

Supplemental information for: *Pama-Nyungan grandparent systems change with grandchildren, but not cross-cousin terms or social norms*

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Further details on phylogenetic methods

Tests of phylogenetic signal

A λ -transformation scales the branches of the tree by a factor, λ , that assesses how well the observed trait distribution matches the expected trait distribution for that tree under Brownian motion. A value of $\lambda=1$ indicates a perfect phylogenetic signal and returns an output tree identical to the input; a value of $\lambda=0$ indicates no observed phylogenetic signal and returns a star-like phylogeny where the only internal branches are between the tips and the ancestral state, a single unresolved polytomy. To determine the significance of the λ -transformed grandparent tree, we compared the log likelihood of the λ -transformed original tree to models where we forced $\lambda=0$ and $\lambda=1$ using a likelihood ratio test approximated by a χ^2 -distribution with a single degree of freedom.

Ancestral state reconstruction

Ancestral states were calculated on both the full dataset and on a dataset restricted to just the four most common systems, each under two sets of assumptions: (1) equal transition rates among states, and (2) symmetric transition rates among states (so a transition from state 1 to state 2 is equally probable as a transition from state 2 to state 1, but that probability need not be related to any transitions to state 3). The 'ace' command does allow a third mode, in which all transition rates are allowed to vary; our sample size, however, was too small to accurately compute so many independent transition rates (12 separate rates on the restricted dataset, or 56 on the full dataset). This command also returns the ancestral states for each internal node; the phylogeny shown in Figure 2 applies the assumption of equal transition rates (assumption 1 above). For this analysis, the branch lengths of the consensus tree were scaled by 1/100 to make the units comparable to those of biological phylogenies; in theory this should not affect any calculations, but in practice we found that some models failed to converge because their parameter spaces are restricted to those sensible for biological rates measured over millions of years rather than the much faster cultural evolutionary rates.

These analyses use a maximum-likelihood framework, but Bayesian estimates of the root state are also possible. The 'Multistate' analysis used to describe transitions between states (see main text) also provides an estimate of the ancestral Pama-Nyungan grandparent system, in a model that allows transition rates to vary asymmetrically but is restricted to the four most common systems; for completeness, these results are also presented.

Binary Bayesian phylogenetic mixed models

These models fit logistic regressions with phylogenetic co-variance (under a Brownian motion model of evolution) as a random effect. We began each BBPMM with an initial burn-in on an arbitrary tree with 11,000,000 iterations to determine starting values, then sequentially ran on each tree 2,000,000 iterations, with a per-tree burn-in of 1,000,000 and

a sampling rate of 10,000, for a total posterior sample of 1,000 (10 for each tree). Priors for the fixed effects were set using the command 'gelman.prior' (Gelman et al., 2008) with a scale of $1 + \frac{\pi^2}{3}$; the prior for the phylogenetic random effect was set to be an inverse-Wishart distribution with $V = 1$ and $\nu = 0.02$. The residual variance was fixed at 1, which is standard for a logistic regression.

Non-phylogenetic models

Many studies of cross-cultural and cross-linguistic variation are not performed in a phylogenetic context, both historically and in present research. For our study to be comparable to such works, and to highlight the importance of phylogenetic comparative methods in the field of cultural evolution, we also tested our hypotheses in a non-phylogenetic framework, using Fisher's exact test.

When treating each ethnolinguistic society as an independent sample, we found no evidence of a correlation between grandparental term systems and linguistic exogamy ($p = 0.938$), nor between grandparental term systems and post-marital residence ($p = 1$). The observed link between grandparent-grandchild reciprocals and grandparental term systems, however, is statistically significant in a non-phylogenetic framework ($p < 0.001$), as are the links between grandchild and grandparental systems (specifically, that MG systems are more likely to also merge grandchildren terms by gender of the referent and less likely to merge by the identity of the parent, both $p < 0.001$).

Correlations between grandparental systems and community marriage organisation

In the main text, we present the correlation between the grandparental systems and community marriage organisation, with endogamy (few marriages outside the language group) and agamy merged into a single category and compared with exogamy (many marriages outside the language group). When instead agamy and exogamy are merged into a single group, and compared with endogamy, the results are similar.

Under this slightly different definition of community marriage organisation, there is also no relationship between this variable and whether the language distinguishes the female grandparents ($p\text{MCMC} = 0.728$), the male grandparents ($p\text{MCMC} = 0.690$), the parallel grandparents ($p\text{MCMC} = 0.546$), or the cross grandparents ($p\text{MCMC} = 0.348$).

When each language is considered an independent data point, there is no relationship between grandparental system and community marriage organisation (Fisher's exact test, $p = 0.634$); neither does a relationship exist in a phylogenetic framework ($p\text{MCMC} = 0.974$).

Data sources

All terms for grandparents and many of the terms for grandchildren and cross-cousins came from the online database of indigenous Australian languages, CHIRILA (<http://chirila.yale.edu/>) (Bowern, 2016) and the Austkin project (<http://www.austkin.net/>) (Dousset et al., 2010). We also consulted the following sources (with glottocodes in brackets, see Hammarström et al. 2018):

- Alyawarr (alya1239): Yallop (1977)
- Badimaya (badi1246): Dunn (1988)
- Bandjalang (band1339): Cunningham (1969); Geytenbeek and Geytenbeek (1971); Wafer et al. (2008)
- Biri (biri1256): Gargett (2011)
- Dharumbal (dhar1248): Terrill (2002)
- Diyari (dier1241): Austin (1981)
- Djapu (dhuw1249): Dixon and Blake (1979); Heath (1980)
- Dyirbal (mamu1253, dyir1250): Dixon (2015)
- Gamilaraay (gami1243): Giacon (2014), Wafer et al. (2008)
- Gumatj (dhuw1249, guma1253): Dixon and Blake (1979); Heath (1980)
- Gumbaynggir (kumb1268): Wafer et al. (2008)
- Gunya (guny1241): Wafer et al. (2008)
- Jaru (jaru1254): Tsunoda (1981)
- Karajarri (kara1476): Scheffler and Jorion (1981)
- KukuYalanji (kuku1273): Hershberger and Hershberger (1982); Patz (2002)
- MartuWangka (mart1256): Jones (2012)
- Muruwari (muru1266): Wafer et al. (2008)
- Ngadjumaya (ngad1258): Brandenstein (1980)
- Ngiyambaa (wang1291): Wafer et al. (2008)
- Paakantyi (darl1243): L. A. Hercus (1982); Wafer et al. (2008)
- PintupiLuritja (pint1250): Hansen (1978)
- Pitjantjatjara (pitj1243): Scheffler and Jorion (1981)
- Warlpiri (warl1254): Scheffler and Jorion (1981)
- Warumungu (waru1265): Luise Anna Hercus (1999)
- Warungu (waru1264): Scheffler and Jorion (1981)
- WikMungkan (wikm1247): Needham (1971)
- Wiradjuri (wira1262): Wafer et al. (2008)
- Yandruwandha (yand1253): Wafer et al. (2008)
- YortaYorta (yort1237): Wafer et al. (2008)

Table 1 in the main text defines the relevant terms with reference to the speaker. Some Australian languages also have trirelational kinship terms, where the propositus is defined in relation to another person. These terms affect which items are used for cognate reconstruction using linguistic comparative methods but do not affect the splits in systems discussed here.

Many of the community marriage organisation scores were obtained from Binford (2001), via the online cross-cultural database D-PLACE (<https://d-place.org/>) (Kirby et al., 2016). We also consulted the following sources:

- Adnyamathanha: Houseman (1997)
- Arabana: Hercus (1994); Nursey-Bray et al. (2013)
- Badimaya: Dunn (1988)
- Bandjalang: Harvey (2011)
- Batyala: Bell (2013)
- Bilinarra: Harvey and Garde (2016)
- CentralAnmatyerr: Young (1987)
- Dharawal: Toner (2015)
- Dharumbal: Morton (2017)
- Dhurga: Toner (2015)
- Djabugay: Henry (2000); McDonald and Lane (2000)
- Djinang: Waters (1984)
- Gupapuyngu: Munro and Nathan (2005); Vaughan (2018)
- GuuguYimidhirr: Haviland (1979)
- Jiwarli: Aikhenvald and Dixon (2001)
- KuguNghanhcara: Baldi (2011)
- Kukatja: Denham (2013a); Dousset (2012)
- Kunjen: Ogilvie (1994); Sommer and Marsh (1969)
- KuukThaayorre: Gaby (2016); Harvey (2001)
- KuukuYau: Hill (2011, 2016, 2018)
- Mabuig: Rivers (1900)
- MangalaMck: Denham (2013b)
- Martuthunira: Dench (1995)
- Mudburra: Dorian (2004)
- Ngarinyman: Harvey and Garde (2016); Raynes (2000)
- Ngarluma: A. C. Dench (1995)
- Ngarrindjeri: Jenkin (1976)
- Nyamal: Read and Coppin (2014)
- Nyangumarta: Hargrave (1982)

- Panyjima: Dench (1987)
- Parnkala: Mathews (1900)
- PittaPitta: Conybeare (1898); Harvey (2011)
- Purduna: Goode et al. (2014); McConvell et al. (2018)
- Ritharrngu: Altman et al. (1999); Peterson and Myers (2016)
- Thanggati: Bower (2010)
- Tharrgari: Dench (1995)
- Wangkangurru: Hercus (1994)
- Wardandi: Dousset et al. (2010); Gunn et al. (2011)
- Warlmanpa: Simpson (1985)
- Warnman: Tonkinson (1989, 2002)
- Warriyangga: Austin (2015)
- Warumungu: Simpson (2013)
- Yannhangu: Bower and James (2005)
- YortaYorta: Bower and Morey (1999)
- Yugambah: Sharpe (1985, 1998)
- Yuwaalaraay: Austin (1993)

All post-marital residence data came from Moravec et al. (2018).

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