Molecular ecology of the peach-potato aphid and a relative

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The peach-potato aphid (*Myzus persicae*) is one of the most widespread and important virus vector aphids. In Scotland, its impact is particularly high in the seed potato industry as it spreads many destructive potato viruses such as potato leaf roll virus (PLRV). Like all aphids, it can reproduce asexually (without mating) during the summer months and this allows numbers to build up very quickly on plants. The process of asexual reproduction generates many genetically identical offspring (a clone) from a single female. Winged forms are also generated, usually as a result of overcrowding, and these move freely between fields carrying viruses. To stop this spread, farmers have to control the vector using intensive prophylactic spraying regimes, aided by monitoring of aphid numbers by agency advisers. Despite the obvious importance of aphid movement to agriculture, little is known about this part of their ecology. To understand what is happening, discriminating features either for individuals or populations are required. Previous studies, using methods such as allozyme electrophoresis, found very little variation between different peach-potato aphid clones. The only allozymes found to vary were the esterases which are known to be involved in insecticide resistance. This led to the suggestion that the genetic composition of this species consisted of a small number of genotypes or clones.

The population structure of these clones, and therefore the accuracy of this model, could not be determined without a more sensitive method for differentiating individual genotypes. To provide a means of doing this, SCRI has studied this aphid by directly analysing highly variable regions of its DNA. The method has already been applied to analyse biotypes of the large European raspberry aphid (*Amphorophora idaei*). The technique uses natural variation in the length of the IGS spacers found between the ribosomal genes. Within any individual eukaryote, there are many copies of these regions, and each can be a different length. Figure 1 shows examples of the types of patterns which can be obtained for different clones of the peach-potato aphid. In each lane, genomic DNA from an individual aphid clone isolated from the field, has been digested using a combination of restriction enzymes. When these fragments are separated and transferred to a nylon membrane, they can be detected using a short labelled probe. The combination of different sized fragments gives a unique profile (an IGS fingerprint) for each aphid clone. Those that share all bands are likely to be the same clone.

Using this technique, we have found, for the first time, that a closely related species, *Myzus*

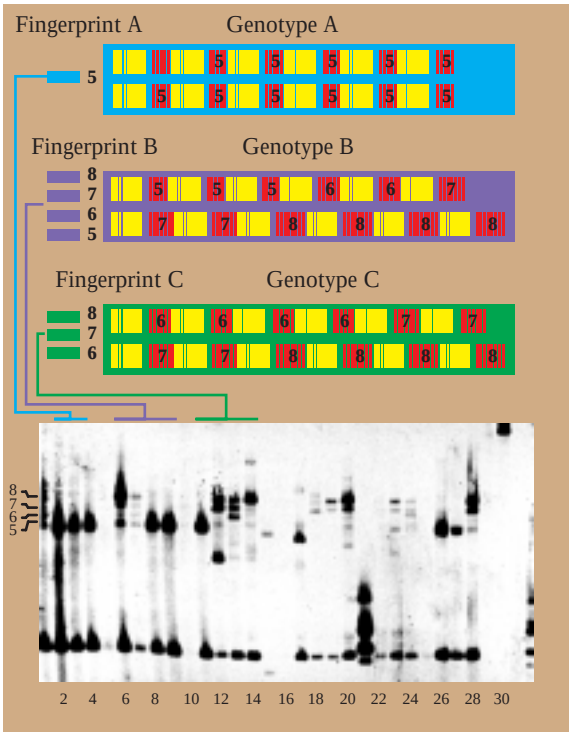

Figure 1 The main panel shows the results of IGS fingerprinting of *M. persicae* collected from a single field. Lanes 2, 3, 4, 8, 9, 11, 26 and 27 contain a pattern which was present in 30 percent of all samples. Unique genotypes are present in most other lanes except lanes 6 and 7 which contained a 4-banded pattern. A much larger band pattern was found in samples of *M. antirrhinii* (lanes 29 and 30). Above the main panel, a schematic diagram shows how these bands originate from different copies of rDNA. Three genotypes are represented by different colours and their patterns are shown on the left. Each gene can have a different number of repeats (shown in red with the numbers of repeats indicated) between the genes (shown in yellow).

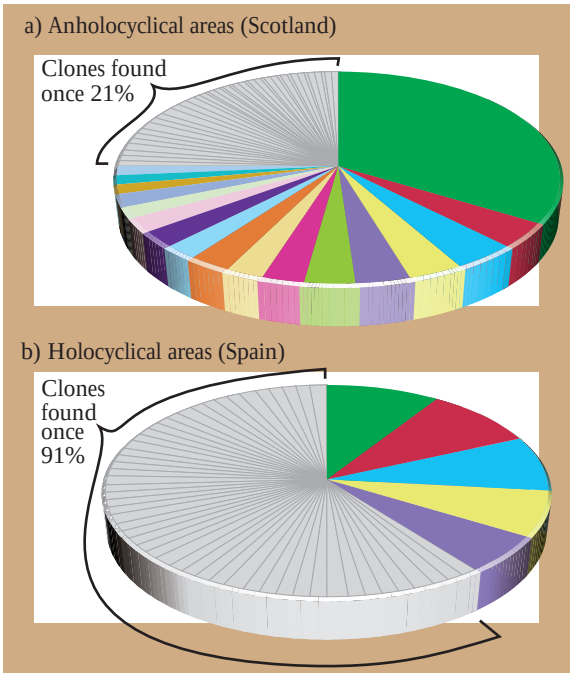

Figure 2 Pie charts illustrating the results of genetic analysis of *M. persicae* from two areas. The lower chart illustrates the distribution of genotypes found in areas of holocyclical reproduction (after Martinez-Tores *et al.* 1997[1]). The upper chart illustrates areas of anholocyclic reproduction (work at SCRI). Each pie segment represents a single genotype and its area represents the frequency with which it was collected. The smallest segment in each case represents a single genotype, found once. There were far more unique genotypes in Spain than in Scotland.

antirrhinii, was present in samples collected from crops in Scotland. This aphid is very similar in appearance to *Myzus persicae*. The only physical feature which can give a clue to its presence is that it is always dark green. However, there are *Myzus persicae* clones which are also dark green. But, using the IGS fingerprinting method, it is quite clear that *Myzus antirrhinii* has a distinct pattern (Fig. 1).

The work has also demonstrated that the peach-potato aphid consists of a large number of different genotypes. There are at least 80 among the 276 samples examined. Within these results, there are other interesting trends. The proportion of genotypes is not distributed evenly. A large number (30%) of samples appear to be exactly the same clone (Fig. 2). By comparing peach-potato aphid clones from elsewhere in Europe and the world, it was possible to see that this genotype appeared only in Scottish samples. Amongst the other genotypes, 29 were found more than once, but most (49/80) appear only once (Fig. 2). The clonal expansion of genotypes appeared to be greater in Scottish samples when compared to those from Spain. In Spanish samples, only five genotypes were sampled more than once and the greatest proportion of a single genotype was 8% (Fig. 2). These differences in distribution patterns are most likely to be due to the frequency of sexual reproduction (holocycly). The peach-potato aphid, as its name suggests, needs peach trees to complete its sexual life cycle. Peach trees are scarce in Scotland, compared to Spain, and tend to be restricted to sheltered environments such as glasshouses. Therefore, the aphid must survive winter by continued asexual propagation (anholocycly) on hardy secondary hosts or suitable hosts in glasshouses. The details of this part of the survival of the aphid are not fully understood, but an ability by the aphid to find

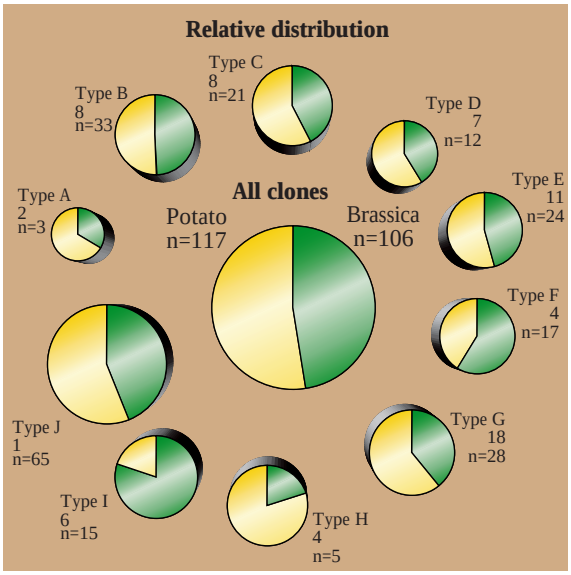

Figure 3 Fingerprints from aphids collected on potato or brassica were analysed and grouped into those that were most similar (groups A - J). The total numbers collected are shown in the central pie, with those from potato in yellow and those from brassica in green. Each group is also represented as a pie and is divided into those from the two crops. The size of each pie represents the total number of samples in that group (this is also given numerically beside each). The total number of genotypes in the groups is shown as the central number beside each pie. For example, Type J has only 1 genotype but this was found in 65 samples.

suitable plants and/or to withstand winter temperatures will be necessary. There are already field observations that demonstrate that some clones are better at over-wintering than others. The aphid type which we find in 30% of Scottish peach-potato aphid samples, has been found in December and February, when peach-potato aphid numbers are extremely low. While the numbers we could examine were small, these observations tend to suggest that this clone is particularly well adapted to over-wintering in Scotland. In the following seasons, this clone will predominate because it is already reproducing before any long distance migrants arrive.

The representation of different clonal groups on two crop plants was examined using the fingerprinting technique. Each group had representatives on both potato and brassica (Fig. 3), suggesting that there were no genotypes associated with a specific crop as has been found in some cereal aphids.

Future work will use the molecular markers, which we have developed, to try to determine exactly where different genotypes can be found over-wintering. This will allow a much clearer model of aphid numbers to be constructed and this, in turn, should enable more targeted use of insecticides and other control measures.

References.

[1] Martinez-Torres, D., Carrio, R., Latorre, A., Simon, J. C., Hermoso, A. & Moya, A. (1997). *Journal of Evolutionary Biology* 10: 459-477.