted to melons might lay a few larvae before taking off again.

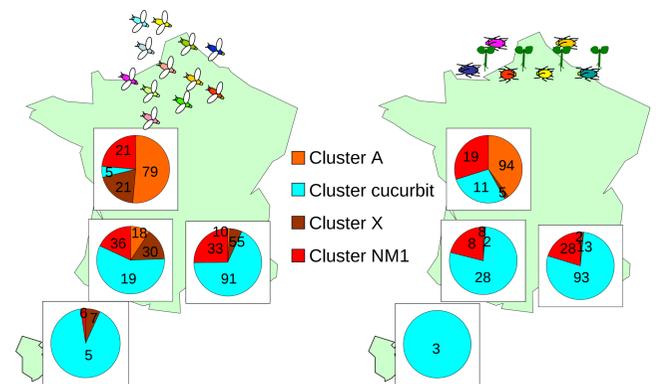
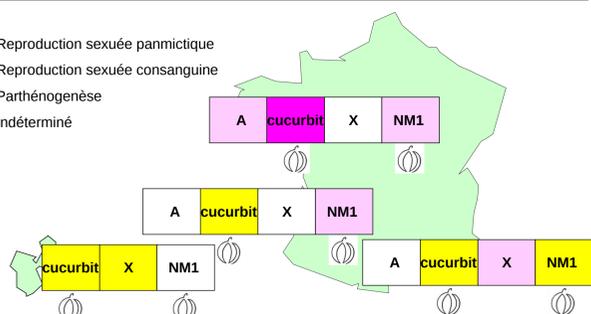


Figure 4 : Distribution of the alate and apterous *A. gossypii* samples according to the genetic clusters. The proportion of individuals is represented by sectors and the numbers of multilocus genotypes is shown in each sector in the four melon-growing areas according to the division into four genetic clusters.

	Equilibre d'Hardy-Weinberg	Déséquilibre de liaison	F_{is}
Reproduction sexuée panmictique	$H_{obs} = H_{att}$	$r_{obs} = r_{att}$	0
Reproduction sexuée consanguine	$H_{obs} < H_{att}$	$r_{obs} < r_{att}$	1
Parthénogenèse	$H_{obs} > H_{att}$	$r_{obs} < r_{att}$	-1

■ Reproduction sexuée panmictique
■ Reproduction sexuée consanguine
■ Parthénogenèse
□ Indéterminé



Reproductive mode

We examined the genetic variability of the alate populations to track the genetic fingerprints of sexual reproduction. We calculated three parameters: the Hardy-Weinberg equilibrium (HWE), the linkage disequilibrium (LD) and the F_{is} index (Tab. 2). To reduce the Wahlund effect, we split the populations a) according to their cluster membership (A, X, Y or Z) and their area (SE, SW, W or LA) (Fig. 5). The values of the genetic indices strongly suggest that these individuals correspond to obligate parthenogenetic lineages. The genetic analysis suggested that sexual reproduction occurred in the populations from the SW and W. The positive values of F_{is} argued in favour of a high level of inbreeding but they could also be artificially inflated by pooling different reproductive units (Wahlund effect) or because of a mix of asexual and sexual lineages. The genetic analyses within the populations belonging to the sub-clusters A suggested that sexual reproduction occurred with a high level of inbreeding in these populations. These aphids are assumed to colonise wild plant species. The uncultivated plant compartment could be considered as a heterogeneous and disturbed environment, in which the maintenance of sexuality confers advantages, while crop plants correspond to simplified and uniform environments that favoured a few host-adapted asexual lineages

Conclusion

Our results clearly demonstrate that the melon plant acts as a selective filter against the reproduction of non-specialised individuals. We showed that olfactory cues are unlikely to be decisive in natura for host recognition by spring-migrant aphid populations that are not specialised on Cucurbitaceae. The agroecosystem structure and history of the four studied regions may have partially shaped the genetic structure of the spring-migrant populations of *A. gossypii*. Cucurbitaceae-specialised genotypes corresponded exclusively to anholocyclic lineages, regardless of the environmental conditions. However, some genotypes that were genetically close to the host-specialised genotypes and some genotypes that probably originated from wild plants had never been previously sampled; both were holocyclic.