

QUANTITATIVE AND MOLECULAR VARIATION IN GEOGRAPHICALLY CENTRAL AND MARGINAL POPULATIONS OF *ULMUS LAEVIS*, THE EUROPEAN WHITE ELM

RACHEL WHITELEY, SANNA BLACK-SAMUELSSON, GÖSTA ERIKSSON

Swedish University of Agricultural Sciences

Box 7027, SE 750 07 Uppsala, Sweden

U. laevis, the European White Elm, is widespread and fairly continuously distributed throughout eastern Europe and western Russia, often forming a component

of riparian forests. In western Europe it has a very fragmented distribution. The species is listed as vulnerable on the Swedish red list. It is tolerant of very wet

conditions and is often found on sites which experience periodic flooding. It is an out-crosser, but the relative importance of wind and insect pollination to the species is not known. It is thought to be at least partly wind-dispersed and pollinated, but water may also play a role in dispersal. The importance of vegetative propagation in the species is also uncertain.

Potential threats to *U. laevis* populations include Dutch Elm Disease which appears to be a particular problem in the eastern part of the range; deforestation clearance and drainage of flood-plains for agricultural or industrial activities; and risks associated with habitat fragmentation increased vulnerability to catastrophic events and demographic fluctuations, and inbreeding depression in the long term.

Our project aims to obtain an overview of the genetic structure of *Ulmus laevis* in Europe with respect to variation in adaptive traits and at molecular marker loci. Additionally, we plan to conduct an investigation

of gene-flow and mating patterns within one or more of our study populations. We intend that our results should be used to inform decisions about the gene conservation of *U. laevis*.

Seeds will be collected from study populations in Sweden (the Baltic island of Öland), southern France (Garrone valley), eastern Germany (Elbe and Mulde valleys) and western Russia (Moscow area). Families of around 20 progeny from 20 mother trees per population will be grown in a fully randomised common garden experiment at SLU in Uppsala.

Quantitative traits to be measured include growth rate and rhythm over three growth periods. The molecular markers chosen as being most suitable for this project are microsatellites, as they can be used both to obtain population-level measures of genetic identity and, in a gene-flow study, to illuminate relationships between individuals. These markers are currently being developed.