

# Assessing the genetic local adaptation within the wild population of a narrow endemic tree species: the case of *Cedrus brevifolia* Henry.

## DATE & TIME

📅 Wednesday, December 10th, 2014

🕒 17:45 - 19:15

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## SPEAKERS



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## DESCRIPTION

A basic argument in the study of adaptation of trees is that natural selection in different environments generates genetic clines that correlate with the environment's clines. Thus, temporal changes in gene frequency resulting from climate change mirror spatial changes. This study aims to address these general arguments in a narrowly distributed endemic species. Thus, it investigates the gene variation in *Cedrus brevifolia*, as a result of adaptation within its natural population. This adaptation is expected to reflect the demographic and ecological forces on the species throughout its survival in different environmental conditions. *Cedrus brevifolia* is an endemic conifer tree of Cyprus flora, with narrow distribution in a fragmented population (~398 ha). It is listed in the Red Data Book of the Flora of Cyprus as vulnerable, while its habitat type (9590\*) is characterised as priority habitat according to the Habitats Directive (92/46/EC). Recent studies have shown that the species is characterised by high genetic variation and significant genetic differentiation between five relic patches. Here, needles from 320 trees were collected from 16 sampling plots (20 trees / plot), covering the natural and ecological boundaries of the species' distribution. Successful DNA extraction led to the testing of 20 candidate adaptive genes, where six of them showed polymorphisms (total of 44 SNPs). Analysis of gene diversity patterns based on these six genes revealed a mean nucleotide diversity of  $\theta_w = 2.842 \times 10^{-3}$  and an average pairwise difference between sequences of  $\pi = 2.052 \times 10^{-3}$ . However, neutrality test showed evidence of positive selection in only one out of six candidate genes.

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