

## Abstract Forest Genetic Monitoring in a Biodiversity Hotspot<sup>+</sup>

Filippos A. Aravanopoulos <sup>1,2,\*</sup>, Nikolaos Tourvas <sup>1</sup>, Ermioni Malliarou <sup>1</sup>, Fani G. Lyrou <sup>1</sup>, Vasiliki-Maria Kotina <sup>1</sup> and Anna-Maria Farsakoglou <sup>1</sup>

- <sup>1</sup> Laboratory of Forest Genetics, Faculty of Agriculture, Forestry and Natural Environment, Aristotle University of Thessaloniki, 54124 Thessaloniki, Greece
- <sup>2</sup> Hellenic Agricultural Academy, 11855 Athens, Greece
- \* Correspondence: aravanop@for.auth.gr
- + Presented at the 3rd International Electronic Conference on Forests—Exploring New Discoveries and New Directions in Forests, 15–31 October 2022; Available online: https://iecf2022.sciforum.net/.

**Abstract:** The genetic monitoring of forest trees is of the utmost importance for securing the maintenance of species' adaptive potential. Genetic monitoring, the quantification of temporal changes in a population's genetic variation and structure, introduces prognosis and assists in defining tools for the management of genetic resources. Forest genetic monitoring (FGM) is imperative in biodiversity hotspots such as Greece, one of the most species-rich European countries, where >7000 native plant taxa (~20% endemics) exist and 28% of its land base is included in the Natura 2000 Special Areas of Conservation network. Moreover, (meta-)analyses of genetic data have shown that Greek forests' tree populations present significantly higher values of polymorphism and differentiation compared to the average values reported in the international literature. FGM studies in Greece involve the following species: *Abies borissi regis, Castanea sativa, Fagus sylvatica, Quercus petraea, Q. robur, Pinus nigra*, and *Prunus avium*. FGM uses a genealogical approach and employs 11–26 Simple Sequence Repeat (SSR) loci in different cohorts (mature and juvenile trees), while the average time internal between assessments is 12.9 years. The results so far for *A. borissi regis* and *F. sylvatica* indicate a maintenance of genetic diversity over time, but with a slight drop of Ne in the juvenile cohort of hybrid firs compared to the mature trees.

Keywords: conservation genetics; genetic monitoring; forest trees; Greece

**Supplementary Materials:** The following are available online at https://www.mdpi.com/article/10 .3390/IECF2022-13127/s1.

**Author Contributions:** Conceptualization, F.A.A.; Methodology, F.A.A., E.M., N.T., A.-M.F.; Software, F.A.A., E.M., N.T.; Writing-original draft preparation, F.A.A.; Writing-review and editing, F.G.L., V.-M.K., N.T., A.-M.F.; Supervision, F.A.A. All authors have read and agreed to the published version of the manuscript.

**Funding:** The research was partially supported by project Crown Genome, funded by the General Secretariat for Research and Innovation, Greece and the Aristotle University of Thessaloniki. It has also been supported by the European Union's LIFE financial mechanism (LIFEGENMON project, LIFE13 ENV/SI/00148).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

**Data Availability Statement:** Raw data will become available at the Dryad Digital Repository upon completion of this study.

Conflicts of Interest: The authors declare no conflict of interest.



Citation: Aravanopoulos, F.A.; Tourvas, N.; Malliarou, E.; Lyrou, F.G.; Kotina, V.-M.; Farsakoglou, A.-M. Forest Genetic Monitoring in a Biodiversity Hotspot. *Environ. Sci. Proc.* 2022, 22, 33. https://doi.org/ 10.3390/IECF2022-13127

Academic Editor: Rodolfo Picchio

Published: 31 October 2022

**Publisher's Note:** MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



**Copyright:** © 2022 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/).