

Additive and non-additive genetic parameters for multipurpose traits in a clonally replicated incomplete factorial test of *Castanea* spp.

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Abstract Second-year traits of growth, stem form, terminal flushing, and survival were assessed in 1770 ramets from 295 clones of 16 full-sib families of *Castanea* spp. Additive, dominance, and epistatic genetic variances were estimated in a clonally replicated incomplete 5 × 4 factorial test. Parents of the mating design were selected mainly on their phenotypes for wood quality (*Castanea sativa* traditional varieties) and their proven resistance to *Phytophthora* spp. (Asiatic species and *Castanea crenata* × *C. sativa* hybrids). Additive genetic variances were estimated to be 1.7–9 times greater than the dominance components. Inferred epistatic variance components showed a significant role in controlling growth traits and branch length. Narrow- and broad-sense heritability estimates showed that terminal flushing date was the most heritable trait, followed by height. The high estimates of half-sib, full-sib, and clonal mean heritabilities for almost all traits suggest that different strategies of backwards and forwards selection could be proposed. The ranking of the breeding values of parents allow us to select the best parents for new crosses and extend the mating design. Favorable genetic correlations were found between growth traits and straightness, so multi-trait selection looks promising. Our results provide the first information on the partitioning of genetic variance in *Castanea* spp. and a starting point for devising new selection strategies.

Keywords *Castanea* spp. · Additive variance · Non-additive variance · Clonal testing · “C” effects

Introduction

Most studies related to long-term tree-improvement programs are based on recurrent selection for general combining ability, in which basically only additive genetic variance is captured by selection on the basis of open-pollinated progenies. However, the non-additive (dominance and epistatic) portion of genetic variation may be an important component of genetic variance (Stonecypher and McCullough 1986; Paul et al. 1997; Wu and Matheson 2005) and should be considered in the design of efficient deployment strategies for tree breeding programs (Burdon and Shelbourne 1974; Foster and Shaw 1987; Isik et al. 2004). Propagation by vegetative methods allows capture the total genetic variation, and maximum genetic gains in both long and short terms can be expected from clonal selection. Moreover, heterosis for vegetative growth is characteristic of interspecific hybrids in many plant genera, and it could be explained by dominance and pseudo-overdominance effects (Falconer 1989; Williams and Savolainen 1996). Clonal propagation has also been used to capture hybrid vigor in some other forest species of the genus *Eucalyptus* (Potts and Dungey 2004), *Populus* (Yu et al. 2001), and *Pinus* (Cappa et al. 2013).

Trials established with full-sib offspring of selected parents and with clonally replicated progeny allow for further partitioning of genetic variance into additive, dominance, and epistatic components. The largest studies employing this design feature have been carried out in conifers to improve rooting ability and growth traits, mainly in loblolly pine (*Pinus taeda* L.). In this species, additive genetic variance was the most important component of the total genetic

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