

MOLECULAR ESTIMATES OF SIMILARITY IN *EUCALYPTUS GLOBULUS*

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The base populations used in most forest tree genetic improvement programs usually lack detailed pedigree information. Molecular markers, such as microsatellites (SSR), can be used to estimate individuals' pairwise relatedness, which is based on the probabilities' ratios of the identity in state between the individuals compared and the reference unrelated population. These estimates can be very useful to infer the level of relationship among sub-populations of elite material and/or for the design of controlled crosses between putatively unrelated parents.

Using 113 putatively unrelated individuals - genotyped with 18 SSR - self, full-sib, half-sib and unrelated were simulated, and four pairwise similarity coefficients were tested: Queller & Goodnight 1989; Li *et al.* 1993; Ritland 1996, and Lynch & Ritland 1999. The Lynch & Ritland (1999) coefficient was selected (Figure 1), for it displayed a better adjustment with the expected level of relatedness and narrower standard errors (SE). SE were calculated through Monte-Carlo techniques, to avoid unequal sample size bias, by using 10^5 simulations for each relatedness group.

To illustrate the usefulness of molecular estimates of similarity in genetic improvement programs, a clustering (UPGMA) based on the pairwise Lynch & Ritland (1999) coefficient (LR) values was performed to infer about the putative relationship among individuals of the subgroups of *E. globulus* elite individuals. From that analysis at least two pairs might be related and a PCA analysis confirmed the clustering results.

REFERENCES

- Li, C.C., Weeks, D.E. and Chakravarti, A. (1993) *Hum Hered* 43: 45-52.
Lynch, M. and Ritland, K. (1999) *Genetics* 152: 1753-1766.
Queller, D.C. and Goodnight, K.F. (1989) *Evolution* 43: 258-275.
Ritland, K. (1996) *Genet Res* 67: 175-185.

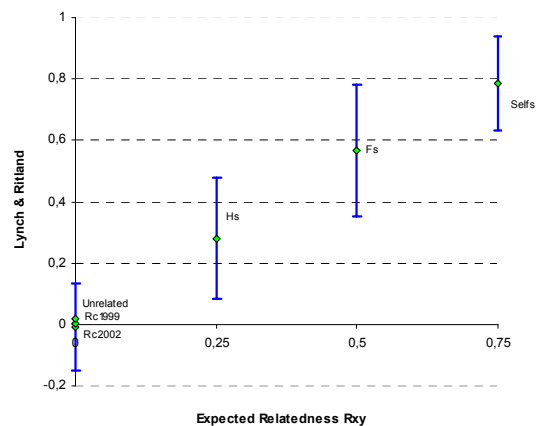


Figure 1. Mean values (diamonds) and confidence interval (95%) based on the LR coefficient for the groups: Sells, full-sibs (FS), half-sibs (HS), unrelated. The two *E. globulus* elite individuals subgroups were plot as Rc1999 and Rc2002