

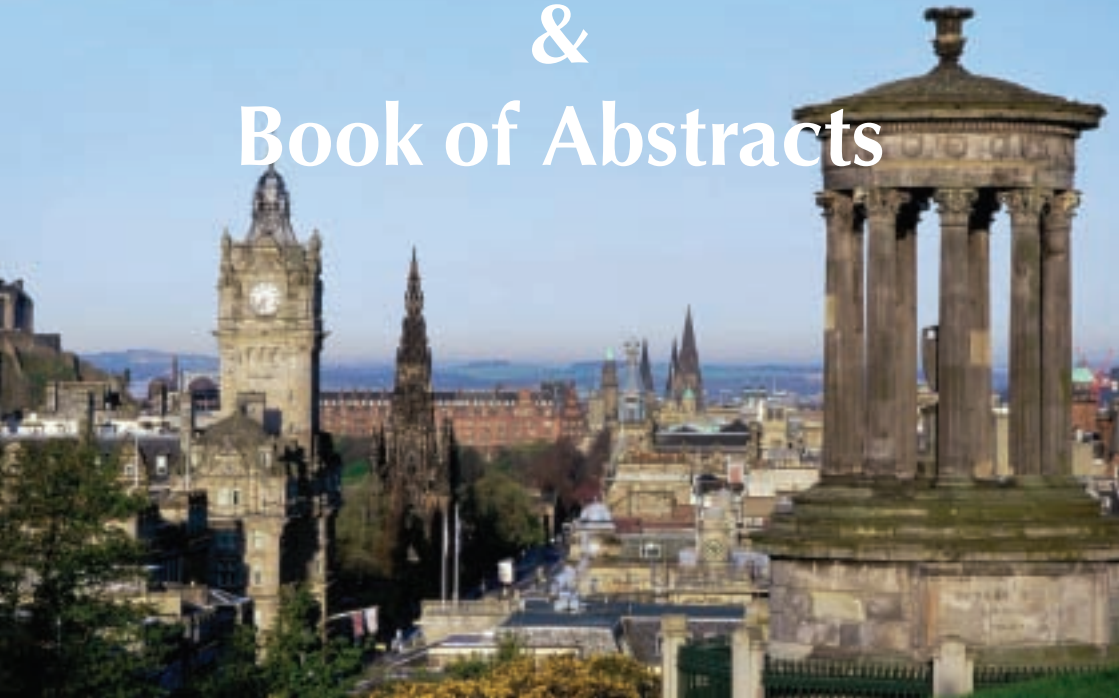


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their allelic effects. Preliminary results showed that the following loci from the flowering time pathway had an effect on seed production in both years in plants grown in Oulu: *CONSTANS*, *PHYB*, *FT*, *VRN1* and *VRN2*.

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PEDIGREE RECONSTRUCTION FOR COSEXUAL SPECIES USING SIMULATED ANNEALING: CASE STUDY OF OIL PALM (*ELAEIS GUINEENSIS*)

*David Cros*¹, *Jesus Fernandez*², *Jean-Marc Bouvet*¹, *Leopoldo Sanchez*³

¹CIRAD, Montpellier, France, ²INIA, Madrid, Spain, ³INRA, Orléans, France

The approach of Fernandez and Toro (2006) to reconstruct pedigrees from molecular data of contemporaneous individuals using a *simulated annealing* algorithm was extended to hermaphroditic and monoecious species. New features also include the possibility of selfings, accounting for a predefined coancestry matrix between founders and specifying different number of individuals per generation. The new method was validated using 16 individuals from the last generation of the Yangambi breeding population of oil palm. Their pedigree was known for 5 generations and they were genotyped with 166 SSR. In the study, the number of used SSR varied from 6 to 166 and the percentage of unknown parentages from 20% to 100%. The Pearson correlation between the pedigree-based coancestries calculated on the true and on the reconstructed genealogies ranged from 0.74 to 0.99. The RMSE ranged from 0.02 to 0.12. When pedigree was assumed completely unknown, reliable reconstruction required at least 38 SSR. Using 100 SSR or more, the Pearson correlation was very high (0.98) and the RMSE very low (0.06). The new method was also applied to 104 individuals from the last generation of a key breeding population (Deli) originated from 4 oil palms. The individuals were genotyped with 160 SSR. Records of their pedigree only existed for the recent past. Results of pedigree reconstruction detected a family coming from old selfings looking as outliers, with pedigree-based coancestries much higher than molecular coancestries, indicating old selfings were erroneous. After correcting the recorded pedigree, pedigree-based coancestries calculated on the reconstructed genealogy and molecular coancestries were highly correlated (> 0.9) when using 80 markers or more. In conclusion, this method gave likely pedigrees with satisfactory reliability for cosexual species, using a realistic number of polymorphic markers. Also, it seems very helpful to correct historical pedigrees. The methodology has been implemented in the software *MOL_COANC_v2*.

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SCREENING PRIMATE GENOMES FOR ENDOGENOUS RETROVIRUSES.

Katherine Brown, *Richard Emes*, *Ed Louis*, *Rachael Tarlinton*

University of Nottingham, Nottingham, UK

Endogenous retroviruses (ERVs) are retroviruses which have integrated into the DNA of the germline cells of a host and are transmitted horizontally from generation to generation. Once a retrovirus has become endogenous, it behaves like any other genetic element, so it is subject to selection, mutation and genetic drift and can spread through the host population to fixation, or be eliminated from the population entirely. By analysing the ERV content of a genome it is possible to gain insight into the evolutionary history of both the virus and its hosts. Several large-scale genome screening projects have been carried out on mammalian genomes to identify ERVs and the human and chimpanzee genomes have been comprehensively screened. However, although all primate genomes have basic RepeatMasker annotation there is limited information about their retroviral content.

This project is based on use of the Exonerate algorithm (Slater and Birney, 2005) to screen the 10 available primate genomes for regions resembling retroviral genes. An input database has been created with comprehensive coverage of known retroviral diversity and these sequences are used as queries to locate