

Plus du tiers des Symphytes qui ont été réunis sont communs aux deux stations. En faisant appel aux plantes-hôtes et à leur écologie, on constate qu'il s'agit d'insectes dont les larves se nourrissent de plantes qui affectionnent les milieux ouverts humides.

La faune fréquentant le site du Dorperbroek est très marquée par les espèces vivant aux dépens des Salicacées et des Bétulacées ainsi que par d'autres Symphytes fréquentant des milieux plus mouilleux qu'au Busselziep.

La singularité de la faune du Busselziep est de compter des espèces liées à des milieux assez fortement marqués par les activités humaines.

L'étude des Symphytes aboutit ainsi aux mêmes conclusions que celles dégagées après l'examen des Syrphides et des Sphécides: l'intérêt biologique de la vallée du Bosbeek est le corollaire de la grande diversité des biotopes qui s'échelonnent d'amont en aval.

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Host plant range and genetic diversity in phytophagous insects: case studies in the Chrysomelidae*

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Phytophagous insects

Phytophagous or herbivorous insects depend on one or more host plants for survival and reproduction. As a consequence many of these insect species have special adaptations to optimize the relation with the plants they feed on. The life history characters of the host plant will be reflected in the adaptations of the phytophagous insect and ecological, behavioral and genetic characteristics of the insects will be influenced by the dependence on the host plant.

Within the phytophagous insects different levels of specialisation occur. Some species live on a wide variety of host plants (often from many different plant families), while others are specialised in a single plant species. In general a division is made in three levels of herbivory: monophagous species feeding on plant species belonging to a single genus, oligophagous species feeding on plants of a single family and polyphagous species feeding on plants from different plant families (BERNAYS & CHAPMAN, 1994, MENKEN, 1996).

One of the phytophagous insect groups in which the relationships between insect and host plants have received already a lot of attention are the leaf beetles or Chrysomelidae. With an estimated number of about 40.000 species described (and many still unknown) the leaf beetle family groups an enormous variety of species. Many of them have been studied because of their economical impact on agricultural crops, the most famous examples being the Colorado Potato Beetle (*Leptinotarsa decemlineata*), the corn rootworms (*Diabrotica* sp.) on mays crops and the cruciferous flea

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beetles (*Phyllotreta*) on oilseed and other cruciferous crops. Larvae and adults feed on the same host plants and apart from the feeding damage they also spread plant pathogenic viruses.

Niche width and genetic variation

In 1965 Leigh VAN VALEN formulated the hypothesis that animals that have wider niches are phenetically more variable. This hypothesis, called the "niche width variation hypothesis" was first based on morphological evidence, but later on was extrapolated to genetic variation (LAVIE & NEVO, 1981). Thus species occupying a wider niche are expected to be genetically more variable than species with a more restricted niche.

This hypothesis has, since its original definition, been tested several times and in most cases been confirmed. Unfortunately many of the performed studies used vaguely defined niches (based on geographic range or habitat temperature variation) or used species belonging to different genera or even to different families of animals for their comparison of genetic variability.

Phytophagous insects as a model to test the niche width variation hypothesis

Phytophagous insects offer good opportunities for testing the niche width variation hypothesis. The niche of a herbivorous insect is mainly determined by its host plant range, as it depends on these plants for development and reproduction. To test the value of the hypothesis in phytophagous insects we analysed genetic data of five genera of Chrysomelid beetles (*Phyllotreta*, *Galerucella*, *Ophraella*, *Oreina* and *Gonioctena*), comparing allozyme detected genetic variability with host plant range (monophagous [narrow niche] versus oligophagous [broad niche] species).

The results of our analyses show that for the genera *Galerucella*, *Ophraella* and *Oreina* no significant differences in genetic variation were found between mono- and oligophagous species. In the genus *Gonioctena* genetic variability is lower in monophagous species and in *Phyllotreta* the monophagous species show higher genetic variability than the oligophagous species. Thus, out of the five Chrysomelid genera studied only *Gonioctena* supports the hypothesis. The results for the genus *Phyllotreta* even oppose to the predictions of the niche width variation hypothesis.

Conclusion

As a conclusion we can say that the niche width variation hypothesis, which has been proven to be supported in a lot of animal taxa should not be generalized towards phytophagous organisms. Even within one family of phytophagous beetles we find contrasting relations between genetic variability and niche width. An explanation for the detected genetic differences may be found in a "host plant timing" hypothesis, stating that spe-

cies that feed on host plants which are very unpredictable in timing, abundance and distribution are subjected to changing selections for differently adapted genotypes and show an increase in genetic variability (this effect might overrule [or mask] the niche width effect), whereas species feeding on predictable host plants are not influenced by this and follow the niche width variation hypothesis.

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