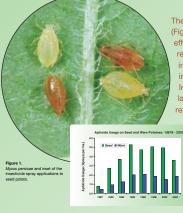
# A genotypic analysis of peach-potato aphids caught in Scottish suction traps

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The peach-potato aphid, Myzus persicae (Figure 1), is an important pest and a very efficient vector of potato viruses. This has resulted in the application of high levels of insecticides to seed potato crops (Figure 1 inset)

In Scotland, the absence of peach for egg laying limits *M. persicae* to asexual reproduction. Molecular markers can now

provide information on the genetic composition of *M. persicae* populations. The Scottish population is comprised of a small number of identical clones or genotypes (Table 1). This is in contrast to many other populations where sexual reproduction generates a complex mixture of genotypes. To monitor and forecast the activities of aphids including *M. persicae*, a network of suction traps collects specimens daily. When the levels of *M. persicae* reach a threshold in a trap then local crop monitoring can commence, such as on seed potato in Scotland. Suction traps are believed to operate at a landscape scale, representing the flying aphids within a 50km radius. The results of suction traps can be



2001 the entire Scottish M, persicae population consisted of seven genotypes. Genotypes A are carried all known resistance mechanisms and these are indicated with red colours in all the iagrams. Genotypes C, D and E carried some resistance mechanisms and these are indicated in ellow colours. Genotypes I and J carry no known resistances and they are green. Genotypes C, I and J had been the predominant local clone in previous years.

made more powerful by determining the overall genetic composition in a trap and then linking this to the aphid ecology determining where the flying populations are coming from and how much of a threat they pose. This should refine the predictive capabilities of the traps. It has been difficult to genotype M. persicae in traps as high quality DNA is not easily obtained from specimens stored in a fluid chosen for preserving morphology. This problem is compounded for samples stored for long periods. We have now developed a DNA extraction method for such samples and here, as an example, we examined the genetic composition of specimens caught in the Dundee suction trap in 2001, a year when exceptionally high numbers of dispersing M. persicae were collected.

# Aim

To examine the genetic

numbers of alatae were

caught (Figure 2) and

relate this to field

distribution.

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composition of M. persicae in the

Dundee suction trap in 2001, a

year when exceptionally high

# Materials and methods

# Field collected M. persicae.

In 2001 *M. persicae* were collected from field sites around the Dundee suction trap. Figure 3 shows the relative positions of the field sites and the trap. These consisted of both insecticide treated (mostly seed potato) and untreated fields. The Dundee trap is located within a large experimental farm and it was possible to control the agroecosystem for 2km around the trap. Fields of oilseed rape and potato were grown within this radius. These were

not treated with insecticides and were sampled at regular intervals throughout the season. Commercial fields were visited at various times during the growing season and those within a 30km radius were included.



ap showing the location of the suction trap (yellow star) and the field sites. Insecticide treated fields are shown with a red quare and the untreated with a green circle.

#### M. persicae in the suction trap.

Four alternative methods of extracting and amplifying DNA from aphids that had been preserved in trap fluid were assessed (see Figure 4). Method A was the most successful and was used thereafter. The methods will be

subjected to publication and are not described herein. The method was finalised in 2003 and it was applied retrospectively to the 2001 collected *M. persicae* alatae. This meant that the samples were at least two years old. Four microsatellite loci were used to characterise the trapped alatae (M35, M86, M63 and M49; Sloane et al 2001).

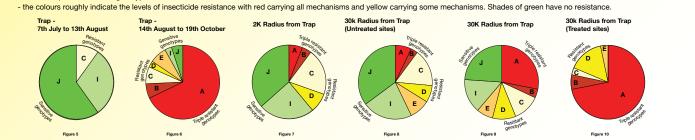


unit individual ML persidea specimene collecteri in the East Craigs suction pp in 1995 were extracted using one of four extraction methods (A, B, C or A microstellite marker (M80) was amplified using the PCR PCR products are separated using 10% polyacrylamide gel electrophrees in a scontinuous buffer system. Method A was found to be the most

# Results

Relative frequencies of each genotype

ided into those in the weeks ust (Figure 6). The 14<sup>n</sup> of Au



# Conclusions

- The clonal composition of treated (Figure 10) and insecticide untreated fields is different (Figure 7).
- Selection of resistant *M. persicae* occurs on treated seed potato fields and in 2001 'MACE' aphids, (resistant to dimethyl carbamates as well as all the other main classes of insecticide) were at the greatest advantage (Figure 10).
- Despite their presence on unsprayed crops in the early part of the season, MACE resistant *M. persicae* did not increase in numbers in untreated crops near the suction trap (Figure 7).
- In the early part of the season the suction trap was filled with the long-term successful clones, types I, J and C (Figure 5).
- Despite the continued success of clones I, J and C on untreated crops (Figures 7 & 8), the numbers of winged aphids originating from MACE genotypes (A and B) on treated potato increased and eventually dwarfed *M. persicae* from all other sources (Figures 2 & 10).
- These MACE aphids arrived in two large flights which almost certainly originated from the burning down of firstly seed, and then two weeks later, ware potatoes (Figure 2).
- The ability to analyse the genotypes in suction trap material and relate this to the field distribution of these genotypes will lead to a new understanding of the population dynamics and agroecology of *M. persicae* in Scotland.

#### References

Sloane MA, Sunnucks P, Wilson ACC, Hales DF (2001). Microsatellite isolation, linkage group identification and determination of recombination frequency in the peach potato aphid, *Myzus persicae* (Sulzer) Genetical *Research* (Camb.) 77: 251-260.

#### Acknowledgements

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