

Supplementary Material

Hybridisation rates, population structure, and dispersal of sambar deer (*Cervus unicolor*) and rusa deer (*Cervus timorensis*) in south-eastern Australia

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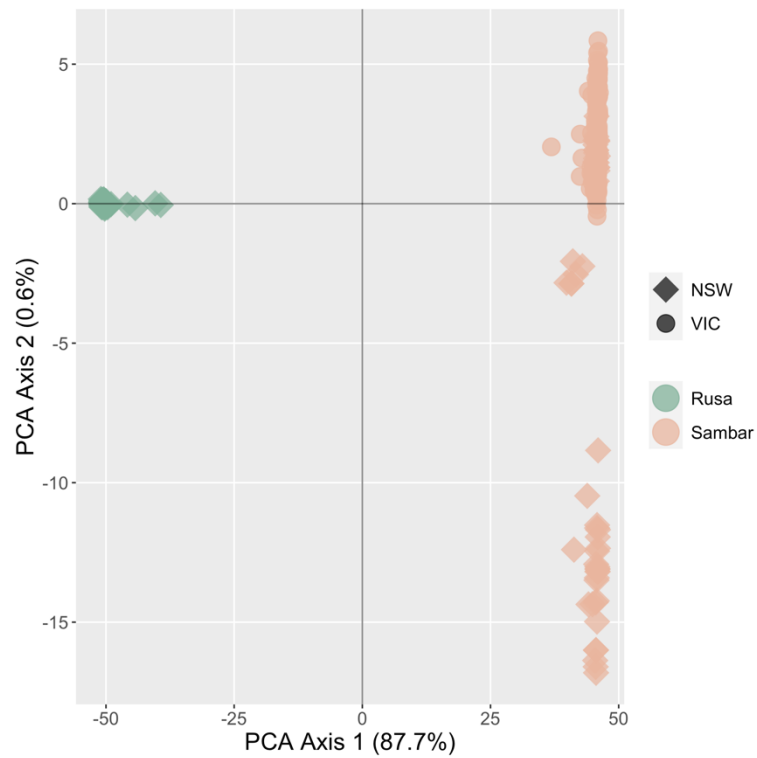
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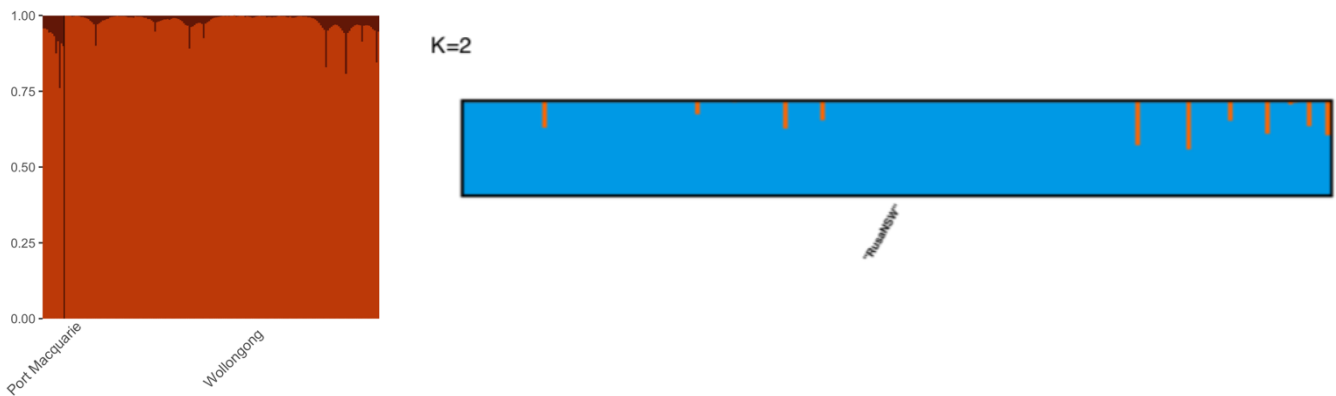
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Supplementary material Fig. S1 Principal component analysis plot showing collapsed groups identified through fixed difference analysis, following the removal of suspected hybrid samples. A total of 2798 loci were fixed between these two groups

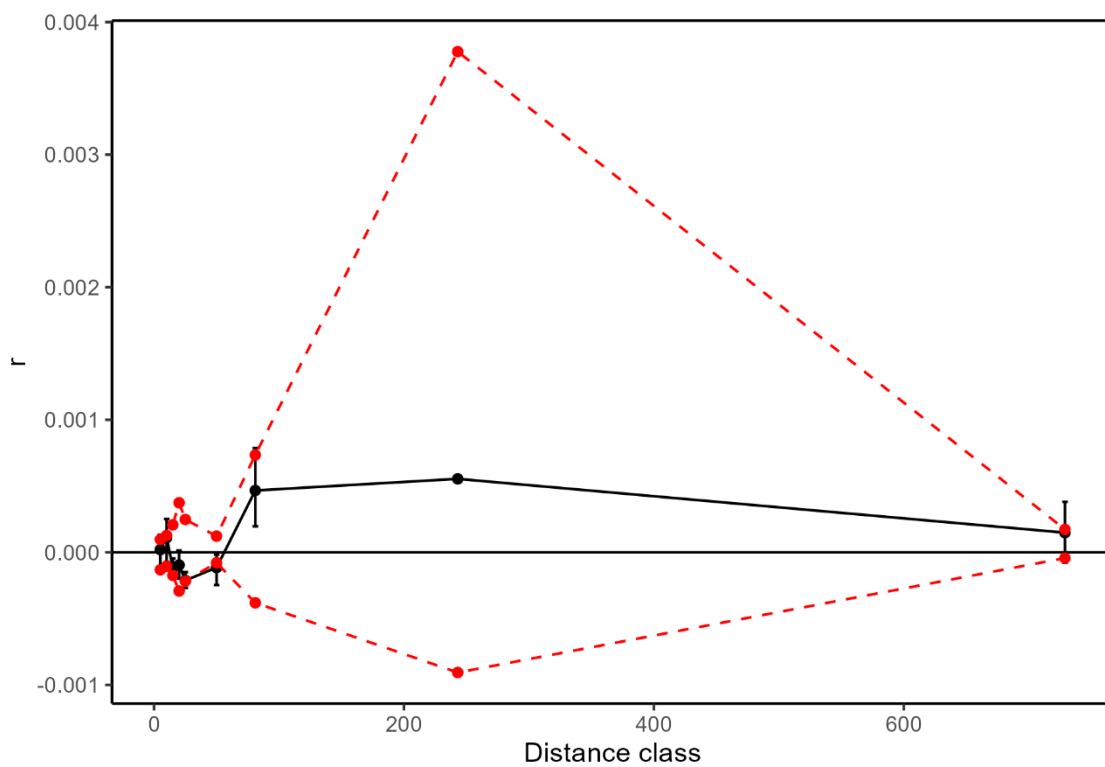


Supplementary material Fig. S2 *Tess3* output (left) and *fastStructure* output (right) for the Rusa NSW samples at $K = 2$

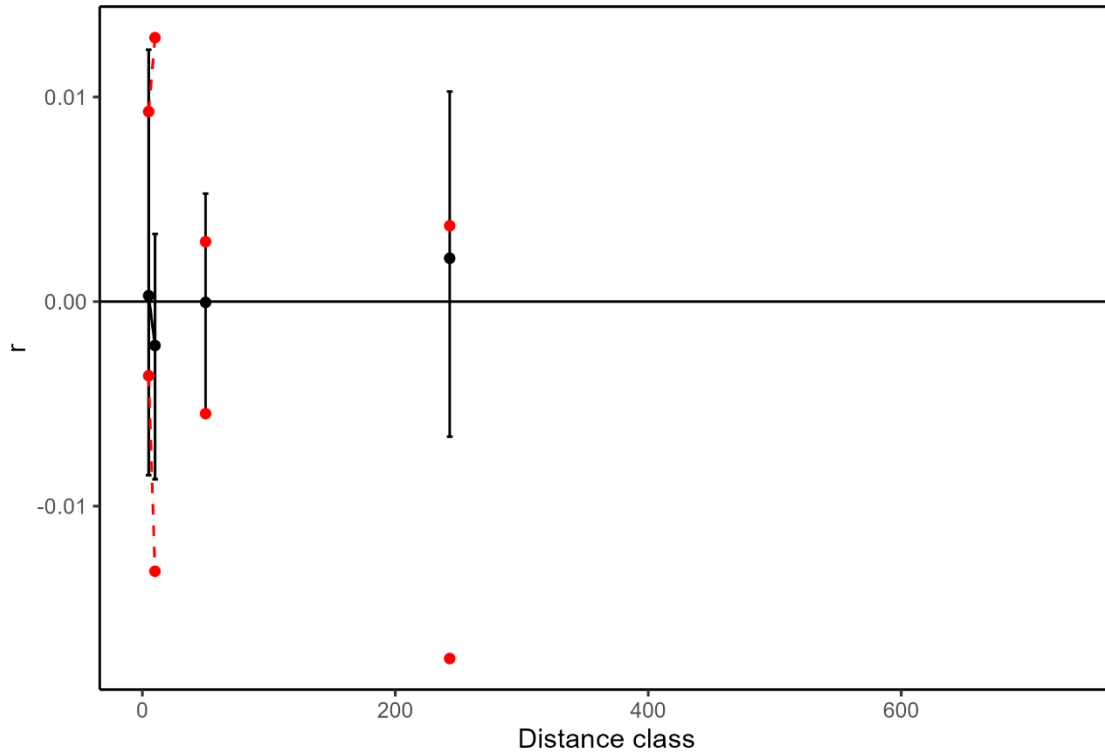
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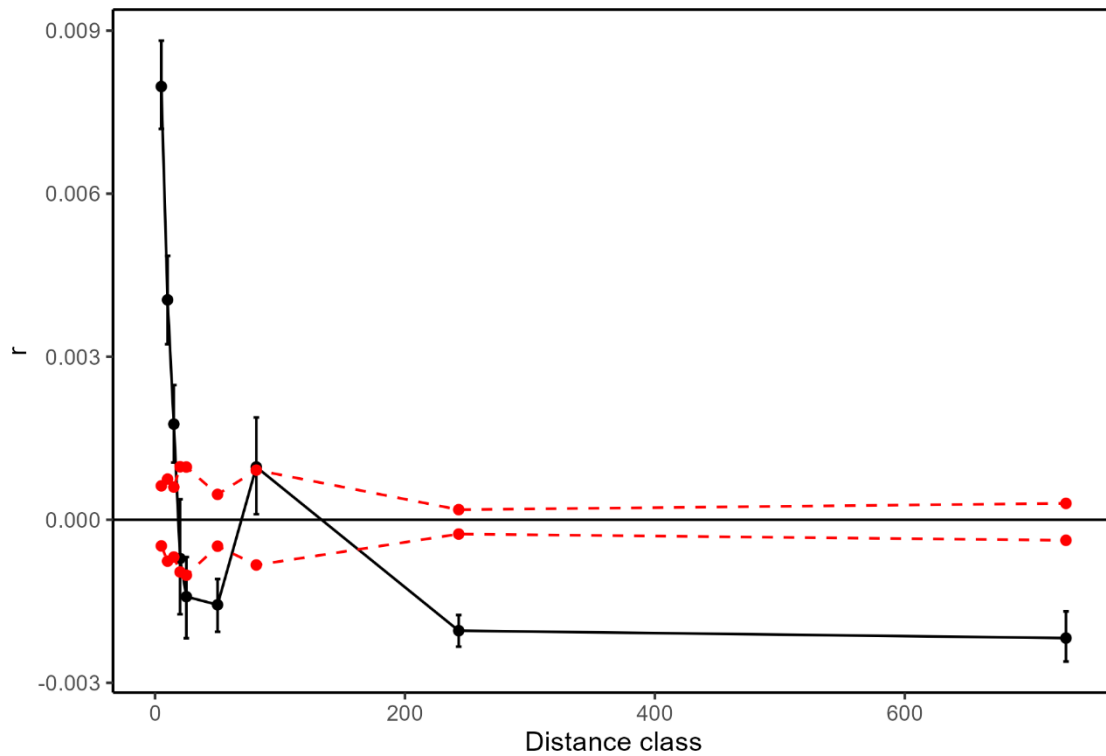
Supplementary material Fig. S3 *fastStructure* best fit for K (K = 2) for all sambar deer samples



Supplementary material Fig. S4 Auto correlogram with distance classes (km) on the x-axis and spatial correlation coefficient (r) on the y-axis for rusa deer. Error bars are estimates of the 95% confidence intervals obtained via bootstrap analysis. Red dashed lines indicate 95% confidence intervals around the null hypothesis of no spatial correlation



Supplementary material Fig. S5 Auto correlogram with distance classes (km) on the x-axis and spatial correlation coefficient (r) on the y-axis for sambar deer from the northern cluster. Error bars are estimates of the 95% confidence intervals obtained via bootstrap analysis. Red dashed lines indicate 95% confidence intervals around the null hypothesis of no spatial correlation. Points are not connected with lines if the data did not have at least one sampled pair in the intermediate distance class



Supplementary material Fig. S6 Auto correlogram with distance classes (km) on the x-axis and spatial correlation coefficient (r) on the y-axis for sambar deer from South NSW/Gippsland and Melbourne. Error bars are estimates of the 95% confidence intervals obtained via bootstrap analysis. Red dashed lines indicate 95% confidence intervals around the null hypothesis of no spatial correlation

Supplementary material Table S1 Akaike Information Criterion generated for each candidate distribution tested to fit the kinship dispersal data estimated from *Colony*. These were calculated separately for the rusa deer samples (Rusa NSW), the sambar populations present in northern NSW (Sambar North) and the sambar deer populations present in South NSW/Gippsland and Melbourne (Sambar South). Values with an asterisk (*) show the most supported distribution for each group

	Negative binomial	Poisson	Log-normal	Half-normal	Pareto
Rusa NSW	1440.4*	588571.3	1460.2	1658.3	1507.2
Sambar North	487.7*	517601	496.4	522.4	503.6
Sambar South	349.2	306260.7	342.3*	394.8	343.1