**Poster Abstract – A.34**

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# ANALYSIS OF SPATIAL GENETIC STRUCTURE IN AN EXPANDING *PINUS HALEPENSIS* POPULATION REVEALS DEVELOPMENT OF FINE-SCALE GENETIC CLUSTERING OVER TIME

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*spatial genetic structure, spatial autocorrelation, Pinus halepensis, population expansion, microsatellites*

We analyzed the change of spatial genetic structure (SGS) of reproductive individuals over time in an expanding *Pinus halepensis* population. To our knowledge, this is the first empirical study to analyze the temporal component of SGS by following the dynamics of successive cohorts of the same population over time, rather than analyzing different age cohorts at a single time. SGS is influenced by various factors including restricted gene dispersal, microenvironmental selection, mating patterns and the spatial pattern of reproductive individuals. Several factors that affect SGS are expected to vary over time and as adult density increases. Using air photo analysis, tree-ring dating and molecular marker analysis we reconstructed the spread of reproductive individuals over 30 years beginning from five initial individuals. In the early stages, genotypes were distributed randomly in space. Over time and with increasing density, fine-scale (<20m) SGS developed and the magnitude of genetic clustering increased. The SGS was strongly affected by the initial spatial distribution and genetic variation of the founding individuals. The development of SGS may be explained by fine-scale environmental heterogeneity and possibly microenvironmental selection. Inbreeding and variation in reproductive success may have enhanced SGS magnitude over time.