Bio-systematics of predatory mites used for control of the coconut mite
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General discussion

In biological pest control it is not only important to identify and characterize the pest species, but also the natural enemies that are found in association with the target pest species (Moraes et al. 1987; McMurtry 2010). However, the traits of the natural enemies may vary with the genetic entities considered. Such entities may be represented by genotypes, bio- or eco-type, geographic populations, cryptic species or species. In this thesis, I focused on geographically isolated populations and studied the extent to which these populations are reproductively incompatible, because this has consequences for mass rearing and for introducing a strain from one geographic area into the area of another strain. For one thing mixing different geographic strains in mass culture may have negative effects on population growth rates if the strains are reproductively incompatible (Stouthamer et al. 2000; Mochiah et al. 2002). For another, reproductive incompatibility ensures reproductive isolation, thereby possibly maintaining the genetic integrity of the geographic strain even after it has been released in the geographic area of another strain. Having established the reproductive isolation between geographic populations of the natural enemies (Chapters 2, 3 and 4), I reviewed and assembled data to demonstrate the extent to which these geographic populations exhibit genetic variation in traits relevant to biological pest control. Moreover, by reconstructing the invasion routes of the natural enemies I tried to determine their geographic area of origin, which most likely is the area where they exhibit the greatest genetic diversity. In this way it is possible to plan releases of natural enemies in other areas where their genetic variation is limited.

So, what can be learnt from the results presented in this thesis with respect to geographic populations of mainly two species of predatory mites (Acar: Phytoseiidae) that are found in close association with coconut mites under the bracts of coconuts? I have presented evidence for reproductive isolation between geographic populations of the predatory mite Neoseiulus paspalivorus and N. baraki and showed that this was due to the presence of endosymbionts in one of the two predator species (N. paspalivorus) (Chapters 2 and 3). Moreover, I showed that the other predator species, N. baraki, is actually a species complex with two cryptic species, one from Benin and the other occurring in Tanzania, Brazil and Sri Lanka (Chapter 4). I also argued that a third predator species, N. neobaraki, also belongs to this complex (Chapter 6). Phylogenetic analysis of all Neoseiulus species together (plus an outgroup) suggests that the centre of genetic diversity of Neoseiulus species is in Africa, but there were no differences in genetic diversity among populations of N. paspalivorus from different countries (Chapter 6). This led to the hypothesis that N. baraki moved from weeds to coconut palms in Africa and that one cryptic species from Africa invaded the other continents, whereas N. pas-
palivorus from South-America followed the same invasion route as proposed for its prey, the coconut mites (Navia et al. 2005). If this hypothesis holds, then it makes sense to introduce geographic strains of *N. banakii* from Africa into other continents, but there is as yet no reason to do that with strains of *N. paepalivorus*. Now the question arises which traits are relevant to biological control and whether geographic populations differ in these traits. While this still requires an in-depth analysis, it is good to identify some general trends that may serve as a hypothesis. First, I assumed that two traits are of particular importance: the population growth rate on a diet of coconut mites and the ability to utilize pollen for survival. Then, I observed a trend in that high values of the first trait are associated with lower abilities concerning the second trait (and vice versa). Thus, it seems that there is no master of all trades (good in population growth and in pollen utilization) and that there is a trade-off between two traits that I assumed to be crucial for biological control. Unfortunately, there is no hard theory stating which combination of the two traits is best to achieve (short- or long-term) biological control of coconut mites. In absence of such a theory there is a need to perform experimental tests with strains exhibiting contrasting combinations of the two traits.

Apart from testing which combination of the two traits is best for biological control there are several other issues that need scrutiny before accepting the hypotheses proposed in this Thesis. First, I would recommend doing research that establishes the metabolic and/or genetic reasons for a trade-off between population growth on a diet of coconut mites and the ability to utilize coconut pollen for survival and development. Since the presence of endosymbionts may come at a cost to reproduction (Stouthamer et al. 1999; Bordenstein and Werren 2000), one may wonder how an individual predatory mite can profit from an infection by endosymbionts, unless the endosymbiont confers an advantage, e.g. in digestion of proteins from coconut pollen. Second, I would favour carrying out a more extensive sampling program to test our hypotheses on the centres of genetic diversity (and consequently the invasion routes). Third, I have assumed that the reproductive isolation I have assessed indeed leads to reproductive isolation in the field. If a geographic strain from one area would be released in the area of another, can I assume that reproductive isolation is retained? Clearly, this is a question that needs further research because there is evidence that mating preferences depend on the environment (e.g. diet) (e.g. Kokko et al. 2002) and it is still a major question whether the impact of endosymbionts is under control of the endosymbionts, their host or both.

References


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