

[10.1071/MF22234](https://doi.org/10.1071/MF22234)

Marine and Freshwater Research

Supplementary Material

First evidence of multiple paternity and hybridisation in Australian sawsharks

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Table S1. Means (s.d.) of relatedness estimates for the two sawshark species with the seven estimators available in COANCESTRY.

Species	Relationship	Estimator						
		DyadML	LynchLi	LynchRd	QuellerGt	Ritland	TrioML	Wang
<i>Pristiophorus cirratus</i>	Unrelated	0.01337 (0.01706)	0.00116 (0.03969)	-0.00015 (0.02508)	0.00092 (0.03519)	-0.00019 (0.02510)	0.01330 (0.01695)	0.00084 (0.03935)
	Parent–Offspring	0.51369 (0.01443)	0.49544 (0.02024)	0.49376 (0.03020)	0.49542 (0.02335)	0.49369 (0.04577)	0.51295 (0.01340)	0.49548 (0.02106)
	Full-Sibs	0.51906 (0.02508)	0.49240 (0.02819)	0.49280 (0.02936)	0.49213 (0.02734)	0.49341 (0.04290)	0.51723 (0.02513)	0.49244 (0.02800)
	Half-Sibs	0.26680 (0.02726)	0.24699 (0.03170)	0.24887 (0.03082)	0.24705 (0.03164)	0.25026 (0.03560)	0.26628 (0.02722)	0.24695 (0.03156)
	Correlation coefficient	0.99463	0.98888	0.99014	0.98961	0.98303	0.9947	0.98893
<i>Pristiophorus nudipinnis</i>	Unrelated	0.02206 (0.02908)	-0.00360 (0.07528)	-0.00139 (0.04122)	-0.00252 (0.06325)	-0.00135 (0.04086)	0.02137 (0.02822)	-0.00352 (0.07443)
	Parent–Offspring	0.51475 (0.02391)	0.49003 (0.03812)	0.48886 (0.04668)	0.48934 (0.04120)	0.48938 (0.07034)	0.51254 (0.02113)	0.48999 (0.03927)
	Full-Sibs	0.51724 (0.04855)	0.49259 (0.05081)	0.49143 (0.05303)	0.49405 (0.05066)	0.49240 (0.07414)	0.511006 (0.04848)	0.49240 (0.05070)
	Half-Sibs	0.26529 (0.05127)	0.24979 (0.05710)	0.24485 (0.05399)	0.24959 (0.05406)	0.24586 (0.06260)	0.26324 (0.05120)	0.24871 (0.05736)
	Correlation coefficient	0.98151	0.96349	0.97235	0.96817	0.95518	0.9818	0.96356

Estimates are based on 300 simulated dyads for each relationship category. Correlation coefficients calculated by COANCESTRY for each estimator are also presented. All values have been rounded to five decimal places.

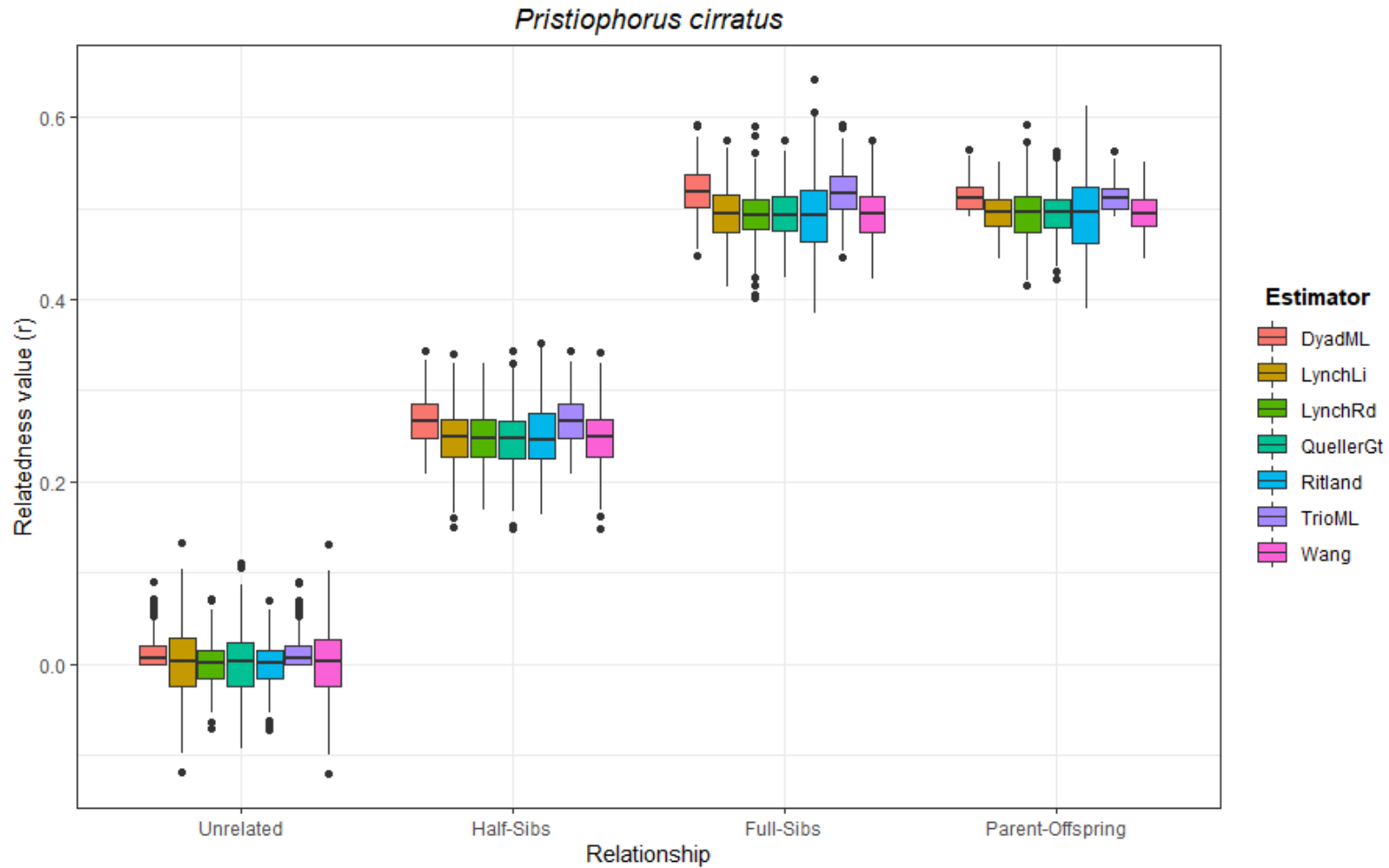


Fig S1. Box plots of relatedness estimates calculated for several relationship categories (unrelated, half-siblings, full-siblings and parent-offspring) for the common sawshark (*Pristiophorus cirratus*). Estimates are based on 300 simulated dyads for each relationship category. Boxes represent the 25–75 percentiles, whiskers represent the 5–95 percentiles, and dots represent outliers.

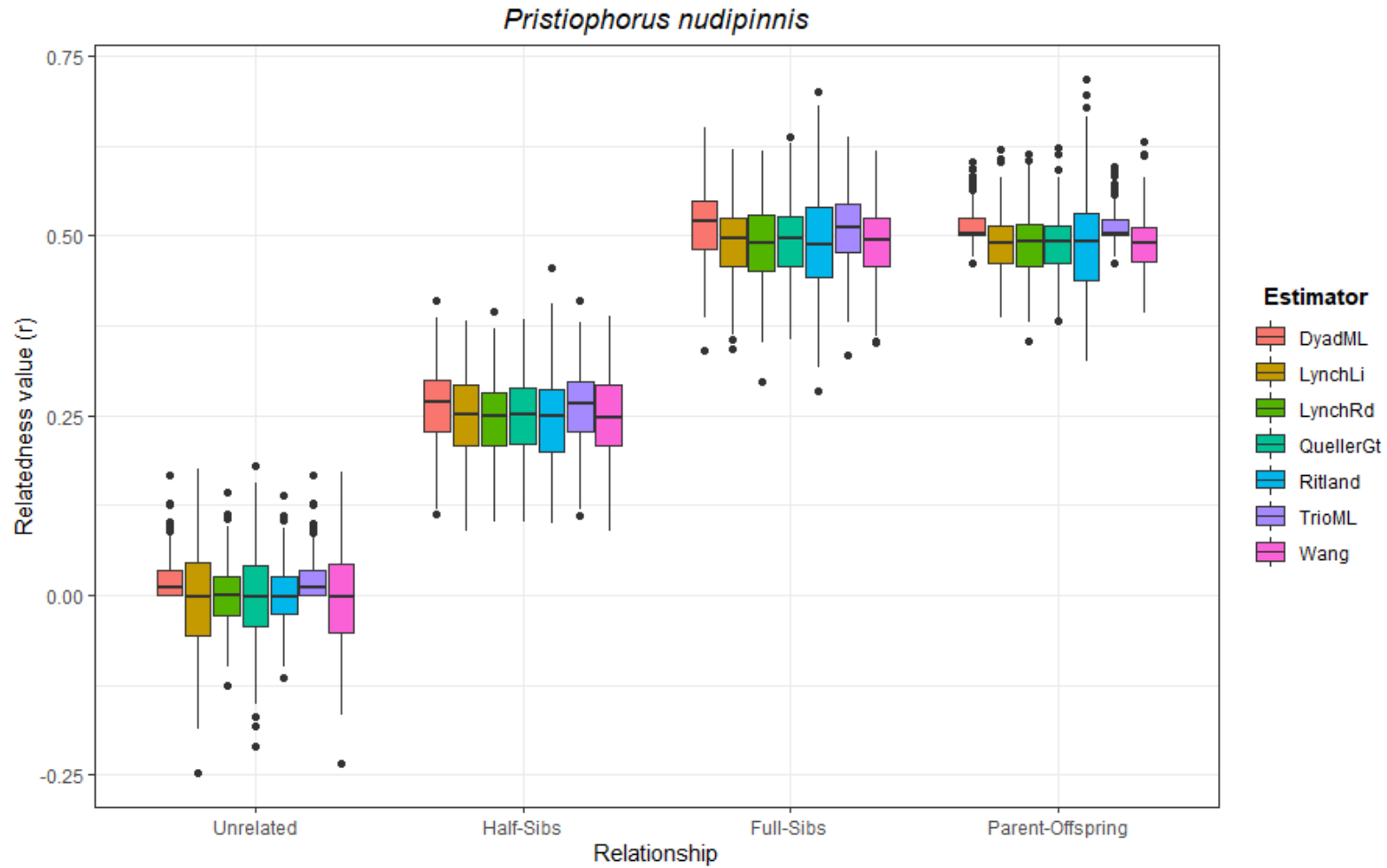


Fig S2. Box plots of relatedness estimates calculated for several relationship categories (unrelated, half-siblings, full-siblings and parent-offspring) for the southern sawshark (*Pristiophorus nudipinnis*). Estimates are based on 300 simulated dyads for each relationship category. Boxes represent the 25–75 percentiles, whiskers represent the 5–95 percentiles, and dots represent outliers.

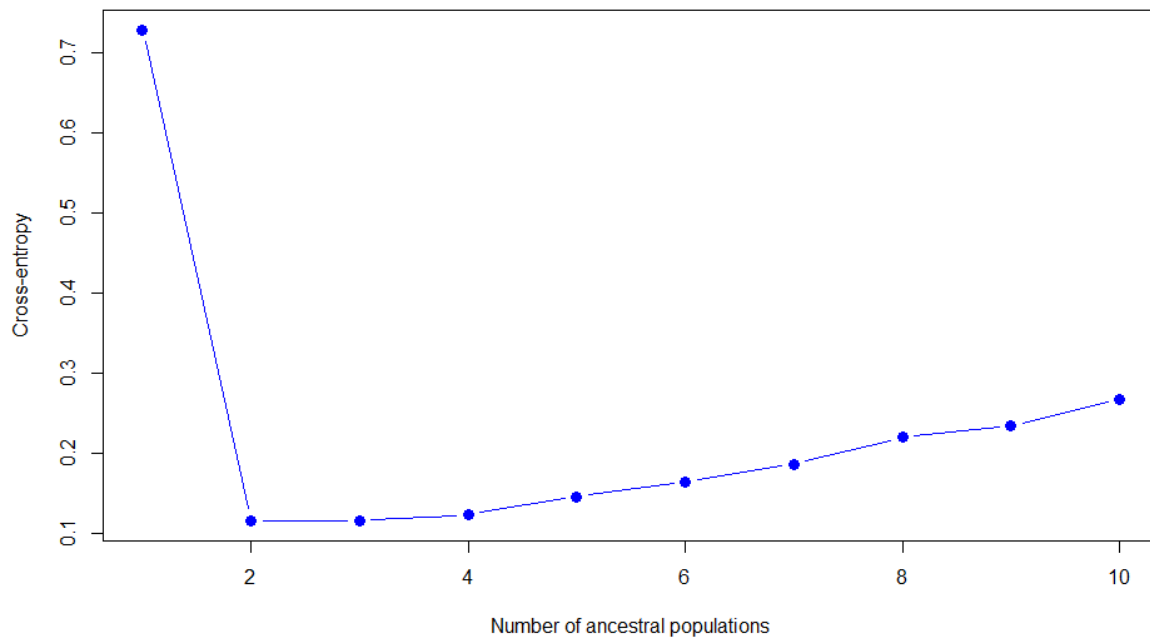


Fig S3. Plot of the calculated cross-entropy criterion for 1–10 ancestral populations.