Genetic diversity of Heterobasidion, the causal agent of conifer root and butt rot

Nicola Luchi1, Donatella Paffetti2, Paolo Capretti2

1 Institute for Sustainable Plant Protection, via Madonna del Piano, 10, I-50019 Sesto Fiorentino (Florence) Italy (nicola.luchi@ispam.unc.it), 2 Department of Agrofood Production and Environmental Sciences, University of Florence (DISPAE), Piazza delle Caccine 28, I-50144, Florence, Italy (donatella.paffetti@unifi.it; paolo.capretti@unifi.it)

Key words: Abies, fungal pathogen, pine, population studies

Background
Heterobasidion annosum s.l. is a root and butt rot fungus that causes losses in timber production. This pathogen is relatively common and can be found in saprophytic habitat on stumps and wood logs in the forest (Woodward et al., 1998). In Italy, within the complex H. annosum s.l., three European species (H. annosum s.s., H. abietinum and H. parvum) have been described (Capretti et al., 1998). Furthermore also the invasive H. irregulare, introduced from North America, was found along the Tyrrhenian coast (D’Amico et al., 2007; Gonthier et al., 2014).

By using molecular markers the diversity of H. annosum s.l. populations have been studied in Italy (Petta et al., 2001; D’Amico et al., 2007; Zamponi et al., 2007). Genetic divergences in H. annosum and H. abietinum populations were found (Zamponi et al., 2007; Luchi et al., 2011). These variations within each fungal population, could be mainly related to the host population but also to the morphology of Italian peninsula that reduced the gene migration among fungal strains.

Objective of this work is to study the population structure and spatialization of genetic diversity in H. abietinum and H. annosum populations in Italy by using minisatellites.

Methods
Fungal isolates collected along the Italian peninsula from different hosts, have been used to study the genetic diversity of H. annosum s.s. and H. abietinum, respectively collected from Pinus spp. and Abies alba in Italy. Mycelium from fungal isolates was grown in vitro and DNA was extracted according to Vainio et al. (1998). PCR amplification using M13 was carried out according to Luchi et al. (2011). The electrophoretic amplified profiles transformed in presence/absence vectors were used for following analyses.

General estimates of genetic diversity in the populations of H. annosum and H. abietinum isolates were calculated using SPCe3DI 1.3a. The spatial genetic structure of the populations was analyzed by Geneland software.

Results and Conclusions
The population of H. annosum isolates shows the higher levels of gene diversity (Nei 1972) than the H. abietinum population (D = 0.37 and D = 0.25, respectively). The morphology of Italian Peninsula may have influenced the rate of spread of Heterobasidion populations (from pine and silver fir). The evolution of Heterobasidion species have probably similar spreading history as tree host species, reflecting genetic variation of fungal populations (Johannesson and Sterlid 2003). However the genetic differences between H. annosum and H. abietinum populations reflect different history of plant host.
In case of *Heterobasidion* subpopulations from Silver fir, like its main host, were never completely isolated showing a diffuse spread from scattered nuclei, such as the glacial refuges. In fact, the considered population of *H. abietinum* isolates appears divided into 4 clusters, but they do not are isolated as demonstrated by the maps of posterior probabilities and by the pairwise genetic distances (Dy, Nei 1972) between the clusters. The other hand, *Heterobasidion* from pine, host isolation reflects establishment of isolated fungal clusters.

Studies on *Heterobasidion* population of can be used useful to understand possible differences in pathogenicity, that may also reduce the biodiversity of conifer stands along Italian peninsula

**Competing interests**
The author declares that they have no competing interests.

**References**


