

Mapping of Loci for Seed Set Incompatibility in the Interspecific Hybrid Between *Pinus elliottii* and *Pinus caribaea* var. *hondurensis*

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Abstract

High density genetic mapping of the Pinus elliottii x Pinus caribaea F₁ hybrid has revealed a number of anomalies suggesting the occurrence of specific gene combinations which may be lethal to seed development. Evidence for hypothesizing the occurrence of lethal genes is discussed and the approach being taken to locate these genes on a genetic map of the hybrid is presented.

Introduction

The F₁ hybrid of *Pinus elliottii* and *Pinus caribaea* is currently the most extensively planted forest plantation species in sub-tropical Queensland. Seed of superior hybrid families produced through controlled mass pollination of mono-clonal seed orchards provides planting stock as seedlings, which are supplemented with rooted cuttings of these families from hedges.

Production of hybrid seed however is inhibited by interspecific incompatibility which significantly reduces seed set relative to that in either of the pure species parents. Many superior families are excluded from testing and the operational F₁ planting programme due to unacceptably low seed set.

Observations Supporting the Hypothesis for a Genetic Basis to Seed Set Incompatibility

High density genetic mapping of a particular F₁ hybrid individual using RAPD markers has revealed a number of anomalies supporting the hypothesis of specific genetic incompatibilities between these two species. These are;

- i) Markers polymorphic between two parents, inherited by and therefore heterozygous in the F₁ individual of their progeny studied, but homozygous in the haploid megagametophytes (female gametes) of the F₁.
- ii) A large proportion (27%) of the total 366 markers identified showing segregation distortion outside the statistically acceptable Mendelian ratio.
- iii) The identification of 18 linkage groups of significantly varying size (16 to 425cM) in a genome comprised of 12 chromosomes of similar physical length.

These observations suggest the possibility of selection against specific gene combinations in the hybrid, accounting for those markers polymorphic between the parents but homozygous in female gametes of the F₁ generation. Markers linked to such lethal gene sites could thus be expected to show segregation distortion (observation ii). Regions of discontinuity in the linkage map can be anticipated to be a consequence of distorted markers, since these cannot be mapped by conventional linkage analysis, thus accounting for the third observation above.

Identification of Loci for Seed Set Incompatibility

On the assumption that reduced seed set and viability in the F_1 and F_2 hybrids of *P. elliotii* \times *P. caribaea* is a consequence of specific genetic incompatibilities between the two species, it has been hypothesized that markers showing segregation distortion in the female gametes of the F_1 generation should show normal Mendelian segregation in the pure species. This hypothesis is currently under investigation. If found to be true, then it should be possible to map and thus join the fragments of linkage groups to provide a complete picture of each of the twelve chromosomes of the *P. elliotii* \times *P. caribaea* hybrid.

Identification and mapping of lethal gene sites is currently of interest in terms of understanding genome organization and the basis of genetic incompatibilities. It may have potential future application in screening individual trees of each species to assess their potential for producing an acceptable level of seed set in hybrid combination.

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