



Breeding insect-resistant brassica crops

The genus *Brassica* contains many important vegetables such as cabbage, broccoli, cauliflower, Brussels sprout and kale, which belong to the species *B. oleracea*, and Chinese cabbage, paksoi and turnip which belong to *B. rapa*. In Europe, brassicas are cultivated across approx. 430,000 ha, of which more than half is grown in the Eastern part. Brassica vegetables suffer from insect pests including cabbage root flies, thrips, aphids, caterpillars and whiteflies. The latter are particularly prevalent in Brussels sprout, savoy cabbage and kale crops. Insects can strongly reduce crop yield and quality (Figure 1). Severe infestations can make the crop unmarketable. Currently, insect pests are dealt with using insecticides. However, insecticides are not always effective and due to environmental concerns alternatives are urgently needed. A possible, environmentally friendly solution is the use of host plant resistance.

IDENTIFYING PLANT MATERIAL RESISTANT TO INSECTS

The first step in breeding insect resistant plants is the identification of plant material that contains resistance genes against the pest insect. Often such genes are present in landraces of the crop or in wild relatives of the crop species. Plant material to be evaluated (accessions) can be obtained from gene banks around the world. To evaluate the accessions, field or greenhouse tests have to be set up in which plants from each accession are infested with the pest insect (Figure 2). Within the PGR Secure project we have evaluated cabbage landraces and wild relatives for resistance against the cabbage whitefly and the cabbage aphid. In other projects we have carried out such evaluations for the cabbage root fly and thrips. For all pest insects, resistant accessions were identified which can be used as the starting point in the breeding process. These include amongst others, landraces and varieties of heading cabbage as well as some wild relatives, including *B. villosa*, *B. incana* and *B. fruticulosa*.

GENETIC ANALYSIS OF THE RESISTANCE

After resistant accessions are identified, the breeder must make crosses between the crop plant that is susceptible to the pest insect and the resistant accessions. Such crosses are not always easy, particularly when wild relatives are involved that are distantly related. When crosses have been successful the breeder needs to find out more about the genetics of the resistance: is it dominant or recessive, and how many chromosomal loci are involved in the resistance. For this, populations are used in which the resistance segregates. These populations are phenotyped for the resistance and genotyped



Figure 1: A kale plant suffering from the cabbage whitefly (A) and a white cabbage with thrips damage (B)



Figure 2: Field evaluation for the cabbage whitefly (A) and clip on cage (B) used to confine cabbage whiteflies to a test plant. In such a test the whiteflies have no choice – they have to feed from the plant on which they are placed.

with molecular markers. After all data are collected, correlations between markers and the resistance can be identified, resulting in the identification of loci involved in the resistance (Figure 3). Often researchers are also interested in finding out how the resistance works. In the past we have found that the presence of a wax-layer plays an important role in the resistance against thrips in cabbage. Within the PGR Secure project we use sophisticated tools like Electrical Penetration Graphs to find out where cabbage aphids encounter resistance factors in the leaf and we have used metabolomics and transcriptomics to identify metabolites and genes that may be involved in the resistance of cabbage plants.

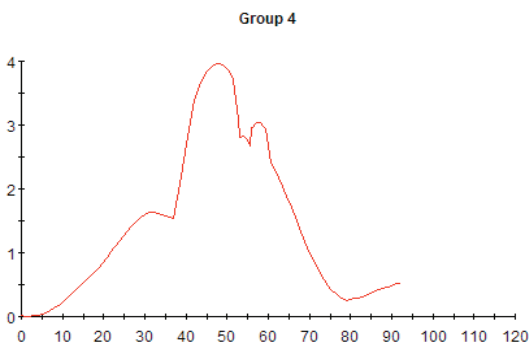


Figure 3: Mapping resistance to whitefly on the genome of white cabbage. The map shows one chromosome containing a region important for the resistance to the whitefly.

THE BREEDING PROCESS

After the identification of a resistance gene against a pest insect, the gene has to be introgressed into the cultivated brassica crop. This is a process that can take more than 10 years, depending on the (genetic) distance between the cultivated material and the donor of the resistance. When wild relatives are the donor there are many characteristics present that are not desired in the crop and have to be removed by repeated backcrossings. For this the molecular markers linked to the resistance gene can be used. Once the introgression of the resistance gene(s) is completed and all undesirable factors are removed, the breeding company can start to produce large amounts of seeds for farmers that want to grow the new variety (Figure 4).



Figure 4: Cabbage field

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