

Molecular estimates of similarity in *Eucalyptus globulus*

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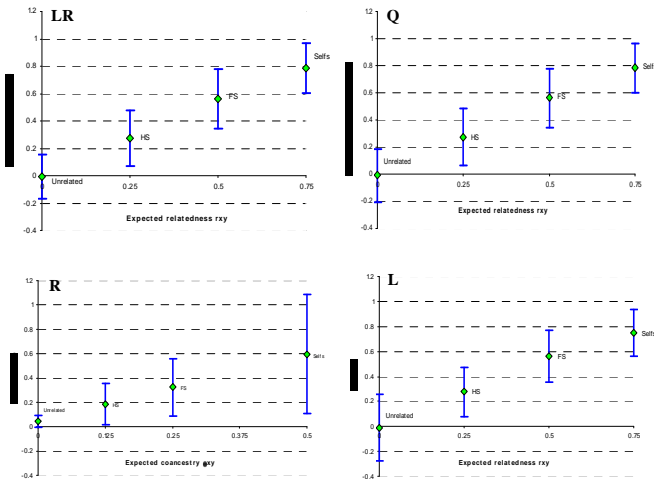
PURPOSE OF THE STUDY

Questions

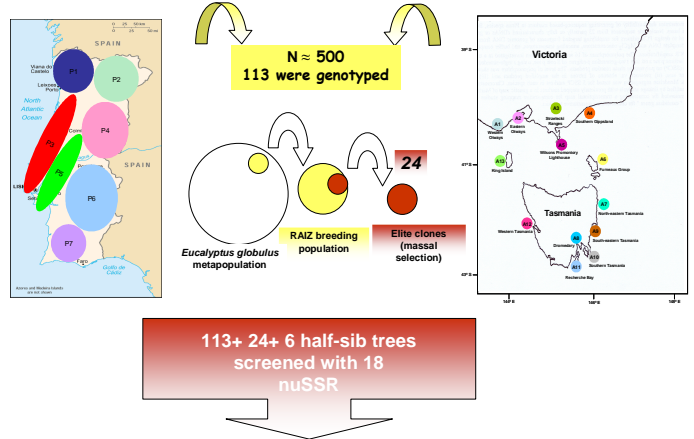
Which relatedness/coancestry estimator is more precise (smaller confidence intervals) ?

How are the relatedness/coancestry estimators of selfs, full-sibs, half-sibs and unrelated individuals uncorrelated with the expected coancestry ?

RESULTS



MATERIAL AND METHODS



Relatedness estimators: Queller and Goodnight (1989) (Q); Li et al. (1993) (L); Lynch and Ritland (1999) (LR)
 Coancestry estimator: Ritland (1996) (R)

Case study

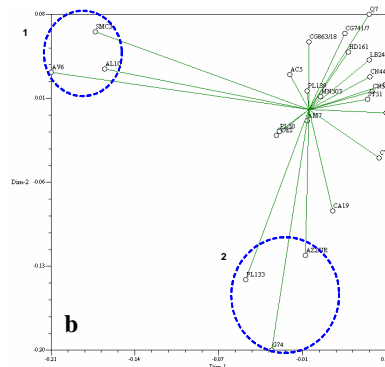
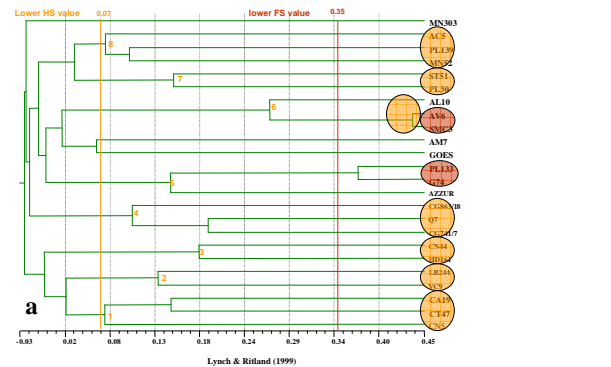
Which index of genetic relatedness seem more useful to avoid related elite material ?

Can the Cluster Analysis together with the Principal Component Analysis (PCA) help in selecting the less related elite clones ?

Fig. 1. Observed values and multilocus 5% confidence intervals (CI) in the different relatedness groups (selfs, half-sibs, full-sibs, and selfs) based on the Lynch and Ritland (1999) (LR), the Queller and Goodnight (1989) (Q), the Ritland (1996) (R), and the Li et al. (1993) (L); relatedness/coancestry estimators. The CI were built by using the ZETA software, with Monte-Carlo simulations (see companion poster, Optimizing the choice of microsatellites for fingerprinting *Eucalyptus*, for details)

CONCLUSIONS

- All the estimators are unbiased (exp. and obs. values are not \neq). The LR, Q and L estimators showed similar CI range, but the LR is more accurate in the case of the unrelated individuals, compared to the other estimators (Fig.1).
- Eight groups have values superior the the lowest HS value based on the LR estimator (Fig. 2a). Two groups of putatively related individuals (blue dashed circles) were identified (Fig 2b). Nevertheless, there is a constrain in the relatedness estimators' precision, due to the recombination process during gamete formation (Fig 2c).
- The study can be improved by adding more SSR, very polymorphic and with even alleles frequencies; a new relatedness estimator model should also be constructed, in order to increase precision



	1	2	3	4	5
1					
2	0.21				
3	0.26	0.15			
4	0.13	0.30	0.27		
5	0.14	0.22	0.18	0.24	
6	0.22	0.18	0.23	0.41	0.04
Mean	0.21				

Fig. 2. UPGMA (a) and PCA (b) based on the 24 elite clones pairwise matrix using the LR estimator, and the pairwise LR matrix using 6 real half-sibs individuals (c). Due to recombination during gametes formation, the pairwise values of half-sibs individuals might have disparate values such as 0.41 or 0.04, but the mean remains close to the expected half-sibs value (0.25).

References : Li CC et al (1993) Similarity of DNA fingerprints due to chance and relatedness. Human Heredity 43:45-52; Lynch & Ritland (1999) Estimation of pairwise relatedness with molecular markers. Genetics 152:1753-1766; Queller & Goodnight (1989) Estimating relatedness using genetic markers. Evolution 43:258-275; Ritland (1996) Estimators for pairwise relatedness and individual inbreeding coefficients. Genetical Research 67:175-185.