Pedigrees are ill-suited to measuring inbreeding in bottlenecked species

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Summary of findings

Valid estimates of individual inbreeding coefficients (F_P) from molecular pedigrees for extremely bottlenecked populations are only feasible when genotypes are available for all (or nearly all) individuals in the pedigree.

Incomplete sampling of such populations results in underestimation of F_P by as much as 23% (Fig 1).

Near 0% bias can be achieved with a complete genetic sample or higher numbers of founders (Fig 1 A-C and F), but the precision of these estimates will still be low unless at least 40 molecular markers are used (Fig 2).

Using more than 40 markers has little effect on either bias or precision of estimates.

Background

Pedigrees have been recommended as the most reliable method for calculating individual inbreeding coefficients (F_P). However, it is difficult to reconstruct valid pedigrees for wild populations.

Pedigrees based on behavioural observations for such populations are often incomplete or absent and it is challenging to build genetic pedigrees for bottlenecked species with low genetic diversity.

We tested the feasibility of constructing genotype-based pedigrees for valid F_P calculations for the little spotted kiwi (*Apteryx owenii*), a species with no behavioural pedigree, a history of severe bottlenecks and very low contemporary genetic variation (average 2.6 alleles per polymorphic microsatellite locus).

Results

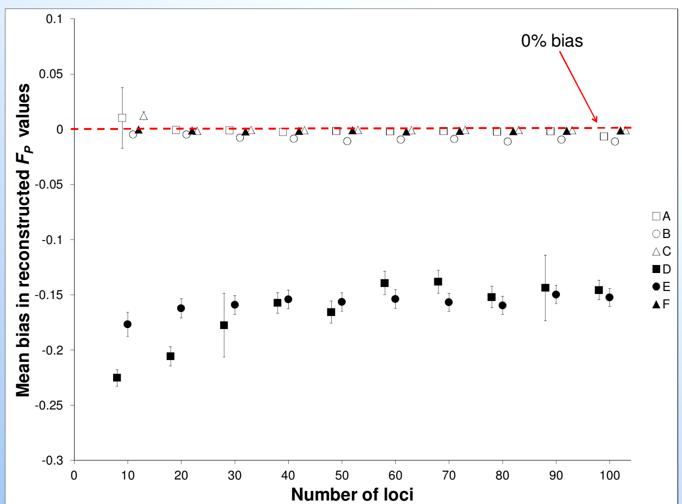


Fig 1: Bias of F_P values (= reconstructed F_P-true F_P) calculated from reconstructed pedigrees under modelling scenarios A-F. Error bars = 95% confidence intervals. X-axis values offset for clarity.

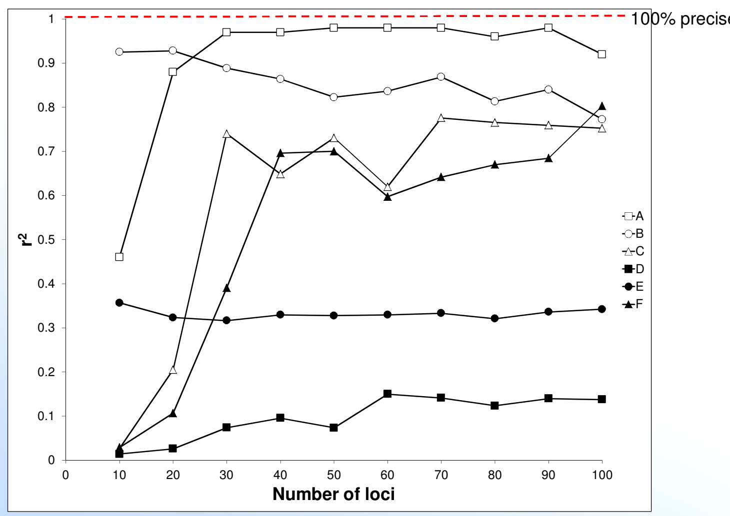


Fig 2: Precision of F_P values (= r^2 of regressions of reconstructed F_P vs true F_P) from reconstructed pedigrees under modelling scenarios A-F.

Methods

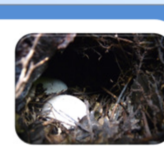
Population simulations - We simulated *A.owenii* populations under six scenarios (Table 1) for 10 to 100 microsatellite loci.

Founder numbers, genotypes and numbers of alleles per locus were based on the extant populations of Long Island and Zealandia Sanctuary except for scenarios B and E where founder genotypes were simulated to maximise genetic variation (Table 1).

Pedigree reconstruction – Pedigrees for simulated populations were reconstructed in COLONY (Jones and Wang 2009) under two alternative sampling regimes (Table 1).

Validity assessment – Bias and precision of F_P values from reconstructed pedigrees were assessed by comparison to F_P values from the corresponding true population pedigree.

Fig 3: Extant *A.owenii* populations



A.owenii eggs

An *A.owenii* chick

Model	Population modelled (number of founders)	Sampling regime	Mean alleles per locus in founders	Average F_P in final population (95% CIs)
A	Long Island (2)	All birds that ever lived sampled (=complete sample)	2.2	0.22 (0.005)
B			4	0.22 (0.005)
C	Karori Sanctuary (34)		2.5	0.0032 (0.001)
D	Long Island (2)	Only living birds sampled	2.2	0.22 (0.007)
E			4	0.22 (0.007)
F	Karori Sanctuary (34)		2.5	0.0032 (0.001)

Table 1: The six modelling scenarios used to simulate populations and the resultant average true F_P.

References

Jones, O. and Wang, J. (2009) COLONY: a program for parentage and sibship inference from multilocus genotype data. *Molecular Ecology Resources* **10**: 551–555

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