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Computational Phylogenetics and the Internal Structure of Pama-Nyungan

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COMPUTATIONAL PHYLOGENETICS AND THE INTERNAL STRUCTURE OF PAMA-NYUNGAN

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We present the first proposal of detailed internal subgrouping and higher-order structure of the Pama-Nyungan family of Australian languages. Previous work has identified more than twenty-five primary subgroups in the family, with little indication of how these groups might fit together. Some work has assumed that reconstruction of higher nodes in the tree was impossible, either because extensive internal borrowing has obscured more remote relations, or because the languages are not sufficiently well attested (see, for example, Bowern & Koch 2004b, Dixon 1997). With regard to the first objection, work by Alpher and Nash (1999) and Bowern and colleagues (2011) shows that loan levels are not high enough to obscure vertical transmission for all but a few languages. New data remove the second objection. Here we use Bayesian phylogenetic inference to show that the Pama-Nyungan tree has a discernible internal subgrouping. We identify four major divisions within the family and discuss the implications of this grouping for future work on the family.*

Keywords: Australian languages, phylogenetics, Pama-Nyungan, family tree, comparative method, historical linguistics, language contact

1. INTRODUCTION: THE PROBLEM OF A PAMA-NYUNGAN FAMILY TREE. Pama-Nyungan languages cover just under 90% of the Australian mainland; they stretch from the islands of the Torres Strait in the northeast to the far southwest of Western Australia. The family contains approximately 290 languages, many of which are internally dialectally diverse. They comprise approximately two-thirds of the indigenous languages spoken in Australia at the time of European settlement.

Pama-Nyungan languages have proved something of a puzzle for linguistic classification thus far. There has been considerable work over the last century on the languages that constitute the Pama-Nyungan family, and more than twenty-five low-level subgroups have been identified (see, among others, Bowern & Koch 2004b, Koch 2004a, O'Grady et al. 1966a, Wurm 1972). As yet, however, there is no consensus regarding the deeper internal branching; that is, there is no agreement as to how these clear subgroups might be related to one another.[1] Some have argued that such consensus is unobtainable. The most forceful statement of the difficulty (or rather, impossibility) of reconstruction of Pama-Nyungan languages is made by R. M. W. Dixon, who denies the possibility of recovering any continent-wide evidence of genetic relationship, not just because any common ancestor is so remote, but more seriously because extensive diffusion has resulted in the elimination of the evidence we would use to recover such relationships.

> Australia provides a prototypical instance of a linguistic area. It has considerable time-depth, fairly uniform terrain leading to ease of interaction and communication, a fair proportion of reciprocal exogamous marriages, rampant multilingualism, and an open attitude to borrowing … There is a basic uniformity to Australian languages which is the natural result of a long period of diffusion.

[1] An exception is Nyungic, the tentative grouping in O'Grady et al. 1966a that contained all the languages of Western Australia, along with Thura-Yura; but even the Nyungic proposal contained no further internal structure.

> Although no justification had been provided for 'Pama-Nyungan', it came to be accepted. People accepted it because it was accepted—as a species of belief. … It is clear that 'Pama-Nyungan' cannot be supported as a genetic group. Nor is it a useful typological grouping. (Dixon 2002:48, 53)

Several reasons have been advanced for the impossibility of higher-order subgrouping within Pama-Nyungan. Explicit in Dixon's work is language contact: it is assumed that extensive borrowing and structural convergence have obliterated any phylogenetic structure that may have existed. Others (such as Bowern 2010 and Koch 2004b) have suggested that lack of data has exacerbated the problem. That is, too many of the languages were too poorly recorded to allow us to have enough evidence to recover their precise position in the family.

Here we present the first proposal for major divisions and higher-level subgrouping within Pama-Nyungan, using a phylogenetic Bayesian analysis based on cognate lexical items identified using the COMPARATIVE METHOD. We show that previous objections to such work within the Pama-Nyungan family are unfounded; loan levels, for example, are not high enough for most of the country to impede accurate tree recovery (Bowern 2011). We discuss the major divisions and internal structure of the family. The results obtained here illustrate the power of combining computational techniques with fine-grained data analysis by specialists in the languages.

The internal structure of Pama-Nyungan is also important for our view of language change more generally. For example, Nettle (1998:9) is explicit in coupling types of split in a family tree with social factors, and regards Pama-Nyungan as standing in contrast to highly branching trees, such as Austronesian.

> A tree-like structure bears witness to a rapid geographical expansion perhaps associated with economic developments in prehistory; less dendritic suggests various possibilities such as a long period of *in situ* development with high rates of exogamy and extensive multilingualism. The fact that no such tree can be established in Australia is not a nuisance but a finding.

We argue here that Pama-Nyungan does, in fact, have a tree-like structure, and that high rates of multilingualism have not made recovering such a tree impossible.

1.1. PREVIOUS CLASSIFICATIONS. Previous work on internal classification of the Pama-Nyungan family has used three types of evidence to determine relationships between languages. The first is lexicostatistic, that is, the inspection of wordlists of basic vocabulary for the identification of likely shared material, and the pairwise comparison of 'sames' within such lists to yield a distance matrix of similarity (Black 1997, Gudschinsky 1964). O'Grady et al. 1966a and 1966b are two influential lexicostatistical classifications of Pama-Nyungan languages, and were the first to cover the whole continent.[2] They found over twenty subgroups that have formed the basis of several subsequent classifications and language lists, including Oates & Oates 1970, Wurm & Hattori 1981, and Gordon 2005.

A second strand of work has taken pronominal and nominal case morphology to be especially diagnostic of relationship. Use of evidence in this area has led to a refinement of the O'Grady et al. 1966a classification, for example, work by Blake (1990a) on the Pama-Nyungan and non-Pama-Nyungan languages that border one another in the eastern part of the Northern Territory; this work has also led to some primary subgroup diagnostics. Dench (1994) used similar evidence, and detailed reconstruction, to argue implicitly for the unity of the Kanyara, Mantharta, and Ngayarta subgroups. Crucially,

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[2] These classifications were not the first attempts to classify Australian languages; there is earlier work such as that by Schmidt (1919), who found two groups, 'Northern' and 'Southern', but did not have data for most of the languages that would now be called non-Pama-Nyungan. See Koch 2004a for an overview of the history of classification.

however, this work has not appeared to have led to many new insights into macro-groupings within Pama-Nyungan. In writing about the close-knit Yardli subgroup, for example, Hercus and Austin (2004) comment on the lack of forms that might be diagnostic of regional groupings at levels between Proto-Pama-Nyungan and Proto-Yardli. Bowern 1998 made the same point for Karnic nominal morphology. A similar position is implicit in Breen and Blake's (2007:70–71) treatment of Kalkatungu and Yalarnnga as 'genetically close' but not a subgroup. Dench (1994:189) also notes that the pronominal reconstructions for Pilbara languages differ minimally from those advanced by Blake (1988) and Dixon (1980) for Proto-Pama-Nyungan.

A third criterion for subgrouping has been typological features. Similarities among Pama-Nyungan languages from around the country have been recognized as long ago as Schmidt 1919; they are largely dependent-marking languages (Nichols 1986) with case but not verbal person/number agreement in declarative clauses; they typically have verbal derivational suffixes but no (or little) nominal derivation; verbs have several conjugation classes in most of the family (Alpher 1990). They typically exhibit ergative morphology and may also show ergative syntax. Many are also nonconfigurational (Hale 1983). These features have typically been used to distinguish Pama-Nyungan languages from languages belonging to other Australian families, but other syntactic features have been adduced as evidence for subgrouping. For example, the Ngumpin-Yapa languages have reconstructible second-position clitic complexes (McConvell & Laughren 2004), Arandic languages are distinguished by their phonological systems and phonotactics, and a subset of Pilbara languages show nominative-accusative alignment. These subgroups have also been further justified on the basis of lexical innovations and sound change.

There has also been work on the features of Proto-Pama-Nyungan itself (e.g. Alpher 1990, 2004, Blake 1990a, McConvell 1997, Sands 1996). From this work, especially Alpher 2004, we now have a set of several hundred reconstructed lexical items. The pronoun (Blake 1990a,b), case (Blake 1993, Hale 1976), and verb conjugation (Alpher 1990) systems are also relatively well known. This work has concentrated on reconstructions of lexical items with wide distribution; thus while the reconstructions are secure, in that they are well attested, comparatively little attention has been paid to the evidence of lexical innovation as possible determinants of higher structure within the family.[3] By definition, words with very widespread distributions are not likely to reveal much about the internal structure of the family, simply because they are conservative features. Conversely, work on material culture (Evans & Jones 1997, McConvell & Evans 1997) has furnished information about the history of lexical items, but appears to have been more revealing about contact patterns than subgroup inheritances.

1.2. CLASSIFICATIONS OF INDIVIDUAL SUBGROUPS. There has been considerable work on individual low-level subgroups themselves, which has resulted in refinement of the earlier lexicostatistical work. Many of these subgroups are well supported through established methods of historical reconstruction, that is, the comparative method applied to lexicon and morphology and the identification of sound changes.[4] Such subgroups in-

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[3] A referee points out that lexicostatistical work inherently (if indirectly) pays attention to this type of evidence. However, the classifications constructed using lexicostatistics in Australia were compiled from distance matrices derived from percentage similarity scores. Such matrices lose the information about specific lexical innovations and reduce the power of the method to recover higher-level groups.

[4] Seven of these subgroups are presented in Bowern & Koch 2004a; these include (but are not limited to) Arandic (Koch 2004a), Thura-Yura (Simpson & Hercus 2004), Yardli (Hercus & Austin 2004), and Ngumpin-Yapa (McConvell & Laughren 2004).

clude Arandic (Koch 1997, 2001), Marrngu (Weber 2009), Maric (Barrett 2005), War-luwaric (Brammall 1991), Mayi (Breen 1981), and Paman (Black 2004, O'Grady 1976, Sutton 1976). A map of the commonly agreed-upon subgroups is given in Figure 1.
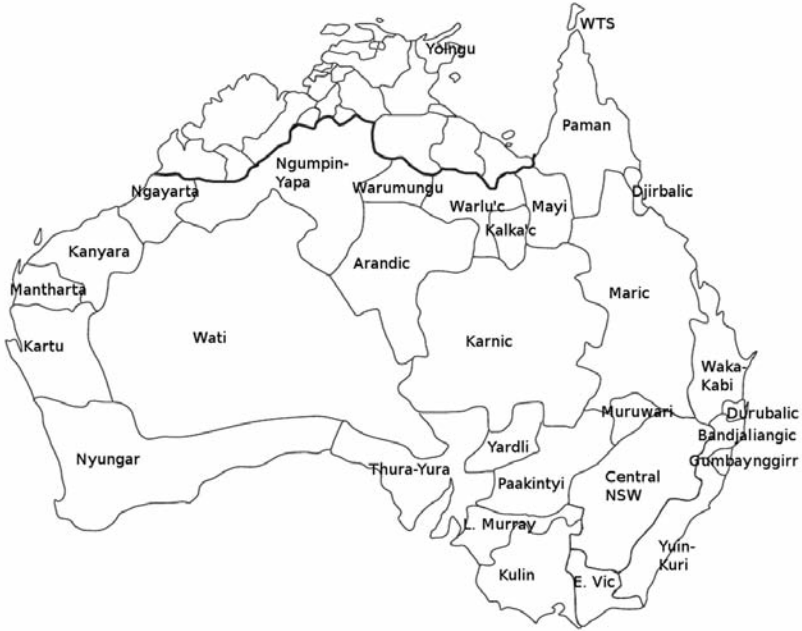

FIGURE 1. Map of major current subgroups of Pama-Nyungan.

Other groups have been more controversial. For example, the Karnic group in Central Australia (Austin 1990a, 1991, Bowern 2001, Breen 1971, Hercus 1994) has been the subject of several studies, and the internal composition of the subgroup differs (a review of the issues appears in Bowern 2010). Similar issues surround Paman (Black 2004, Blake 1979, Hale 1964, Sutton 1976) and perhaps Maric (Barrett 2005), though in this case the problem stems in part from the lack of data about some of the languages. In such cases, problems in internal subgrouping have stemmed from two sources. First is the difficulty in finding subgroup-wide innovations that differentiate the group in question from the rest of Pama-Nyungan, as discussed above. The second problem lies in determining whether a shared feature is a retention or an innovation. In Austin 1990a, for example, the gender marking in third-person pronouns that is present in many (though not all) Karnic languages was treated as an innovation. Bowern 2009, following a suggestion by Harold Koch, showed that it was most likely a retention from Proto-Pama-Nyungan, since cognate forms for both masculine and feminine pronouns are found in scattered languages right across the family.

A final problem concerns the placement of language isolates within the family. Current trees of Pama-Nyungan are also notable in the number of subgroup-level isolates that they posit. Languages such as Gumbaynggirr (Eades 1979), Dyirbal (Dixon 1970), Paakantyi (Hercus 1986), and Warumungu (Simpson & Heath 1982) are clearly Pama-Nyungan languages, judging by their pronouns, case marking, and core lexical items.

Previous work has not, however, found any close ties between these languages and other known subgroups.[5]

There have been some attempts to identify larger clades within Pama-Nyungan. O'Grady and colleagues (1966b) suggest that all of the languages of Western Australia, and some in South Australia (including Thura-Yura), form a single group within the tree, which they termed 'Nyungic'. They did not, however, suggest further structure within Nyungic than ten or more subgroups. More recently, Blake and Reid (1994, 1998) have tentatively suggested that the languages of Western Victoria, comprising Kulin and the isolates Kolkngat and Buwandik, comprise a single group (termed 'Macro-Kulin'). Hercus and Austin (2004) consider the supergroup of Thura-Yura, Yardli, and Karnic (initially proposed by Schmidt 1919) to be as yet 'unproven'; they found no clear evidence for such a group, but no reason to reject it.[6] All such proposals have been tentative, and authors typically caution against higher grouping because of fears that extensive language contact has obscured genetic relations.

1.3. PAMA-NYUNGAN AS A FAN-LIKE FAMILY. Thus the picture that we have of Pama-Nyungan from the current state of research is that the family has a fan-like structure, with little (if any) structure to the upper splits (illustrated in Figure 2).[7] We must consider, however, whether this tree is an accurate reflection of the early splits in the family, suggesting an early and rapid period of divergence into major groups,[8] or whether it is an artifact of inadequate data, intensive language contact, or simply lack of study. This is analogous to the distinctions that biologists often make between hard polytomies (indicating a rapid or simultaneous dispersal of groups) and soft polytomies (where the branching pattern is unknown).

Proto-Pama-Nyungan
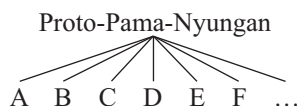
A   B   C   D   E   F   …

FIGURE 2. Fan model of Pama-Nyungan.

Inadequate data can now be ruled out as a factor in Pama-Nyungan. While classifications from earlier years may have had this problem, we have access to a sufficient data set that we are confident in the sampling (see below §2.2 for methods). The classification presented here is based on a lexical database that includes nearly 600,000 unique

[5] Gumbaynggirr has a sister variety Yaygirr (Crowley 1979), which was not included in coding due to lack of data. Paakantyi is dialectally diverse and two varieties were included here. Dyirbal also has internal dialect distinctions.

[6] Bowern 2001 ruled out Thura-Yura languages as being Karnic on the grounds that they do not share several characteristic Karnic innovations; it did not, however, investigate the question of whether there were other features that characterized a higher-level group.

[7] Such families have also been called star-like trees or rakes (Ross 1997).

[8] The question of what demographic processes produce fan-like families in linguistics is a matter of current debate. Nettle (1998) comes to the opposite conclusion from that presented here. That is, Nettle follows Dixon (1997) in assuming that rapid spreads produce only tree-like structures. Examination of recent rapid language dispersals, such as Turkic and subgroups of Austronesian, however, would seem to indicate that rapid migration produces rapid indistinct branching. This happens because populations are losing contact before there is time to build up sufficient distinctive changes.

headwords from 405 varieties and 1,430 doculects.[9] One hundred and twenty-seven languages are attested with more than 1,000 words. Data for this analysis focused on languages that were well attested; moreover, by restricting the sample set to 200 words of basic vocabulary, we were able to include many languages that are attested only from limited sources. Therefore, while data are variable, and some languages are attested only from nineteenth-century sources, we have sufficient resources to make generalizations about family structure.

There is also evidence that the impact of language contact for Australia has been overstated. Contact phenomena have featured prominently in studies of Australian languages (Dench 2001, Dixon 1997, 2002, Heath 1978, Hercus 1979) and rightly so, since many speakers of Indigenous Australian languages were multilingual. However, loan levels for Australia as a whole have been overstated. There are some exceptional areas, but they have received focus precisely because they are exceptional. In a survey of forty-nine Australian languages (Bowern 2011), mean loans in basic vocabulary were found to be 8.7%, with median loans at 5.54% (SD 11.01). Seventy-five percent of the languages surveyed had loan levels under 12% in basic vocabulary.[10] These loan findings are in accordance with those for Cape York in Alpher & Nash 1999, and place Australian loan levels on a par with those found in the rest of the world (Embleton 1986, Nelson-Sathi et al. 2011). Figure 3 gives the distribution of loans in the Australian languages surveyed, with the figures from equivalent wordlists in Haspelmath & Tadmor 2009 (World Loanword Database, WOLD) for comparison.
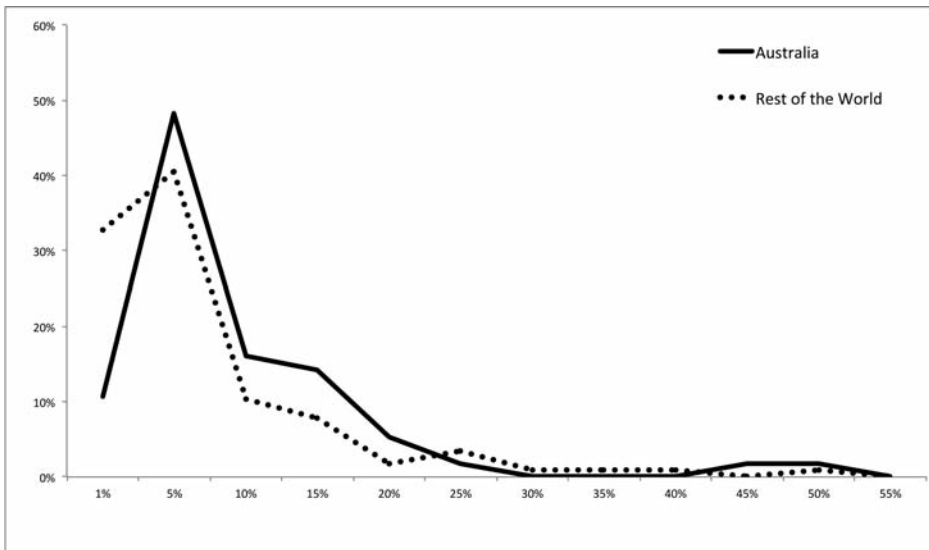
FIGURE 3. Loan rates in Pama-Nyungan languages.

Loan levels in the survey region ranged from 0 to 50% (Gurindji; see McConvell 2009), with only a few languages at c. 25% or higher (Malyangapa, Mudburra, Walma-

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[9] A doculect refers to a linguistic variety that has been described by a single author. It recognizes that the data is representative of a particular set of speakers, but may not represent a whole dialect or language. That is, it is agnostic to phylogenetic levels.

[10] See Bowern et al. 2011 for details. The survey is based on 204 items of basic vocabulary (the same list as used in this study; see §2.2). Loans were identified using standard procedures in historical linguistics (Fox 1995, Hock & Joseph 1996).

jarri). Therefore, while loan levels are, for the most part, not high enough to cause problems for subgrouping, there are some areas where they might interfere with genetic grouping using only lexical material (see further Greenhill et al. 2009).

We can therefore rule out these reasons for a fan-like structure in Pama-Nyungan. Insufficient data is no longer a confounding factor, and loan levels are no more likely to cloud relationships than elsewhere in the world. The (apparent) fan-like structure of so many primary subgroups must therefore either be due to insufficient investigation into the higher-level structure of the tree, or be a reflection of the way in which Pama-Nyungan actually broke up—for example, rapid expansion with languages remaining in contact (e.g. Bowern 2010, Garrett 2006).

1.4. SOLVING THE PROBLEM. Here we apply a model-based Bayesian phylogenetic inference procedure to Pama-Nyungan cognate data in order to reconstruct the internal branching structure of the family. This newly developed approach offers several advantages. First, competing trees are evaluated without prejudice, using a precisely defined set of assumptions based on a likelihood model of cognate replacement. Second, for the 194 languages in our sample, the number of possible trees is astronomical, and it is simply not possible to evaluate all of them. The Bayesian phylogenetic methods we employ use a Markov chain Monte Carlo (MCMC; Metropolis et al. 1953) algorithm to efficiently search the universe of possible trees, sampling trees in proportion to how likely they are, given the model of cognate replacement and the observed distribution of cognates at the tips. Third, it is possible to incorporate into the analysis uncertainty in the data itself. For example, where a word in a particular language is unknown, it can be assigned with equal probability to a range of possible cognate sets. Fourth, rather than producing a single optimal tree, the result is a distribution of trees sampled in proportion to their posterior probability given the data and model. This makes it possible to quantify uncertainty in the tree topology and branch lengths and test competing hypotheses. For example, we can easily estimate the level of support for a particular grouping (the percentage of trees in the posterior distribution with that grouping) or put a confidence interval on the time at which any clade began to diverge. Finally, we can compare the fit of different models of cognate replacement and thereby evaluate the validity and importance of different model assumptions. For example, we can test whether allowing for the possibility of independent innovations of the same form improves model fit, or whether a model that relaxes the assumption of constant rates of change fits better than assuming clock-like rates of change. Such methods are used increasingly in historical linguistics; for examples of phylogenetic work in other families and more detailed explanation of the rationale behind such approaches, see, among others, Atkinson & Gray 2005, Bryant et al. 2005, Dunn 2009, Dunn et al. 2007, Gray et al. 2007, and Holden 2002.

Using this framework, we aim to answer the following questions.

- Does lexical information alone allow us to replicate the lower-level Pama-Nyungan subgroups?
- What higher-level groupings are recovered?
- What degree of support do the major groupings have?
- Does the inferred structure of Pama-Nyungan make sense given what else we know about the languages?

2. DATA AND METHODS. We record the presence or absence of cognate data for 189 meanings across a sample of 194 Pama-Nyungan languages. We use a likelihood approach to model language change as the gain and loss of cognates through time, allowing us to evaluate alternative language family trees and compare model fit across a

range of model assumptions. This approach is combined with Bayesian inference of phylogeny to produce a posterior distribution of trees representing the relationships between Pama-Nyungan languages, accounting for uncertainty in model parameters and stochastic uncertainty in the processes involved. Further details are given below.

2.1. DATA SOURCES.

THE LANGUAGES. A total of 194 doculects were sampled from across the Pama-Nyungan family. The sample represents all family-level isolates, all previously identified subgroups, and all languages with extensive data. Ninety languages satisfy these criteria. The remaining doculects in the sample are drawn from other languages with good data, languages with extensive dialect diversity, and other varieties that ensure even geographical coverage.[11]

A map of the sampled languages is given in Figure 4. Individual language locations can be found at http://austlang.aiatsis.gov.au/.
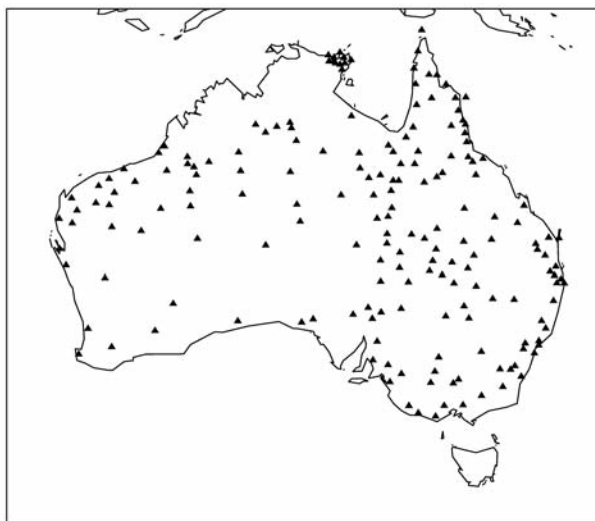
FIGURE 4. Languages included in the sample.

Data quality is variable. Lexical data from published sources in phonemic orthographies were preferred, but where that was not available, other material was used. Some languages are known only from nineteenth-century grammars or dictionaries, others only by wordlists. Other gaps in Fig. 4 represent areas of sparse population rather than missing languages. The mean amount of missing data overall was 23% (median 21%), but it is unevenly distributed. By subgroup, the amount of missing data varies from 2 to 50%. The subgroups most affected by missing data are Kulin (47.8%), Maric (42.4% average), Waka-Kabi (37.3%), and Paman (33.4% average). The supplementary materials provide a list of the languages and sources used.[12]

While the sample is for the most part balanced for both subgroup diversity and geographical areas, a few areas were undersampled. In some cases, there were subgroups

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[11] If we did not sample evenly across the continent, it might be thought that the recovered subgroups are the result of sampling geographically discontinuous areas. While we do not test this hypothesis explicitly, we aim to test it implicitly by ensuring adequate continent-wide language sampling.

[12] Accessible at http://pamanyungan.sites.yale.edu/.

where only one variety had sufficient data for inclusion. The Yardli subgroup, for example, has three languages (Wadikali, Malyangapa, and Yardliyawarra), but only Malyangapa (Austin 2002) had sufficient data to be included. Wadikali is known from only seventy-seven words in total, and Yardliyawarra from little more (Hercus & Austin 2004). The Lower Murray subgroup is also undersampled, because of the difficulty in working out what languages some words belong to. The main source, Taplin 1878, is amalgamated as 'Ngarrindjeri' in current sources, but actually contains data from up to six languages. Pending further research, only two languages from this group were included.

The westernmost languages of the Maric subgroup (formerly spoken in Western Queensland) were undersampled because so many of the languages are very poorly recorded. For some, we have no information whatsoever apart from the name. In other parts of the country, poor attestation was also problematic, but because there were other varieties in the subgroup that are better recorded, the subgroup could still be represented adequately. The Pirlatapa (Austin 1990c) language, for example, is known from only a few phrases, but those phrases place it as fairly closely related to Diyari and Ngamini, both of which are well recorded (Austin 1981).

The other undersampled area is Paman, the northeasternmost subgroup of the family, covering Cape York Peninsula. Many of these languages are recorded only in handwritten field notes, and are not (yet) represented in the electronic database from which most of the data were taken. Moreover, the languages of this subgroup exhibit extensive sound change, which makes the identification of cognates difficult. There is some published work on the sound correspondences in this area (Black 2004, Hale 1964, Sutton 1976), and the changes are complex and the distribution of lexical items likely reflects a period of substantial language change in situ. Seventeen languages from the subgroup were included here, but given that there are more than forty languages in the subgroup, and the subgroup is diverse, the inclusion of more languages would have allowed for greater resolution.

THE LIST OF MEANINGS. A wordlist of basic vocabulary was used in this project. The list includes culturally neutral items that are universally lexicalized and that frequently appear in wordlists. The wordlist is given in 1 below. Many items also appear in the Swadesh 100 (Swadesh 1971) and 200 list (see, for example, Crowley & Bowern 2010). Additional words added here are asterisked. Our list was based on the list used in Greenhill et al. 2008, which was in turn based on Blust 1981, 2000. The original list was 204 items. This was subsequently reduced to 189 items. We removed some words (such as numerals above five) that were not useful for studying Australian languages. Some words from our original list were subsequently excluded, and are given here in italics. Grindstone words appeared in too few language lists; 'man' and 'person' overlapped in many languages, so including both would have biased the results; 'count', 'flower', and 'roof' were frequently loans from English or Kriol in a number of languages, and missing in others. 'Fly' was excluded because many of the wordlists were not explicit about whether the recorded word was the equivalent of the English verb or the English noun. Other words were excluded because they were missing from the attested lists of a substantial number of languages ('winnow', 'hit (with hand)', 'chew').

(1) *above, *again, all, and, *ankle, *ant, *armpit, ash, at, back, bad/evil, belly, *below, big, bird, bite, black, blood, blow, *blowfly/housefly, *boil/pimple, bone, *boomerang/throwing stick, *bottom grinding stone*, breast, breathe, burn, *chew*, child, *climb, cloud, cold, come, cook, *correct/true, *count*, *cry, cut/hack, day, die/be dead, dig, *digging stick, *dingo/wolf, dirty, dog, *dream, drink, dry, dull/blunt, dust, ear, earth/soil, eat, egg, eye, *feces, fall,

far, fat/grease, father, fear, feather, fire, fish, flow, *flower*, *fly*, fog, foot, *fruit*, good, grass, *grow, hair, hand, he/she, head, hear, heavy, *hide, *hit (with hand)*, hold, *house*, how, I, *if*, in/inside, intestines, *itch, *kangaroo/deer, kill, know/be knowledgeable, lake, laugh, leaf, left, leg, lie down, *lightning, live/be alive, liver, long, louse, *lung, *man/male*, meat/flesh, moon, *mosquito, mother, mouth, name, *nape, near/close, neck, new, night, no/not, nose, old, one, *open/uncover, other, *painful/sick, *person/human being*, *pound/beat, rain, red, right, road/path, *roof*, root, rope, rotten, sand, say, scratch, see, sharp, shoot, short, *shoulder, *shy/ashamed, sit, skin, sky, sleep, small, smoke, snake, sniff/smell, spear, *spearthrower, *spider, spit, split, squeeze, stab/pierce, stand, star, *steal, *stick/wood, stone, suck, *sweat, swell, swim, tail, that, *thatch/roof*, they, *thick*, thin, think, this, thou, three, *throat, throw, *thunder, tie up/fasten, tongue, tooth, *top grinding stone*, turn, two, vomit, walk, water, *we.EXCL.PL, we.INCL.PL, wet, what, when, where, white, who, wife, wind, wing, *winnow*, woman/female, work, *yawn, yellow, you.SG

2.2. CODING. Items were first coded by cognacy, such that items presumed to be cognate within each meaning slot were given the same code. This is illustrated in 2 below using words for 'eye'. We take the definition of a 'cognate' as the standard one in historical linguistics. That is, cognates are words that are presumed to descend from a single proto-form via vertical transmission. (For discussion, see Anttila 1989 [1972], Hock & Joseph 1996, and others.)

(2)
LANGUAGE	FORM	CODE	NOTE
Yiningayi	dhili	1	
Gangulu	dhili	1	
Marrgany	dhili	1	
Pirriya	djiloi	1	likely loan
Yarluyandi	milki	2	(see Hercus 1979 for etymology as *mi:l-ki in Proto-Western Karnic)
Mithaka	mirlki	2	
Ngamini	mirki	2	
Yanda	miyil	2	
Kukatja	kuru	3	
Manjiljarra	kuru	3	
Kartujarra	kuru	3	
Yardliyawarra	[missing]	?	
…			

Two caveats are required. The first concerns borrowing. At present, there are no statements of correspondence sets between lexical items in Pama-Nyungan languages. Such work does exist for certain subgroups, but not across the country.[13] This makes the large-scale identification of cognate items more difficult than it would be for a comparable project in Indo-European or Austronesian, where such data are readily available. It also raises the possibility that accidental similarities and loans may have been coded as cognate. As noted in Bowern et al. 2011, rates of borrowing are generally quite low (where they can be determined), and as Greenhill et al. 2009 shows, loan rates have to

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[13] See Barrett 2005 for Maric, Austin 1989 for Kanyara-Mantharta, Austin 1990a for Karnic, Hale 1964 for Paman, and Koch 2004b for Arandic.

approach 40% before they interfere substantially with the recovery of a phylogenetic tree. Therefore we do not expect loans to have distorted the picture unduly, but we flag it as a potential concern. Work in this area is ongoing.

The problem of potentially unidentified loanwords requires addressing. Because correspondence sets that identify words as cognate are not clearly defined yet for much of the continent, and because the phoneme inventory sizes of many of the languages of the family are rather small, there is the possibility of either unidentified loans being treated as cognate, or chance similarities between groups being mistaken for cognates. Both of these problems can be dealt with. In the case of chance similarities, over a data set this size, we expect the proportion of chance similarities to be negligible in comparison to the number of genuine cognates. Chance similarities do not apply to a single word unequally, but to all potential subgroups and potential lexical items. We can therefore treat the possibility of chance similarities as one potential source of residual noise in the data.

With regard to unidentified borrowings, since current knowledge of the family does not allow us to remove all loan data, and removing some loans would result in applying different coding procedures to different subgroups, we favor a uniform coding strategy where we do not explicitly exclude loans from the data set; instead, they are flagged, but treated as cognate. While our subgrouping results may be affected by this decision, we note that where loan rates can be established in Australia, they are mostly below 10% (see §1.3). Low levels of loans will not affect overall identification of subgrouping, as noted above (Greenhill et al. 2009). Even if loans are as common as researchers such as Dixon (2002) claim, we should see the conflicting signal that results from borrowing as low posterior probability values for intermediate subgroups. Our approach to reconstructing ancestry is therefore conservative.

It is recognized that the identification of loanwords (and indeed, cognates more generally) assumes an implicit model of relationship. For example, Pirriya *djiloi* in 2 was tagged as a likely loan because forms related to **dhili* are otherwise confined to languages classified as Maric, while Pirriya is Karnic. This is a reason for not omitting or recoding putative loans at this stage; genuine ambiguities will show up in the posterior probability scores on the tree. If there are small numbers of loans, scores will not be affected unduly. However, if all 'similarities' between Pirriya and Maric languages were omitted on the grounds that Pirriya has been previously classified as Karnic, that introduces the potential for misclassification.[14]

Words were coded for cognacy according to strict semantic correspondence. Semantic shift counts against cognation for coding purposes (though not, of course, for wider study of the family). That is, words were not counted as cognate—or included in this data set—if they were present in the language in a different meaning. An example comes from words for 'eye' in Pama-Nyungan languages (see 2), which show a variety of polysemy and semantic cognate patterns. Western Desert *kuru* 'eye', for example, has likely cognates in Cape York Peninsula in the word **kuru* (Proto-Paman 'seed pod').

The cognate data analyzed here comprise 189 English glosses from 194 Pama-Nyungan languages. For phylogenetic analysis, these data were converted to binary char-

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[14] A referee points out that if cognates and loans have been identified using the comparative method, then some subgrouping has been presupposed, since the method relies on the identification of both regular sound correspondences and shared phonological innovations. While it is true that accurate loan identification relies on (among other things) knowing regular sound correspondences, knowing the correspondences alone does not give adequate subgrouping for a data set of the size and complexity of Pama-Nyungan. Many of the sound changes are either common or confined to a few languages, and thus of poor diagnostic power for family-wide subgrouping (though of considerable value for low-level subgrouping and for cognate identification).

acters representing the presence (1) or absence (0) of each cognate set in each language, producing a matrix of 14,613 binary characters (cognate sets) across the 194 languages.

2.3. BAYESIAN PHYLOGENETIC INFERENCE OF LANGUAGE TREES.

PHYLOGENETIC INFERENCE. We use Bayesian phylogenetic inference as implemented in BEAST (Drummond et al. 2012) to model language evolution as the gain $(0 \rightarrow 1)$ and loss $(1 \rightarrow 0)$ of cognates along the branches of a language family tree or 'phylogeny'. For a given tree and model of language evolution it is straightforward to estimate the likelihood of observed cognate data at the tips (Felsenstein 1981). The likelihood of a tree represents the probability of the observed data given the tree topology and our model of cognate replacement. One approach to phylogenetic inference is therefore to report the maximum-likelihood tree—that is, the tree that makes the observed cognate data most likely under our model. As mentioned above, however, the number of possible trees grows faster than exponentially with the number of languages (Felsenstein 2004), such that even for small numbers of languages we cannot hope to evaluate all possible trees. Further, even if we could evaluate the likelihood of all trees, the maximum-likelihood tree may not be the true tree. Other trees may fit the data almost as well, and inherent uncertainty due to the stochastic nature of the evolutionary process may mean we simply cannot differentiate between them. We examine the implications of this in the discussion section below (§4).

The Bayesian approach we employ here (Drummond & Rambaut 2007) uses Markov chain Monte Carlo (Metropolis et al. 1953) sampling algorithms to efficiently explore the universe of possible tree topologies and branch lengths describing the relationships between languages. An informal description of the algorithm is as follows. From a random starting tree, changes are proposed to the topology and branch lengths. Changes that improve the likelihood are kept, while changes that reduce the likelihood are accepted in proportion to the change in likelihood (such that changes to the tree that dramatically reduce the likelihood of the data are rarely accepted). This procedure produces a posterior distribution of language trees sampled in proportion to their posterior probability given the observed cognate data, some model of cognate evolution, and our prior beliefs about tree topology (such as knowledge about the existence of certain language groups or the age of those groups). Rather than committing to a single 'best' tree, the posterior distribution represents a sample distribution of trees we should consider plausible, given our data and assumptions. This distribution elegantly captures uncertainty in the parameters of interest—in this case, the tree. For example, a clade present in 90% of the sample thereby has an estimated posterior probability of 90%.

COGNATE REPLACEMENT MODELS. We begin by comparing the fit of three proposed models of cognate evolution (Atkinson & Gray 2006, Gray & Atkinson 2003, Gray et al. 2009, Nicholls & Gray 2006). First, following Gray and Atkinson (2003), we fit a simple binary model, which estimates the rate of cognate gain and loss through time, accounting for differences in the frequency of cognate presence (rare) versus absence (common) in the data and allowing for rates to vary across cognates according to a gamma distribution. Second, we fit the covarion model (Gray et al. 2009, Penny et al. 2001, Tuffley & Steel 1998), which extends the simple model by allowing the evolution of certain cognates to turn on and off through time. This is consistent with linguists' intuition that the rate of change of some cognate sets may vary across the tree. Finally, the stochastic Dollo model (Nicholls & Gray 2006) assumes that cognates can be gained once but lost multiple times. This may be a more natural model of language change and is consistent with the assumption (upon which much of historical linguistics is based)

that languages are highly unlikely to independently gain the same cognate, whereas cognates can be independently lost in descendant lineages. For example, given a tree in which languages A and B are sisters, with C as an outgroup, if a form *dhili* is present in A and C but not B, unlike the other two models, the stochastic Dollo model will always infer an origin of the *dhili* form at the common ancestor of A and C (and, necessarily, B), with subsequent loss in B.

RATES OF CHANGE. The amount of inferred change along each branch is used to estimate branch lengths proportional to time. These branches can be converted to an absolute time scale using known divergence events to calibrate rates of change. Here we use an arbitrary time scale because we are interested in the tree structure, not the absolute timing of events. While we do not infer absolute dates, any tree model implies a fixed amount of time from the root of the tree to the present. It is possible, however, that some lineages evolve more quickly than others. We therefore compare model fit under the assumption of a 'strict clock', in which cognates are assumed to evolve at a constant rate, to a lognormal relaxed clock model in which rates can vary across the tree (Drummond et al. 2006).

The analyses we report assume a yule prior distribution on branch lengths in the tree. The yule prior is commonly used in biology when inferring species trees and is based on a model of exponential waiting times between the emergence of new lineages. The yule prior distribution fits the data significantly better than the more flexible Bayesian skyline plot (Drummond et al. 2005), a prior based on models of lineage coalescence within genetic populations that allows the rate of lineage formation to vary through time. The choice of branch length prior did not affect our results. This is because the considerable branch length information in the language data tends to outweigh any reasonable priors we assign.

MCMC AND MODEL TESTING. We used BEAST (Drummond & Rambaut 2007) to run multiple independent MCMC chains for between fifty and one hundred million iterations each, sampled every 10,000 iterations, with the first ten million iterations discarded as burn-in. We used the Tracer component of BEAST to examine the post-burn-in likelihoods and other parameters of interest across the Markov chain. This revealed that runs had reached convergence by this time and effective sample sizes for all parameters were above 2,000. To compare the fit of the different models we used an importance sampling estimator of the marginal likelihood to obtain (the natural logarithm of) Bayes factors (Suchard et al. 2003). We report results for the best-fitting model.

We used the TreeAnnotator tool in BEAST to summarize trees in the form of maximum clade credibility (MCC) trees. Well-supported subgroups (both low-level and higher) will have high posterior probability scores.[15] Groups with extensive borrowing or parallel development will show up as conflicting subgrouping, which will lower posterior support for the corresponding clades. If a fan model is appropriate, we will see well-supported lower-level groups with large amounts of conflicting signals (and low posterior probabilities) for higher-level groups. While we assume all of the languages in the sample are related (the method we present was not designed to test the coherence of a Pama-Nyungan clade), unrelated languages are not a problem for the method. Isolates or unrelated groups will appear as outgroups with low posterior support.

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[15] There are no established cut-offs for 'excellent' versus 'adequate' support in consensus trees. We consider nodes to be well supported if the posterior probability is above 0.8, and to be poorly supported if the probability is below 0.5.

3. RESULTS. Table 1 shows results from the model comparison procedure. The stochastic Dollo model with relaxed clock produced the best fit to the data, with the highest ln P(model/data) (that is, the highest posterior probability). The Bayes factors show that this model is a significantly better fit than the next best model (BF > 100).[16] This supports the idea that the assumption of the stochastic Dollo model, that cognates are gained once and then differentially lost in descendant lineages, is a more natural model of vocabulary evolution than is captured under the simple time-reversible (binary) or covarion models. The better fit of the stochastic Dollo model also suggests that the borrowing of basic vocabulary terms in our data is rare and the chance of two languages independently innovating the same form for a given meaning is very low. This is consistent with the findings of Bowern et al. 2011.

MODEL	ln P(model/data)	SIMPLE		COVARION		S. DOLLO	
		strict	relaxed	strict	relaxed	strict	relaxed
Simple strict	–112700	—					
Simple relaxed	–112306	117	—				
Covarion strict	–112530	74	–97	—			
Covarion relaxed	–112118	253	81	179	—		
S. Dollo strict	–112060	277	107	204	25	—	
S. Dollo relaxed	–111791	394	223	320	142	117	—

TABLE 1. Log probability of simple binary, covarion, and stochastic Dollo models of cognate replacement with and without a relaxed clock. Also shown are the log10 Bayes factors (BFs; Newton & Raftery 1994) for all pairwise model comparisons. A BF of 5–20 is taken as substantial support, over 20 as strong support, and BFs greater than 100 are considered decisive (Kass & Raftery 1995).

A consensus tree of the stochastic Dollo (relaxed clock) model showing subgroups and their posterior probability values is given in Figure 5. A full tree showing all languages is provided in the supplementary materials. Subgroups that are not concordant with the previous literature on the languages are preceded by !. The maximum clade credibility tree for the relaxed covarion model is given in the supplementary materials.

4. DISCUSSION.

4.1. MODELING OF PRIMARY SUBGROUPS. Twenty-five of the twenty-eight previously identified Pama-Nyungan subgroups are supported by our analysis. This agreement bolsters support for these groups and provides further validation for our method. In addition, several of the tentatively proposed macro-groupings are well supported. These include Macro-Kulin (Blake & Reid 1994, 1998), the Pilbara languages (Kanyara-Mantharta and Ngayarta), and Nyungic, though without Thura-Yura. Kalkatungic is supported, contra Breen and Blake (2007), though with a deep ancestral node, reflecting early branching of the languages and a long period of independent development. Subgroups with posterior probabilities above 90% are Thura-Yura, Arandic, Wati, Marrngu, Nyungar, Kartu, Ngayarta, Kanyara-Mantharta, Warluwaric, Yolŋu, Kalkatungic, Mayi, Maric, Central New South Wales, Durubalic, Waka-Kabi, Kulin, Eastern Victoria (a macro-group including Yorta-Yorta, Gannai, and Pallanganmiddang), and Lower Murray.

Most isolates were plausibly placed within the tree as sisters to previously established groups: Bunganditj with Kulin, as proposed by Blake and Reid (1998); Gumbaynggirr with Durubalic, Bandjalangic, and Waka-Kabi; Muruwari as a sister to the

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[16] The covarion model with relaxed clock produced the second best fit to the data. We note that this model remained a significantly poorer fit than the stochastic Dollo model with relaxed clock regardless of whether we estimated the hidden frequencies of fast and slow evolving sites.
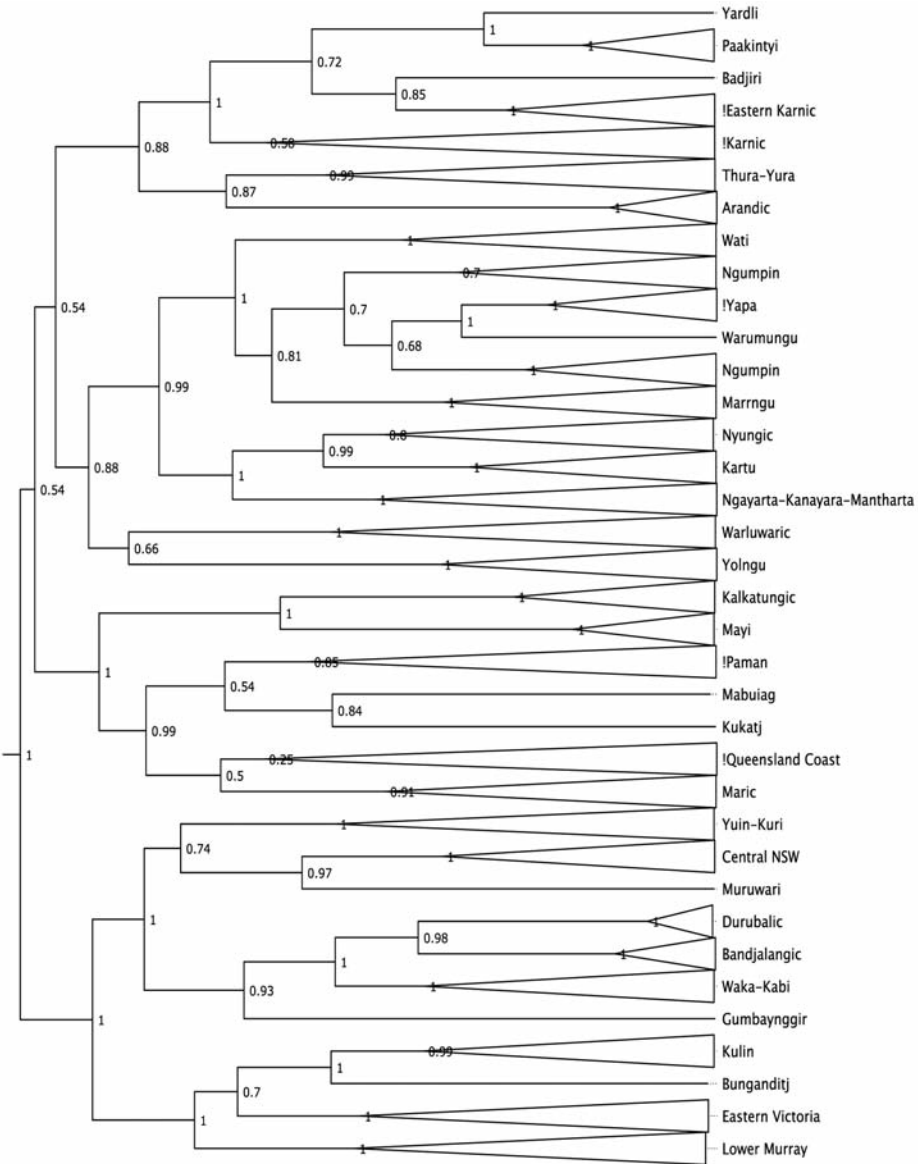
FIGURE 5. Pama-Nyungan subgroups. See the supplementary materials for a representation of the tree using DensiTree, which clearly represents the posterior uncertainty in certain subgroups, and for a full tree including individual language names.

Central New South Wales languages; and Paakantyi as a sister to Yardli (though see §4.2 below). The only isolates that were placed within established subgroups were Warumungu, which split Ngumpin-Yapa, and the Western Torres Strait language, which split Paman. These groups are discussed below.

   Discussion here focuses on the consensus tree of the relaxed stochastic Dollo model, though we give the tree of the covarion model in the supplementary materials for comparison. Although the covarion model returned much lower posterior probabilities overall, we note that the covarion model recovered Ngumpin-Yapa in accordance with the

existing literature, unlike the stochastic Dollo model. The covarion had an alternative grouping for both Karnic and Paman, which, while different from the stochastic Dollo model tree, also does not accord with results combined from phonology, morphology, and syntax. Given that the relaxed covarion model had a much lower posterior probability overall than the stochastic Dollo overall, we do not pursue systematic comparisons here.

4.2. NONRECOVERED SUBGROUPS. Out of the twenty-eight subgroups identified from the previous literature, three were not recovered in the consensus tree. These are the primary groups with the lowest posterior probabilities. The Karnic languages were not treated as monophyletic in the tree; instead, Eastern Karnic is grouped with Paakantyi and Yardli. Paman languages are split by Mabuiag, which is a Western Torres Strait language (Alpher et al. 2008). The languages of the North Queensland coast also appear to form a clade within Paman, which has not been previously suggested; this clade includes some languages previously considered to be Paman. Finally, the Ngumpin-Yapa subgroup is internally inconsistent, and includes Warumungu. Each is discussed in turn.

Before discussing the details of the nonrecovered groups, it is worth noting that Yardli and Ngumpin have some of the highest loan rates recorded for basic vocabulary. Furthermore, Paman and Maric languages were disproportionately affected by missing data, where 50% and 60% of languages in the subgroup respectively have more than 30% missing data. Karnic has 26% overall missing data, with half of the languages showing more than 30% missing data.

KARNIC AND YARDLI. Yardli is a small group of three languages (Yardliyawarra, Wadikali, and Malyangapa) to the southeast of the Lake Eyre Basin. These languages were previously grouped with the Karnic languages to the North, primarily on the basis of lexicostatistical evidence (O'Grady et al. 1966a), and this is the grouping that we find in the Bayesian analysis here (with posterior of 0.72); see Figure 6. Hercus and Austin (2004) and Bowern (2001) provide evidence that Yardli is not a subgroup of Karnic, however, using evidence from shared innovation in morphology. Yardli languages do not share the change of locative case to dative that is found in all Karnic languages, for example. The languages also have different pronouns and do not share a cluster of innovations in the Karnic pronominal system (see Bowern 2001 and Hercus & Austin 2004 for details).

There are several pieces of evidence that would make us question the strength of the lexical classification for this group. First, only one of the three Yardli languages has any data to speak of; Wadikali is known from only seventy-one words, and Yardliyawarra does not have many more. Only Malyangapa has decent attestation.[17] However, Malyangapa has high levels of missing data on the sample wordlist (31%), coupled with high loan rates (over 20%), with most of the loans coming from Karnic languages. This is a case where the combination of missing data and high levels of lexical loans may have biased results. Furthermore, Karnic languages themselves have been problematic for linguistic classification; see Austin 1990a, Bowern 1998, 2001, 2009, Breen 2007, and Hercus 1994 for details of the conflicts. Bowern 2010 concludes that the classification of Karnic is genuinely ambiguous and results from irreconcilable conflicts in the data, reflecting old, overlapping isoglosses (some morphological, some lexical). Within Karnic, apart from the placement of Yardli, the stochastic Dollo model provides lower-

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[17] The languages had low speaker numbers, and many speakers were killed in the Mindiri Massacre of the early 1880s (Hercus & Sutton 1986).
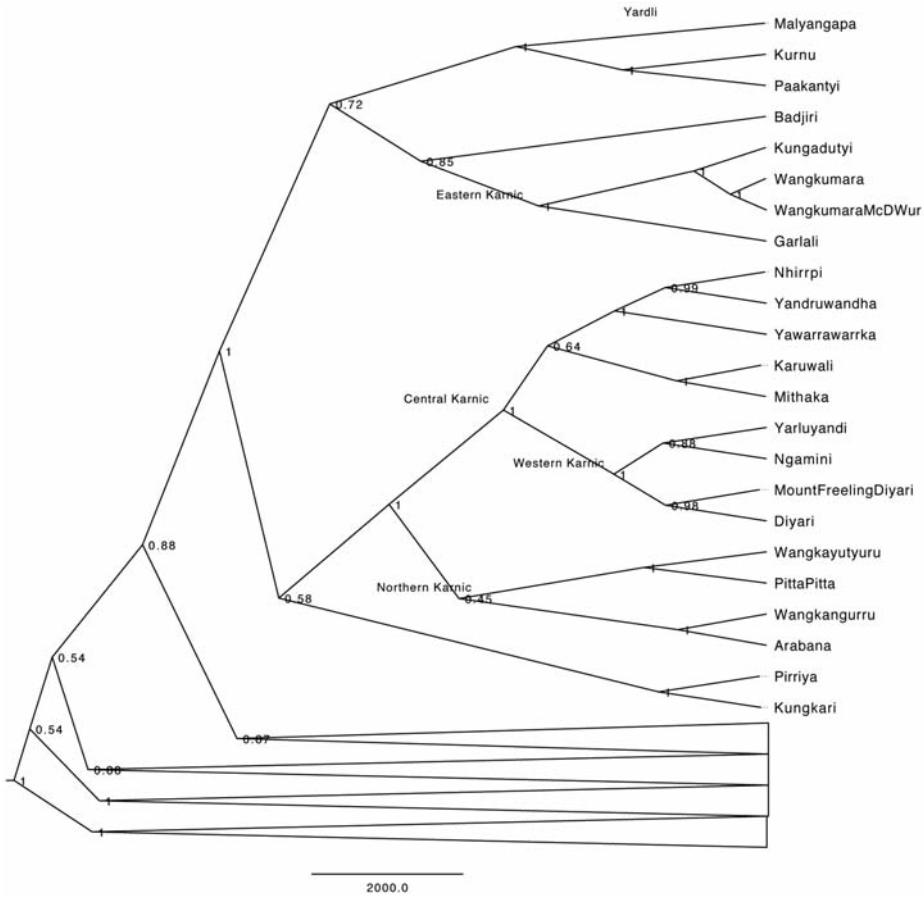
FIGURE 6. Karnic languages.

level internal groupings that are consistent with previous work. For example, our consensus tree includes Austin's (1990b) Central and Western Karnic groups, along with Northern Karnic (Bowern 2009, Hercus 1994).

WESTERN TORRES STRAIT AND PAMAN. The Western Torres Strait language (with the Mabuiag dialect represented in this survey) is grouped with Paman, as shown in Figure 7. This is unexpected, since no previous work has suggested that Western Torres Strait would be a likely member of the Paman subgroup. It has not undergone the sound changes that are characteristic of Northern or Middle Paman languages (Hale 1961, 1964, O'Grady 1976), and the morphology and syntax of the languages are quite different. Alpher and colleagues (2008) show that Western Torres Strait is clearly Pama-Nyungan, but the data they used did not allow them to be specific about further internal classification.

In this case, the difficulty of cognate identification is likely skewing results. Western Torres Strait has a very high percentage of unique data. Sixty-six percent of the words in the list had no identifiable cognates in other languages in the family (the highest level for any language in the sample), and many of those that do have good etymologies throughout the family are reconstructible to proto-Pama-Nyungan. That is, they are widely attested and not diagnostic for internal classification. These include *kosar* 'two'
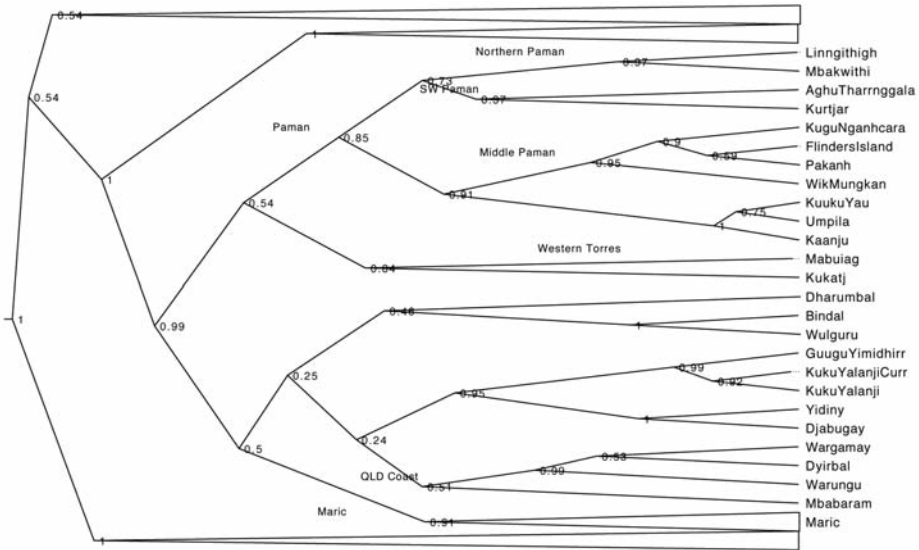
FIGURE 7. Paman languages.

<*kutyarra*, *tana* '3PL' < *tyana*, *ŋa* 'who' < *ŋan* (cf. Proto-Paman *wanytyu*), *sib* 'liver' < *tyipa*, *kalk* 'spear' < *kalka*, and so forth. In this case, the subgrouping with Paman (and Kukatj in particular) is likely being driven by very few cognate sets.

As noted above, Paman was undersampled; in particular, the diverse Southwest and Norman Paman subgroups (Alpher 1972, Alpher & Nash 1999, Black 2004) are represented by just three languages (Kurtjar, Kukatj, and Aghu-Tharnggala), two of which (Aghu-Tharnggala and Kurtjar) are sisters here. The grouping here recovers Northern Paman and Middle Paman, but higher grouping does not concord with the literature. One must consider, however, that our existing knowledge of Paman subgrouping is still preliminary. Hale (1964:263) notes that Paman itself is lexically diverse, and that the Northern Paman languages share considerably more vocabulary among themselves than they do with their southern neighbors. Alpher and Nash (1999:35–36) summarize the supporting evidence for existing Paman subgroup classifications, noting the slenderness of the evidence on which some groups are based. The position of Kukatj (Alpher & Nash 1999:36) is also noted as problematic. We leave aside further discussion of the internal structure of Paman, and its immediate neighbors, for future research.

NGUMPIN-YAPA. The Ngumpin-Yapa subgroup was identified first in McConvell & Laughren 2004,[18] though O'Grady and colleagues (1966a) earlier identified both Ngumpin and Yapa (which they called Ngarrga) as two of the twelve coordinate subgroups comprising Nyungic. McConvell and Laughren (2004:154) identify features that are Ngumpin-Yapa innovations, along with other features that are shared by Ngumpin-Yapa languages and are not found elsewhere in Nyungic, but cannot be shown to be exclusively shared innovations.

Ngumpin has two branches: Eastern and Western. In the results of the stochastic Dollo model, Eastern Ngumpin and Western Ngumpin do not form a single subgroup; rather, Eastern Ngumpin is split: the easternmost languages are a sister to Yapa and Warumungu,

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[18] Note, however, that McConvell and Laughren do not discuss lexical data in any detail in their presentation of evidence for subgrouping.

while the other Eastern Ngumpin languages are a sister to Western Ngumpin. This is shown in Figure 8. In addition, Warumungu, usually considered an isolate within Pama-Nyungan, is placed within the Ngumpin-Yapa subgroup as a sister to Yapa (Warlpiri and Warlmanpa).
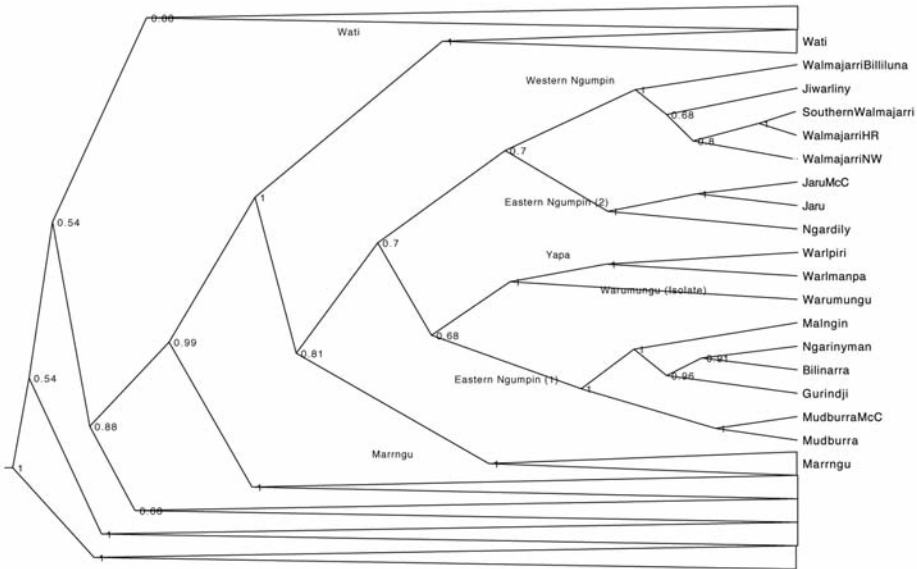

FIGURE 8. Ngumpin-Yapa languages.

The most likely reason for this is the very high number of loans between Eastern Ngumpin languages and surrounding non-Pama-Nyungan languages. The loans into the Eastern Ngumpin language Gurindji are discussed in some detail in McConvell 2009, while Bowern et al. 2011 provides more information about the regional context for the loans. Several Ngumpin languages are among the highest borrowers in the Australian sample in Bowern et al. 2011. Fifty percent of Gurindji's vocabulary on the list used here is borrowed from surrounding languages, and Mudburra has 38% loans. Many of these loans are shared within Eastern Ngumpin. For example, *purrp* 'all' is a loan from the non-Pama-Nyungan language Jaminjung into Gurindji, Mudburra, and Bilinara, and *majul* 'stomach' is from Wardaman into Gurindji and Mudburra. These loan patterns thus make some Eastern Ngumpin languages lexically quite distinct from their Western Ngumpin and Yapa neighbors.

Regarding the placement of Warumungu in Ngumpin-Yapa, an inspection of the cognate items that give this result shows that many are likely to be shared retentions from a shared ancestor beyond Ngumpin-Yapa. The languages share very few forms, and most of those that are shared have been reconstructed to Proto-Pama-Nyungan. These are (in total) *kana* 'digging stick', *pali-* 'die', *warlu* 'fire', *mayi* 'vegetable food', *Nuna-* 'lie down', *kuyu* 'meat', *puka* 'rotten', *waŋka-* 'speak, say', *nya:-* 'see', *parnti* 'smell', *wapa-* 'walk, go', and *ŋapa* 'water'. Other shared words are *wawirri* 'kangaroo', which is a loan from Arandic (see Koch 1997), *papulu* 'house' (found only in Warlpiri,[19] Warumungu, and the other Yapa language Warlmanpa), *jiman, jimanta* 'shoulder' (only found in Warlpiri and Warumungu and a likely loan), *junga* 'true',

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[19] A referee points out that *papulu* is only found in Eastern Warlpiri.

which has an areal distribution (Northern Wati, Yapa, Warumungu, and the Ngumpin language Ngardily), and *muku* 'all', found in Yapa and Warumungu. This suggests that Warumungu's placement here may be disproportionately affected by the small number of loans it shares with Warlpiri.

4.3. INTERNAL STRUCTURE IN LOWER-LEVEL SUBGROUPS. Where there are previous internal classifications within the primary subgroups, our tree recovers them. For example, we recover Eastern and Western Kulin (Blake & Reid 1998), the internal structure of Yolŋu (Schebeck 2002) (though see further below), Warluwaric (Brammall 1991), Thura-Yura (Simpson & Hercus 2004:183), Kartu (Marmion 2012:11), Central New South Wales (Austin 1997), Ngayarta and Kanyara-Mantharta (Dench 1994), Mayi (Breen 1981:17), and, as discussed above, the internal structures of Karnic.

Our internal Maric classification does not accord in all details with that presented by Barrett (2005). His Northern Maric (represented in our data sources by Warungu and in Barrett 2005 by Warungu and Gugu Badhun) groups in our tree with Dyirbal and Mbabaram. Barrett (2005:171) mentions these languages specifically as possible closer relatives to Maric within Pama-Nyungan, and Tsunoda (2011:10–12) discusses problems with the classification of Northern Maric within Pama-Maric. Within Yuin-Kuri, we recover all groups (though with more structure than previous classifications (e.g. Eades 1976), which list languages within major divisions of the subgroup). Wafer and Lissarrague (2008:167) group Birrpayi with Katthang rather than in the Iyora group. In our data set, Birrpayi clearly groups with Iyora rather than Katthang. This is shown by lexical differences, such as Iyora and Birrpayi *wiri* 'bad' (vs. Katthang *watyutu*), Dharuk and Birrpayi *muthaŋ* 'be alive' (vs. Katthang *kirraŋ*), Dharuk, Iyora, and Birrpayi *marri* 'big' (vs. Katthang *manuk*), and so on. We have no explanation for this discrepancy at present, though we note, following Wafer and Lissarrague (2008:168–69), that the name 'Katthang' (their 'Gadhang') is used ambiguously in the literature to refer to several different groups.

In some cases, we have more resolution within the tree than previous classifications. For example, Kite and Wurm (2004) give three coordinate branches of Waka-Kabi: Goreng, Waka, and Kabi. We find evidence that Goreng and Waka comprise their own clade within the subgroup. Likewise, previous treatments of the Central New South Wales subgroup do not discuss internal groupings, whereas we find evidence for a closer relationship between Wiradjuri and Ngiyambaa, with Gamilaraay and dialects as a sister. See above for discussion of Yuin-Kuri.

For the internal structure of Yolŋu, Schebeck (2002) lists ten languages without further higher structure. Heath (1980:1) has three groups: Western (Djinang and Djinba), Southern (Dhuwal(a), Dhay'yi, and Ritharrngu), and Northern (Dhaangu, Djaangu, Nhaangu). Our tree does not find evidence for Northern Yolŋu, with Nhaŋu (represented by Yan-nhaŋu) a sister to Southern Yolŋu plus Dhaŋu/Djaŋu. Heath's (1980) classification is highly tentative. Bowern 2007 tentatively concluded that Heath's Western and Northern groups formed an intermediate subgroup, but did not regard the evidence for Northern Yolŋu as conclusive, since so many of the features the languages share are retentions from Proto-Yolŋu. The internal classification of this group must therefore at this stage be regarded as underresearched.

Thus in summary, of the subgroups that were not recovered by this method, one has been the subject of continuing debate in the linguistic literature and two were compromised by isolates with high levels of unique data. Furthermore, while some of our internal classifications for lower-level subgroups do not accord with published standards,

we note that in those cases, the standards are either disputed or themselves regarded as tentative or problematic by their authors.

4.4. The major divisions of pama-nyungan. Let us now consider the novel upper groups identified in this consensus tree. Four major divisions have strong support in the consensus tree. These groups are summarized in 3 below, along with other well-supported internal divisions and lower-level subgroups identified in previous comparative work on Pama-Nyungan languages. Example 3 gives major divisions, but note that not all nodes identified in Fig. 5 are represented here; the text summary is intended as a schematic guide only.

First is a southeastern group, comprising (i) the languages of Victoria and southeast South Australia (the Lower Murray subgroup), the languages of Central New South Wales, and the languages east of the Great Dividing Range from south of the Victorian border to Brisbane.[20] Second is a northern group, with a primary split between the Gulf subgroups Kalkatungic and Mayi on the one hand, and the languages of Queensland (Pama-Maric and other languages of the Northern coast, such as Dyirbal) on the other. As discussed in §4.2 above, however, the internal classification of these languages requires further work. The third major division is the languages of central australia and 'corner country' (the area where South Australia, Queensland, and the Northern Territory adjoin), with a divide between Arandic and Thura-Yura on the one hand, and Karnic, Paakantyi, and Yardli on the other. The fourth major division is the languages of the western half of the country, with a (albeit poorly supported) split between Yolŋu and Warluwaric versus the rest of the languages in the group, and then a further split between the languages of the Western Desert regions (Wati (Western Desert), Ngumpin-Yapa, and Marrngu) and those of the Southwest (extending from the Pilbara to Kartu and Nyungar, including Mirniny, spoken along the Great Australian Bight).

(3) 1. Southeastern
    (a) Victorian
        i. Lower Murray
        ii. Victorian
            A. Eastern Victoria
            B. Macro-Kulin (Kulin and Bunganditj)
    (b) New South Wales
        i. Yuin-Kuri
        ii. Central NSW (+ Muruwari)
    (c) North Coast
        i. Durubalic
        ii. Bandjalangic
        iii. Gumbaynggir
        iv. Waka-Kabi
  2. Northern
    (a) Gulf
        i. Kalkatungic
        ii. Mayi
    (b) Pama-Maric (weakly supported; see §4.2)

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[20] Note that parts of the tree are 'flattened' in the text description in 3 in order to avoid giving names to many new internal nodes.

    3. Central
      (a) ...
          i. Thura-Yura
          ii. Arandic
      (b) Southwest Queensland
          i. Karnic (see §4.2)
          ii. Northwest NSW (Yardli and Paakantyi)
            A. Yardli
            B. Paakantyi
    4. Western
      (a) ... (weakly supported)
          i. Warluwaric
          ii. Yolŋu
      (b) Nyungic
          i. Desert
            A. Marrngu
            B. Ngumpin-Yapa (and Warumungu; see §4.2)
            C. Wati
          ii. Southwest
            A. Pilbara (Ngayarta and Kanyara-Mantharta)
            B. Kartu
            C. Nyungar

There is also weak evidence that the Central and Western groups may group together, and that the Northern group may be a sister to that group. Posterior probabilities for those nodes are low, however, at 0.54. Many other trees have the Northern group as a primary division; there is also support for a combined Central and Northern group, as can be seen in the DensiTree figure (Bouckaert 2010) in the supplementary materials.[21] Given this uncertainty, we treat these four groups as involving soft polytomies, and treat the highest level of classification as, at this point, unproven. It is possible that further work on the Northern group (which includes Paman) will clarify this issue.

One might wonder whether these groups reflect long-standing areal contact rather than shared genetic inheritance, especially where rates of lexical replacement have been high and the posterior support is low. There is certainly geographic patterning in the tree, in that (with the exception of Yolŋu and parts of Warluwaric, which are separated from other Pama-Nyungan languages by intervening non-Pama-Nyungan languages) all major divisions and subgroups form continuous blocks. However, contact is not likely to be producing all of the patterns seen here. For example, Thura-Yura and Arandic, though close geographically, are not in contact with one another; Wati and Karnic languages intervene. Central New South Wales and Yuin-Kuri are adjacent, but separated by the natural barrier of the Great Dividing Range. Conversely, some high-contact zones are not reflected in the phylogeny. For example, Wati languages and Wirangu (the westernmost Thura-Yura language) have been in considerable contact, especially in the period around European settlement (Hercus 1999:2–3). Likewise, Waka-Kabic and Maric, Arandic and Ngumpin-Yapa, and Ngayarta and Marrngu languages all have documented loans, trade routes, and strong mythological and cultural connections between them, but none of these contact patterns are reflected in the consensus tree.

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[21] DensiTree plots the tree samples from the MCMC analysis individually. It thus provides a convenient graphical representation of the degree of support for particular nodes, and for competing hypotheses.

5. CONCLUSIONS. In conclusion, the early history of Pama-Nyungan is not beyond the reach of historical work. There are sufficient data, and loan levels are comparable to rates found elsewhere in the world. The only area where loan rates may be distorting the phylogeny is in Ngumpin-Yapa, where Eastern Ngumpin languages are known for their exceptionally high loan rates (some of the highest in the world; McConvell 2009). This work highlights the utility of lexical work in the Pama-Nyungan family, which has previously been overlooked in favor of morphological reconstruction. We hope that the publication of this tree will spur other Australianists to examine their regions of expertise for evidence that may confirm or refute the phylogenetic structure proposed here.

Our work puts to rest once and for all the claim that Australian languages are so exceptional that methods used elsewhere in the world do not work on this continent. The methods presented here have been used with Bantu, Austronesian, Indo-European, and Japonic languages (among others). Pama-Nyungan languages, like all languages, show a mixture of histories that reflect both contact and inheritance. Producing accurate phylogenies is an important part of examining the interplay of these processes in all languages, and Australian languages are no exception here.

This phylogeny provides a unique insight into Australian cultural ancestry and prehistory. We would argue that the best hope for future prehistorical research in Australia is linguistic data. Though there is, of course, much work on the archaeology of Aboriginal Australia, the majority of dating work has focused on the dates for earliest settlement (McConnell & O'Connor 1997, Mulvaney & Kamminga 1999, O'Connell & Allen 2004, O'Connor 1999). Moreover, the Australian archaeological record is not well differentiated and research is not evenly spread across the country. Genetic data for Aboriginal Australia is not plentiful, and since researchers almost never recorded detailed metadata about the people who gave the samples, it cannot be used for detailed research that relies on distinguishing group affiliation. Language data, however, can provide us with detailed information about past contacts, migration, and location.

Finally, Pama-Nyungan research provides us with a unique insight into hunter-gatherer language dynamics. Our lexical reconstructions form the largest data set for any hunter-gatherer language family, and second only in size to Greenhill and colleagues' (2008) Austronesian Basic Vocabulary Database. Pama-Nyungan is the largest attested hunter-gatherer language family, yet until now it has been omitted from discussions of hunter-gatherer language change, on the grounds that it was either atypical of language change, or insufficiently resolved to allow conclusions to be drawn. It also opens up work on studying patterns of language and cultural coevolution (Fortunato & Jordan 2010, Jordan et al. 2009, Mace & Jordan 2011), an area that is severely under-researched in both Australian languages specifically and hunter-gatherer languages more generally.

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