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Sophie Thomas, Nathalie Boissot, Flavie Vanlerberghe-Masutti. What do spring migrants reveal about sex and host selection in the melon aphid. 34. Réunion annuelle du Groupe d'Etude de Biologie et Génétique des Populations (Petit Pois Dérivé 2012), Aug 2012, Avignon, France. 2012. hal-02805852

**HAL Id: hal-02805852**

**<https://hal.inrae.fr/hal-02805852>**

Submitted on 6 Jun 2020

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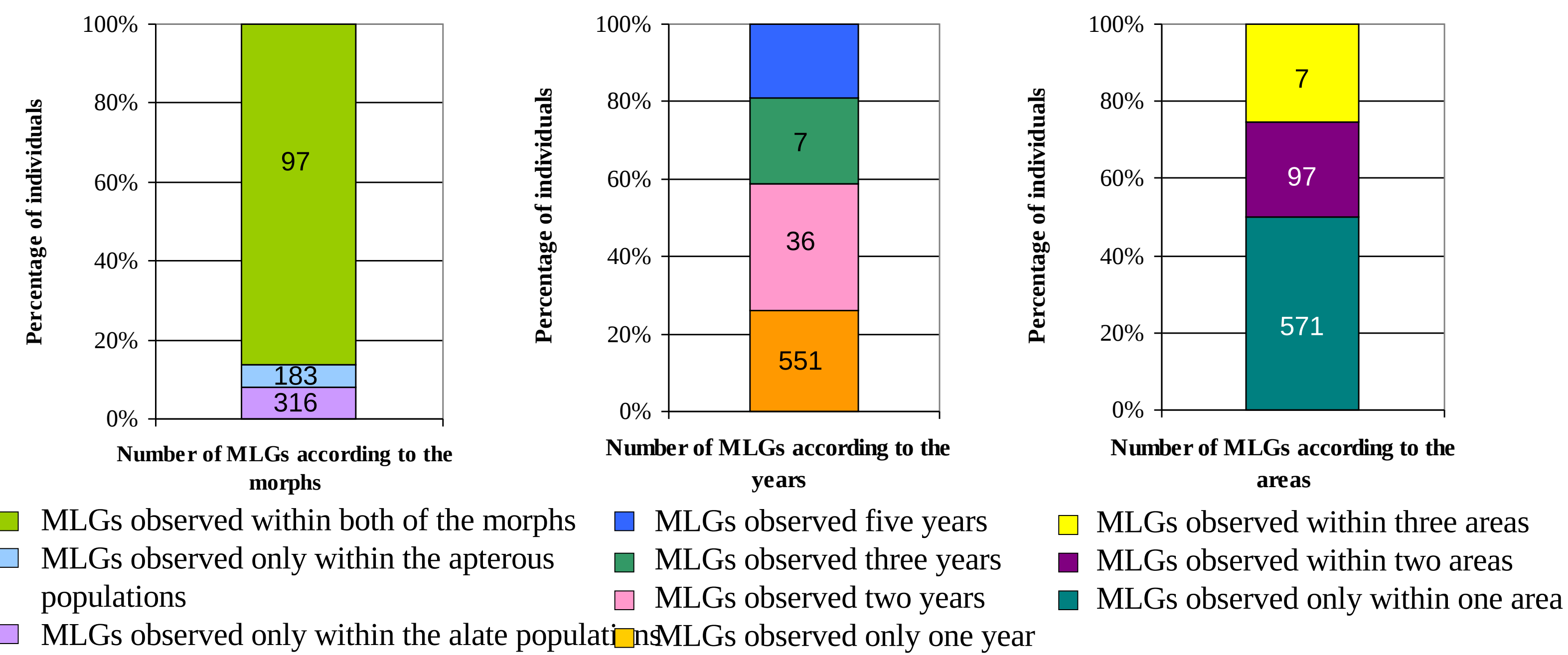
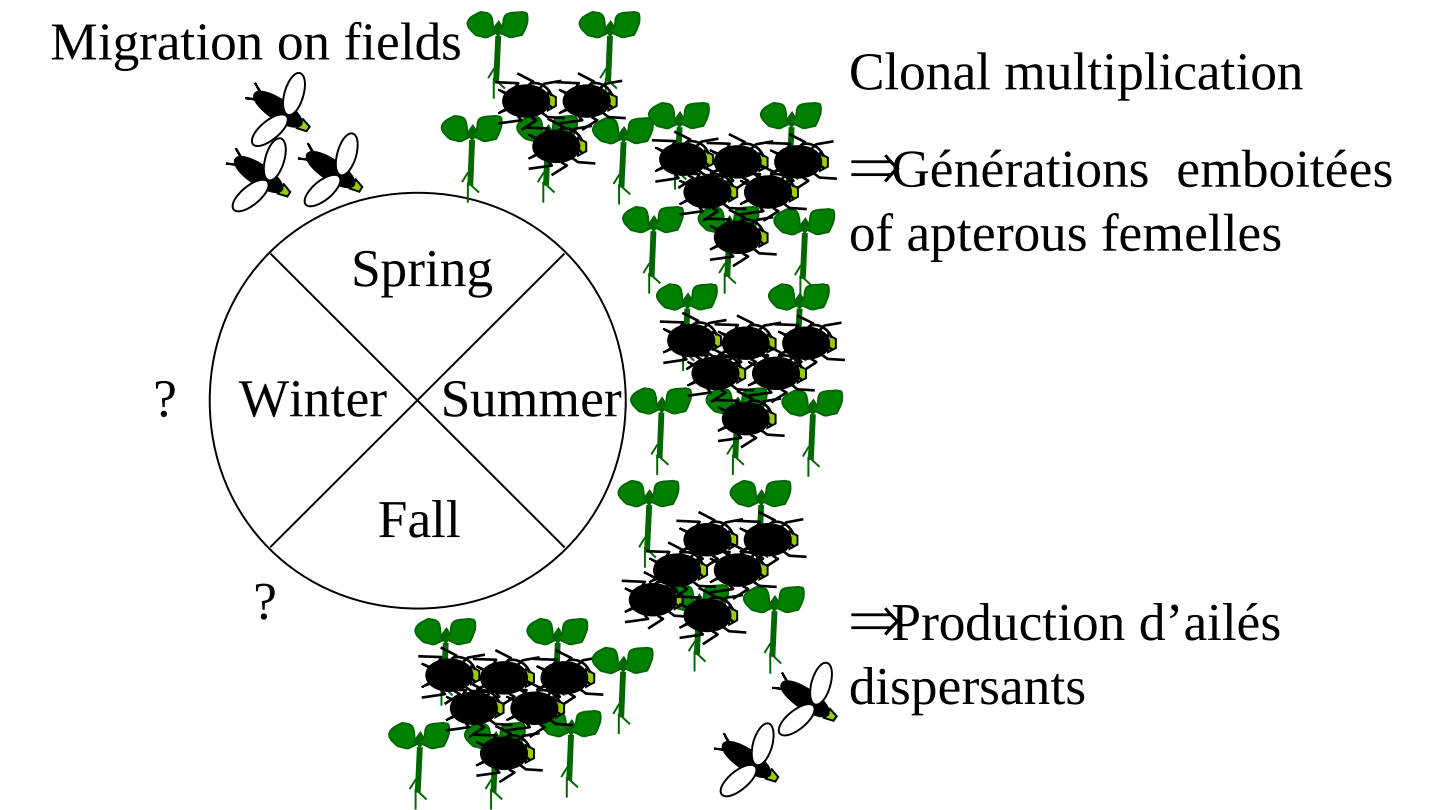
# What do spring migrants reveal about sex and host selection in the melon aphid

Sophie Thomas<sup>1</sup>, Nathalie Boissot<sup>1</sup>, Flavie Vanlerberghe-Masutti<sup>2</sup>

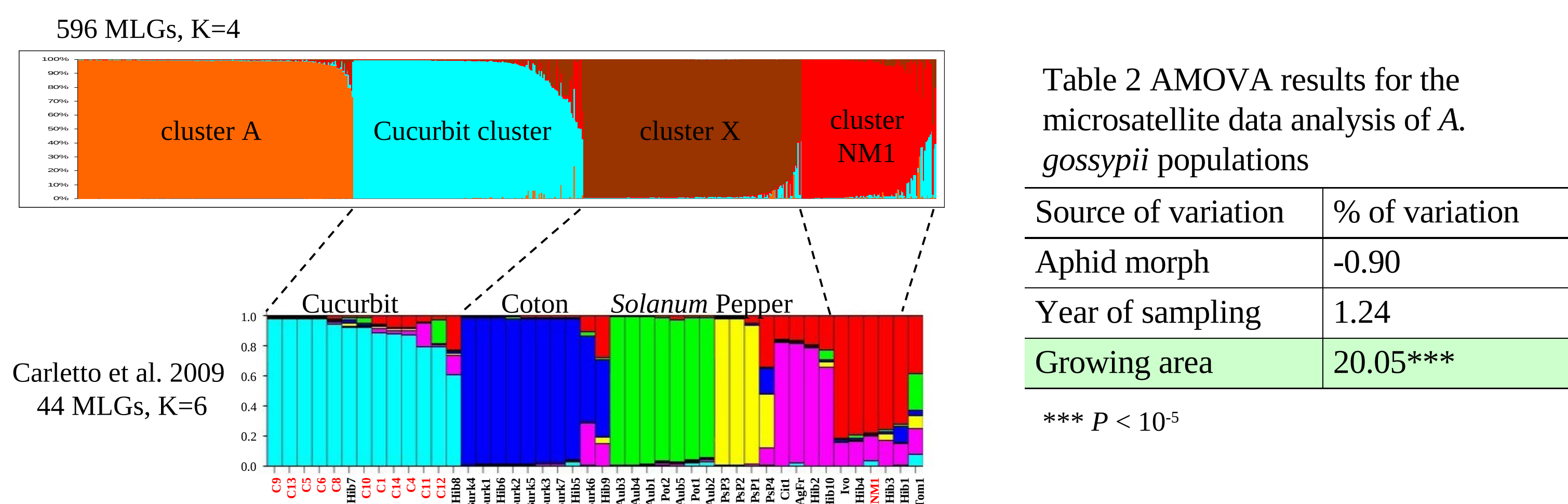
<sup>1</sup>INRA, UR1052, Génétique et Amélioration des Fruits et Légumes, B.P. 94, F-84143 Montfavet cedex

<sup>2</sup>INRA, UMR1062 CBGP, IRD, CIRAD, Montpellier SupAgro, Campus international de Baillarguet, CS 30016, F-34988 Montferrier-sur-Lez, France

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.

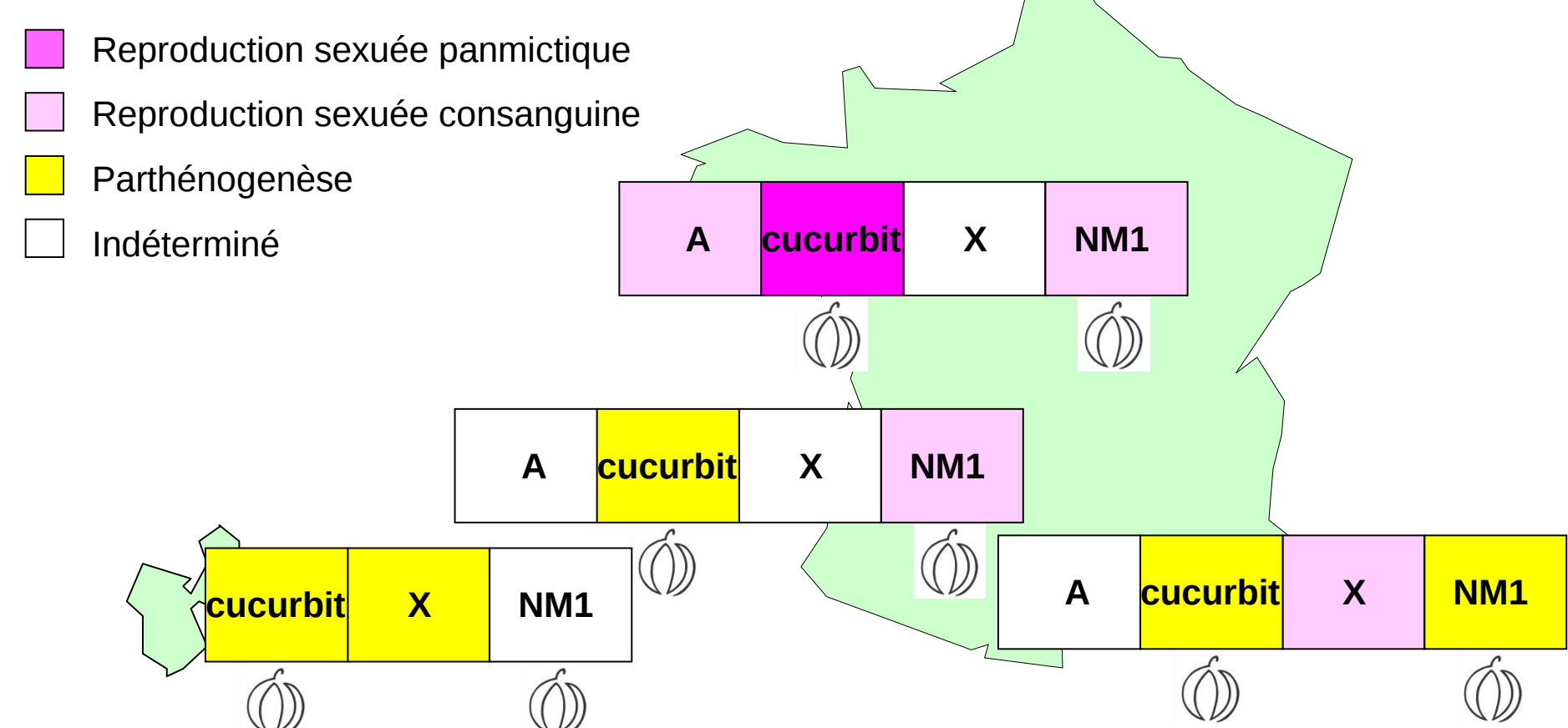


**Figure 3 Results from the Structure program showing the estimated proportion of assignment of the multilocus genotypes.** Assignment of the 596 MLGs with the 44 MLGs previously described and assigned to host races (Carletto et al. 2009).

## 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.

	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



## Conclusion

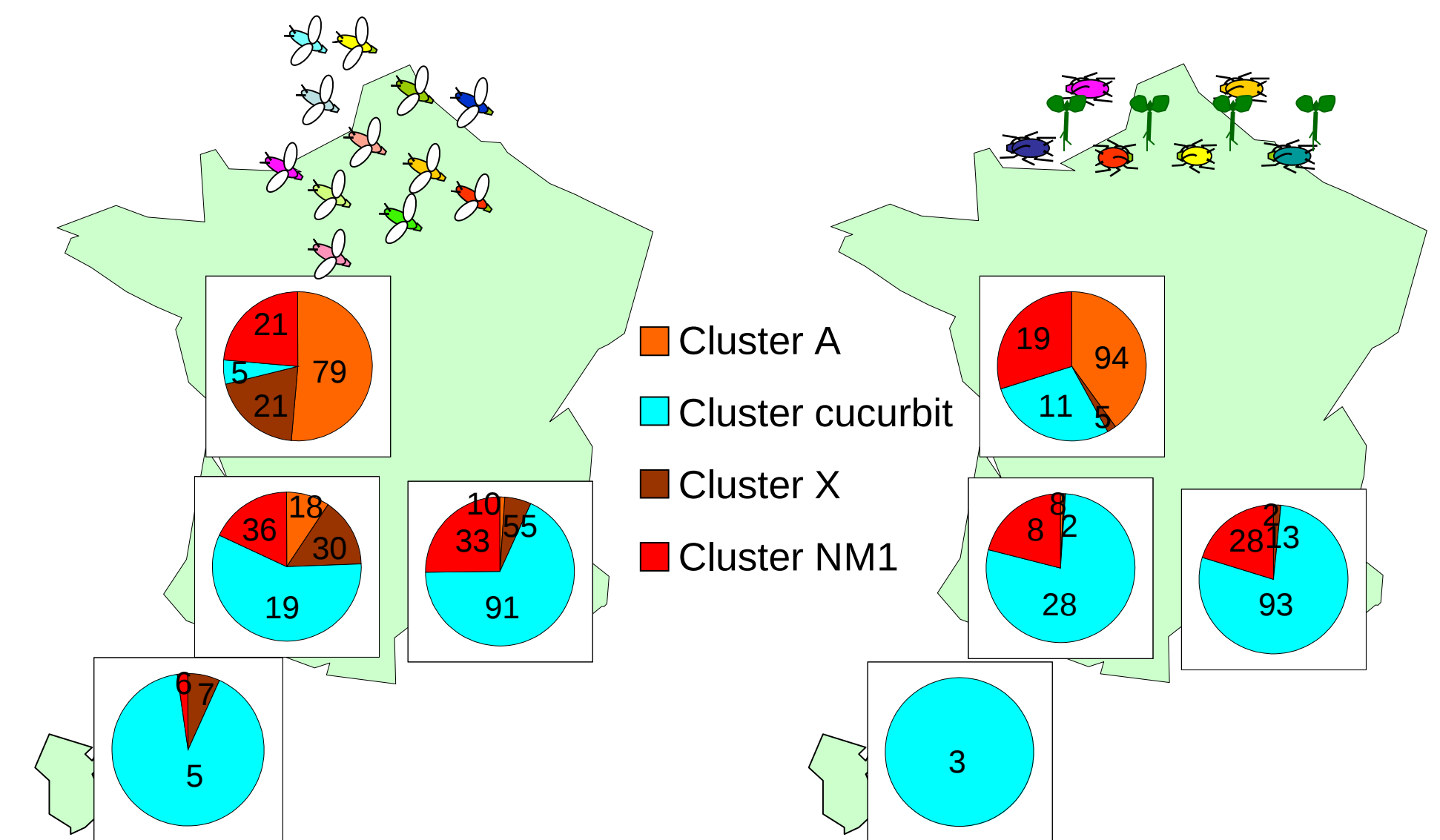
Our results clearly demonstrate that the melon plant acts as a selective filter against the reproduction of non-specialised individuals. We showed that olfactory cues are unlikely to be decisive in natura for host recognition by spring-migrant aphid populations that are not specialised on Cucurbitaceae. 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.

## A strikingly high genetic variability (Fig. 1)

To investigate the genetic diversity of *A. gossypii*, we sampled alate and apterous aphids from 2004 to 2009 in locations in the southeast (SE), southwest (SW) and west (W) of France and in the Lesser Antilles (LA). The aphids were genotyped using eight microsatellite markers.

Among the 4792 aphids analysed (1868 alate and 2924 apterous), we found a high genetic variability with 596 multilocus genotypes (MLGs). Their occurrence were represented in the figure 1. The majority of the MLGs were present as a single or rare copies corresponding to 22% of individuals among the alate aphids and 9% among the apterous aphids. Only four of the MLGs had a frequency higher than 5% of the total number of individual genotypes and the number of clones that recurred over time and space were dominated by only a dozen MLGs.

The analysis of the 596 MLGs revealed four genetic clusters (Figure 3). Three of the clusters had already been identified in previous studies, although the genetic diversity observed within each of them was much higher in the present study. These three clusters contained the MLGs that characterised the aphid clones that were specialised on cultivated plants. Cluster Y contained the MLGs that defined the Cucurbitaceae host race, cluster Z contained some MLGs that specialised on Cucurbitaceae (NM1) and some that specialised on Malvaceae, cluster X contained MLGs from the Solanaceae and cotton host races. In contrast, cluster A contained MLGs that had never been observed in previous studies. The hypothesis that the aphids bearing these MLGs may have originated from a broad array of wild host plants is supported by the huge host-plant spectrum of *A. gossypii*, which consists of more than 900 plant species over 119 botanical families.



**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.

## 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 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