

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

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Background

Heterobasidion annosum s.l. is a root and butt rot fungus that cause losses in timber production. This pathogen is relatively common and can be found in saprophytic habit 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. parviporum*) 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 use 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 SPAGeDI 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 ($D_i = 0.37$ and $D_i = 0.26$, 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 Sterild 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 (D_p , 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 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.

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