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Genetic variability of the invasive *Erigeron annuus* in Europe

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Objectives

One of the major environmental impacts of human activities has been the introduction of non-native species into new areas. A few of these species became serious pests, e. g. *Hypericum perforatum* in California (Holloway 1964; Huffaker 1964), *Opuntia* spp. in Australia (Holloway 1964), *Conyza canadensis* in Europe (Palmblad 1968), and considerable resources are often required to control them (Harper 1977).

Much research has been devoted to the question why some plant species are successful neophytes (Crawley 1987; Di Castri *et al.* 1990; Groves & di Castri 1991). However, it is clear that there is no single reason for the success of invasive species, since many factors, both ecological and genetic, may be important. The majority of the studies published so far have focused on ecological and life history characteristics of the invasive species, whereas rather little attention has been paid to the genetic changes that may facilitate adaptation to local conditions. Therefore the main question asked in this project is: What is the role of genetic variability and micro-evolutionary processes in the success of an invasive plant species?

Erigeron annuus s.l. (Asteraceae) has been chosen as a model system for the following reasons:

(1) It is a native of North America, but also an abundant neophyte in Europe, where it occupies a wide range of habitats and replaces to some extent native species.
(2) Although its reproduction is apomictic, outcrossing between different morphotypes may occur occasionally.
(3) We hypothesize that occasional outcrossing events have played a major part in local adaptation of this species and hence for its success as a neophyte.

Therefore the main question asked in our project is: What is the role of genetic variability and micro-evolutionary processes in the success of an invasive plant species?

The specific objectives of our project are as following:

(1) To compare patterns of genetic and morphological variation within and between native and neophyte populations in North America and Europe, respectively.
(2) To investigate experimentally whether outbreeding or hybridization occurs to understand the origin of local genetic variation.

Proposed methods

Several techniques are available for detecting genetic variation within and between natural populations (Berry *et al.* 1991). These include for example allozymes, restriction fragment length polymorphisms (RFLP), random amplified polymorphic DNA (RAPD) and microsatellites. Each method is suitable for a particular level of an evolutionary analysis, varying from closely related individuals to anciently diverged species.

Many studies on intraspecific genetic variation in plants have concentrated on the chloroplast genome (cpDNA). However, while several authors have successfully used cpDNA for the analysis of interspecific variation and phylogenetic questions, it is unlikely that there will be sufficient variation at the intraspecific level in the family of Asteraceae (Bayer 1993).

Mitochondrial DNA, on the other hand, has been used extensively for population analysis in animals. Unfortunately, the mitochondrial genome of plants consists of multiple subgenomic molecules, and is subject to complex rearrangements, which has been shown with RFLP analysis e.g. for *Betula.* Therefore, mtDNA is not suitable for the study of intraspecific variation. Consequently, we have chosen RAPDs analysis for our project.

RAPD analysis, combined with the polymerase chain reaction (PCR), has recently become popular in studies of intraspecific genetic variation (Williams *et al.* 1990; Adams & Demeke 1993; Marsolais *et al.* 1993; Bachmann 1994) and seems to be the most appropriate method for studies on *E. annuus.* This technique has the advantage of producing considerable results within a short time span, and is sensitive enough to detect intraspecific variation. Furthermore, it is relatively cheap and efficient, and allows the analysis of a large number of samples with limited laboratory equipment.

Analysis of isozyme variability and on phenotypic plasticity has already been applied successfully in *Erigeron annuus* (e.g. Stratton 1988). Therefore, in addition to the RAPD analysis, isozymes are used to detect fixed heterozygosity, which can be expected for obligate apomicts, and other allelic frequency data.

Preliminary results

Preliminary isozyme analysis of eight loci from 179 individuals of European origin revealed about 35 different genotypes. First results of RAPD analyses showed that about 60 different RAPD types could be distinguished with 16 markers for 698 individuals from 104 sampling sites in Europe. Clearly, there are some common types which are widely distributed and show no geographic correlation, whereas other types are found rarely and locally.

These preliminary results demonstrate a significant level of variation, even more than was reported by Stratton (1988) for populations of *Erigeron annuus* in North America. He found phenotypic differences in four enzymes and was able to distinguish during three subsequent years a genotypes-to-sample-size-ratio of 0.18, 0.088 and 0.077, respectively, whereas we found a ratio of 0.19.

The widely distributed genotypes are likely to be constant over several generations and therefore can be assumed to be apomictic, whereas rare and locally distributed genotypes can be either a result of too small sampling resolution or indicate recently developed genotypes, most probably due to outcrossing events. The dichotomy of local and widely distributed genotypes is promising for further studies in the reasons for the distribution of a specific genotype. Therefore, the next step of our research is to explain the origin and the adaptive value of these differences in genetic variation.

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