Supplemental Information for:

Multiple hypotheses explain variation in extra-pair paternity at different levels in a single bird family

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Table A1. Overview of the studies incorporated in the analyses. The numerals refer to the legend of symbols used in Figure 1.

Species	Population	Years
Amytornis modestus	(I) Witchelina Nature Reserve, South-Australia	2013-2014
Malurus alboscapulatus	(I) Porotona, Papua New Guinea	2014
M. alboscapulatus	(II) Garuahi, Papua New Guinea	2011-2014
M. coronatus	(I) Mornington Wildlife Sanctuary, Western-Australia	2006-2014
M. cyaneus	(I) Acton, Australian Capital Territory	1988-2013
M. cyaneus	(II) Newland Head CP, South-Australia	2006-2007
M. cyaneus	(III) Scott Creek, South-Australia	2006
M. cyaneus	(IV) Boho continuous, Victoria	2011
M. cyaneus	(V) Boho linear, Victoria	2011
M. cyaneus	(VI) Lara continuous, Victoria	2011
M. cyaneus	(VII) Lara linear, Victoria	2011
M. elegans	(I) Smithbrook continuous, Western-Australia	2008-2012
M. elegans	(II) Smithbrook‘s surrounding state forest linear, Western-Australia	2009-2012
M. lamberti	(I) Lake Samsonvale, Queensland	2013-2014
M. lamberti	(II) Brookfield CP, South-Australia	2012-2014
M. melanocephalus	(I) Moomin, Queensland	1997-2011
M. melanocephalus	(II) Lake Samsonvale, Queensland	2010-2012
M. splendens	(I) Brookfield CP, South-Australia	1992-1998
M. splendens	(II) Perth, Western-Australia	1986-1987
Stipiturus malachurus	(I) Portland, Victoria	2000-2002

Details about sampling, genotyping and parentage analyses for unpublished studies:

For *M. alboscapulatus*, thirteen microsatellite loci developed for *M. melanocephalus* (Webster and Welklin, unpublished data) were amplified for all individuals captured at two study sites (Porotona 10° 15 S 150° 34 E and Garuahi 10° 13 S and 150° 28 E) in Milne Bay Province, Papua New Guinea between 2011 and 2014. We sampled 47 fledglings. To assign the paternity of each juvenile found on the study site, we assumed the breeding condition female observed in each social group was the genetic mother of all offspring in that group and confirmed maternal identity during parentage analysis. We assigned the most likely sire for each juvenile using CERVUS 3.07 (Kalinowski *et al.* 2007). CERVUS calculates a log likelihood score (LOD) for each male in the population by comparing the candidate parent’s genotype to the offspring’s genotype, while taking into account the known parent’s genotype.

In all cases we accepted the CERVUS assignment of paternity if the male chosen had 0 or 1 mismatch with the juvenile (following Baldassare and Webster 2013, Webster *et al.* 2004). Seventeen offspring did not match their social father, and were classified as extra-pair offspring.

Table A2. Porotona site: microsattellite loci used for *Malurus alboscapulatus,* the number of alleles (*k*), number of individuals typed (N), size range, heterozygosity observed (HO) and expected (HE), polymorphic information content (PIC), non-exclusion probability when one parent known (NE-P2), and non-exclusion probability when neither parent known (NE-PP) are shown for each locus.

Locus	BP Range	*k*	N	HO	HE	PIC	NE-2P	NE-PP
MaMe01	149-185	6	30	0.8	0.761	0.705	0.659	0.303
MaMe02	165-280	11	32	0.875	0.897	0.871	0.387	0.088
MaMe04	145-225	12	30	0.9	0.881	0.853	0.421	0.105
MaMe05	144-194	6	31	0.903	0.786	0.738	0.62	0.259
MaMe06	175-208	2	33	0.212	0.193	0.172	0.982	0.85
MaMe08	166-243	6	32	0.719	0.652	0.586	0.767	0.427
MaMe09	208-276	11	32	0.875	0.879	0.851	0.426	0.108
MaMe10	220-248	15	32	0.875	0.88	0.853	0.418	0.102
MaMe14	288-431	20	32	0.969	0.939	0.919	0.265	0.039
MaMe15	295-385	6	31	0.742	0.711	0.656	0.709	0.345
MaMe18	313-353	6	32	0.781	0.798	0.755	0.593	0.227
MaMe19	319-404	21	32	0.938	0.941	0.922	0.258	0.037
MaMe20	291-353	8	32	0.813	0.8	0.761	0.58	0.212

Table A3. Garuahi site: microsattellite loci used for *Malurus alboscapulatus,* the number of alleles (*k*), number of individuals typed (N), size range, heterozygosity observed (HO) and expected (HE), polymorphic information content (PIC), non-exclusion probability when one parent known (NE-P2), and non-exclusion probability when neither parent known (NE-PP) are shown for each locus.

Locus	BP Range	k	N	HO	HE	PIC	NE-2P	NE-PP
MaMe01	149-185	8	147	0.81	0.793	0.761	0.404	0.219
MaMe15	165-280	9	152	0.566	0.787	0.754	0.415	0.23
MaMe02	145-225	13	153	0.824	0.876	0.86	0.255	0.098
MaMe10	144-194	16	154	0.929	0.9	0.889	0.207	0.068
MaMe14	175-208	27	159	0.956	0.943	0.937	0.121	0.025
MaMe19	166-243	33	158	0.937	0.958	0.953	0.091	0.015
MaMe6	208-276	3	165	0.206	0.292	0.25	0.874	0.792
MaMe08	220-248	8	152	0.776	0.785	0.75	0.421	0.237
MaMe20	288-431	10	167	0.844	0.775	0.739	0.434	0.249
MaMe05	295-385	8	167	0.731	0.731	0.695	0.483	0.288
MaMe04	313-353	18	164	0.902	0.898	0.886	0.209	0.068
MaMe18	319-404	11	164	0.774	0.779	0.752	0.408	0.213
MaMe09	291-353	15	161	0.901	0.88	0.865	0.246	0.091

For *M. lamberti*, twelve species-specific microsatellite loci were developed (Thrasher and Webster, unpublished data) and amplified for all individuals captured at Lake Samsonvale (27O16' S, 152 O 41' E), 30 km northwest of Brisbane, Queensland, Australia from 2011 - 2014. We sampled 210 nestlings from 2013-2014, on day 6 after hatching. To assign the paternity of each nestling we assumed the female that built and incubated the eggs as the genetic mother of all offspring in that nest, and we confirmed maternal identity during parentage analysis. We assigned the most likely sire for each nestling using CERVUS 3.07 (Kalinowski et al. 2007). CERVUS calculates a log likelihood score (LOD) for each male in the population by comparing the candidate parent's genotype to the offspring's genotype, while taking into account the known parent's genotype. In all cases we accepted the CERVUS assignment of paternity if the male chosen had 0 or 1 mismatch with the nestling (following Baldassare and Webster 2013, Webster et al. 2004). 144 nestlings did not match their social father (pairing confirmed by behavioural interactions with known mother), and were classified as extra-pair offspring.

Table A4. microsattellite loci used for *Malurus lamberti,* the number of alleles (*k*), number of individuals typed (N), size range, heterozygosity observed (HO) and expected (HE), polymorphic information content (PIC), non-exclusion probability when one parent known (NE-P2), and non-exclusion probability when neither parent known (NE-PP) are shown for each locus.

Locus	BP Range	*k*	N	HO	HE	PIC	NE-2P	NE-PP
MaLa02	172-316	32	772	0.938	0.937	0.933	0.128	0.027
MaLa03	264-316	8	772	0.247	0.266	0.257	0.852	0.734
MaLa04	302-346	8	770	0.771	0.766	0.726	0.458	0.278
MaLa05	165-275	20	773	0.856	0.855	0.84	0.283	0.115
MaLa06	152-212	11	769	0.817	0.823	0.799	0.35	0.172
MaLa07	257-289	7	773	0.634	0.646	0.591	0.602	0.421
MaLa08	200-248	13	770	0.816	0.815	0.791	0.36	0.179
MaLa10	258-330	26	770	0.853	0.907	0.9	0.185	0.053
MaLa13	290-374	23	770	0.87	0.895	0.886	0.21	0.068
MaLa14	199-309	21	773	0.849	0.894	0.885	0.211	0.069
MaLa16	167-223	14	767	0.618	0.667	0.618	0.571	0.382
MaLa18	234-282	13	771	0.843	0.852	0.835	0.296	0.128

Table A5. The best supported model from our model selection approach (model 1a) compared to the results from a phylogenetic mixed modelling approach (model 1b). Coefficients of model 1a shows estimates with 95% confidence intervals, model 1b shows posterior means with their 95% credible intervals, both are based on standardized predictor variables (z-scores) and are on the logit scale. N.a. means that predictor variables were either not available, or that the variable does not vary at that level of investigation; "-"means that predictor variable was not fitted in that particular model. N = 89 years from 20 populations of 9 species. Note that for small data sets the random effects variances are difficult to estimate. For Bayesian methods the estimates could depend on the chosen "non-informative" prior of the variance parameter (see e.g. Li *et al.* 2011).

						Hypothesis	**Density**		**Constrained female**		**Inbreeding avoidance**	**Life history**
Model	**ΔAIC_c**	**Intercept**	**σ^2_{Phylo}**	**$\sigma^2_{Species}$**	**σ^2_{Pop}**	**Level of variation**	**Log Male density**	**Habitat geometry***	**No. helpers**	**Proportion male care**	**Proportion incestuous pairs**	**Male survival**
1a	0	-0.23 (-0.52-0.03	n.a.	0.0	0.19	Temporal	-	n.a.	-	n.a.	0.14 (0.08-0.20)	n.a.
						Inter-population	-	-	0.49 (0.26-0.70)	-	-	-
						Interspecific	0.80 (0.49-1.20)	-	-	-0.64 (-0.94- -0.37)	-	-
1b	0	-0.34 (-0.75-0.11)	5.7	21.3	0.21	Temporal	-	n.a.	-	n.a.	0.13 (0.12-0.15)	n.a.
						Inter-population	-	-	0.41 (0.31-0.48)	-	-	-
						Interspecific	0.92 (0.56-1.33)	-	-	-0.69 (-0.79--0.59)	-	-

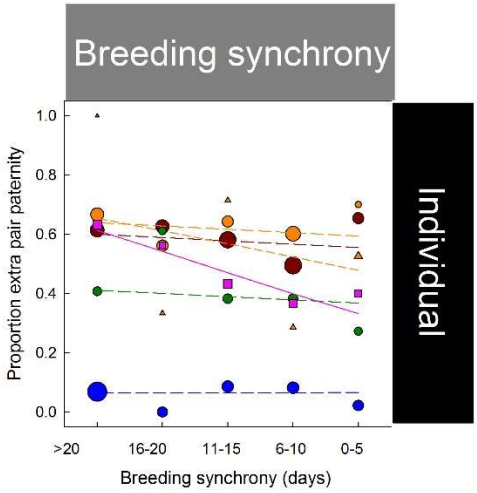

Figure A1. The proportion of extra-pair paternity (number extra-pair offspring/ total number offspring at that category level) for females from different Maluridae populations in relation to breeding asynchrony calculated as the mean difference in lay dates between a focal nest and all of its immediate neighbours. Regression lines for which the 95% CI of the slope did not overlap with zero are depicted by solid lines. The size of symbols is proportional to the cube root of the sample size. For legend see Figure 1.

References

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