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Social complexity and linguistic diversity in the Austronesian and Bantu population expansions

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Reconstructing the rise and fall of social complexity in human societies through time is fundamental for understanding some of the most important transformations in human history. Phylogenetic methods based on language diversity provide a means to reconstruct pre-historic events and model the transition rates of cultural change through time. We model and compare the evolution of social complexity in Austronesian ($n = 88$) and Bantu ($n = 89$) societies, two of the world's largest language families with societies representing a wide spectrum of social complexity. Our results show that in both language families, social complexity tends to build and decline in an incremental fashion, while the Austronesian phylogeny provides evidence for additional severe demographic bottlenecks. We suggest that the greater linguistic diversity of the Austronesian language family than Bantu likely follows the different biogeographic structure of the two regions. Cultural evolution in both the Bantu and Austronesian cases was not a simple linear process, but more of a wave-like process closely tied to the demography of expanding populations and the spatial structure of the colonized regions.

Keywords: social complexity; language family; Austronesia; Bantu; population expansions

1. INTRODUCTION

A fundamental question in anthropology is how and why small-scale societies developed into large-scale societies [1–5] and how and why large-scale societies inevitably fail [6–8]. Cultural evolution from community- to state-level social organization and vice versa entails enormous changes in authority, bureaucracy, complexity, hierarchy and inequality. Here, we compare the spatio-temporal dynamics of social complexity in two major prehistoric linguistic expansions; the Austronesian expansion across southeast Asia and Oceania, and the Bantu expansion in sub-Saharan Africa. Our goal is to understand how social complexity evolved within these expansions, the possible demographic drivers and the resulting impact on language diversification.

Cultural evolution can be viewed as a branching-like process where non-biological information is transmitted among individuals over time and space with varying fidelity resulting in differential success, which is then subjected to various cultural, physical and biological selective processes [9–11]. While the mechanisms that drive cultural evolution are complex, at a broad-scale there is a clear correlation between population size and social complexity. Recent research has shown that technological complexity scales closely with population size [12,13], and the sampling effects of small population sizes or geographical isolation can reduce technological diversity through demographic bottlenecks and consequent cultural founder effects [14,15]. In addition, smaller populations are likely to innovate less than larger populations, as innovation rates in human societies scale super-linearly with population size, and so as a

population increases in size, innovations occur at an increasingly faster rate [16].

Population size is closely correlated with the structural complexity of social systems [1], owing to the inherently modular and self-similar organization of human social networks. In general, the least complex human systems are hunter–gatherer societies where population sizes are generally in the order of a few hundred to a few thousand [17], while the most complex are large-scale states with population sizes in the order of several thousands to millions [18,19]. Thus, the dynamics of cultural evolution must be, in large part, tied to demography, and the need to manage information and resource flows in increasingly larger populations [20]. While all population expansions are internally complex processes, expansions of agricultural populations have the additional dimension of socio-political complexity, as both population size and the level of socio-political organization are closely correlated with economic dependence on agriculture. Indeed, data from 98 societies taken from the ethnographic atlas (figure 1*a*) demonstrate that average population size increases exponentially with dependence on agriculture, where a 10 per cent increase in agricultural dietary dependence results in a 50 per cent increase in the expected population size. Similarly, the maximum level of social complexity exhibited by a society increases predictably with per cent dependence on agriculture (figure 1*b*), such that any level of social complexity higher than the level of 'petty chiefdom' requires a predominantly agricultural economy. Therefore, given the inherent demographic instability of populations during expansion phases, any fluctuations in population sizes during agricultural expansions probably would have impacted local levels of socio-political complexity.
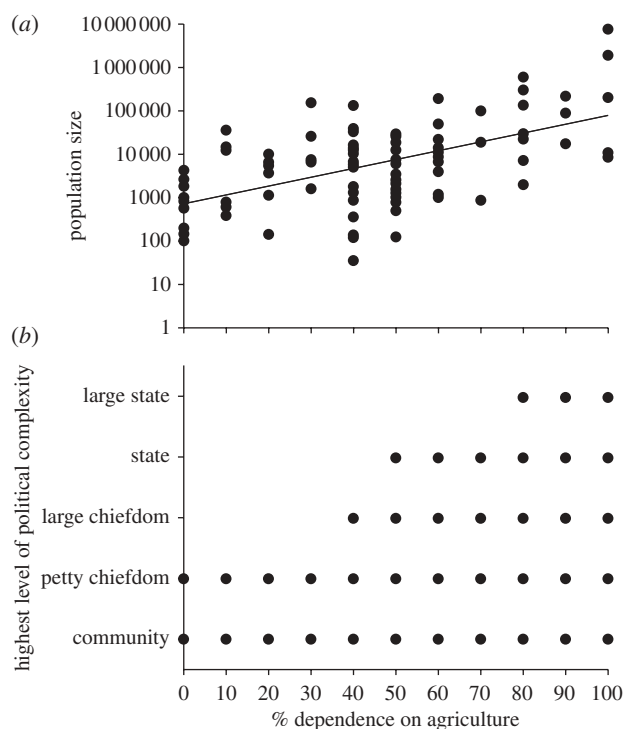
Figure 1. The positive relationships between per cent dependence on agriculture and population size (*a*) and level of political complexity (*b*). Data are global from the Ethnographic Atlas [29] and the Ethnologue [37]. $y = 733e^{0.05x}$; $r = 0.56$, $p < 0.0001$.

Figure 2. Two hypothetical patterns for the evolution of social complexity. (*a*) Complexity gradually increases through time and then crashes (saw-tooth pattern). (*b*) Complexity gradually increases and decreases through time (wave-like pattern).

Here, we use an explicit phylogenetic approach to study and compare the evolution of human socio-political complexity in two of the world's largest and better-studied population expansions: Austronesian languages of southeast Asia and Oceania, and Bantu languages of sub-Saharan Africa. While the exact timings of the initial expansions are unclear in either region, current estimates suggest they were approximately contemporaneous: the Bantu expansion likely began approximately 5000 years ago [21] and the Austronesian expansion approximately 5200 years ago [22]. Both were fuelled, primarily, by populations with agricultural socio-economies [22,23]. Importantly, however, the Austronesian expansion was primarily oceanic, colonizing hundreds to thousands of previously unoccupied islands separated by vast distances, leading to major biotic extinction events and widespread ecological changes throughout the broader region, whereas the Bantu expansion was entirely terrestrial, displacing the indigenous hunter–gatherers and pastoralists of sub-Saharan Africa through a combination of demic replacement, cultural assimilation and the diffusion of agricultural technologies [23].

By definition, historical processes cannot be directly observed, but fortunately phylogenetic methods can help to reconstruct past events. Rigorous methods developed by evolutionary biologists are increasingly used by anthropologists studying the evolution of culture [24,25]. Phylogenetic trees based on language have proven vital for reconstructing human population and cultural histories [22,26,27], and many studies have shown that much cultural variation is well described by a process of descent with modification [10,24]. In this paper, we use Bayesian phylogenetic methods to directly mo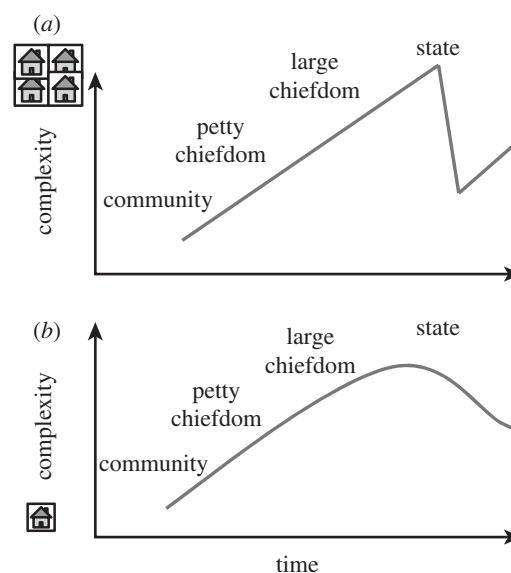del the rates of change from one state of social complexity to another while adjusting for phylogenetic uncertainty inherent to language trees [9,11,28].

2. METHODS

We evaluate two hypothetical patterns for the evolution of social complexity. We then compare these two patterns with the actual modelled rates of social complexity evolution in Austronesian and Bantu language families. Under one hypothetical pattern, social complexity gradually increases through time via incremental steps and then suddenly drops. We call this the saw-tooth pattern. Under another pattern, social complexity gradually increases over time, but then tends to decrease gradually through time. We call this the wave-like pattern (figure 2). We refer to positive state changes in social complexity (e.g. community to petty chiefdom) as ascensions, and negative state changes (e.g. petty chiefdom to community) as descensions. Further, if ascensions or descensions are sequential (e.g. large chiefdom to states or vice versa), we refer to them as *single* ascensions or descensions, but if complexity changes bypass intervening stages (e.g. community to large chiefdom), we refer to them as *multiple* ascensions or descensions.

The Austronesian and Bantu language families are ideal for studying cultural complexity because their constituent societies encompass a wide range of human social organization. The Ethnographic Atlas [29] provides data on 'Jurisdictional hierarchy beyond local community' with five possible levels: (i) no political authority beyond community, (ii) petty chiefdoms, (iii) larger chiefdoms, (iv) states, and (v) large states. Given the rarity of large states in Bantu and Austronesian language families, we collapsed levels (iv) and (v) together into a single category of 'state'. Data are available for 88 Austronesian and 89 Bantu societies.

Bayesian approaches to phylogenetic inference have been increasingly used for estimating phylogenetic trees and assessing the uncertainty inherent to phylogenetic reconstructions [30,31]. Bayesian inference is a statistical framework based
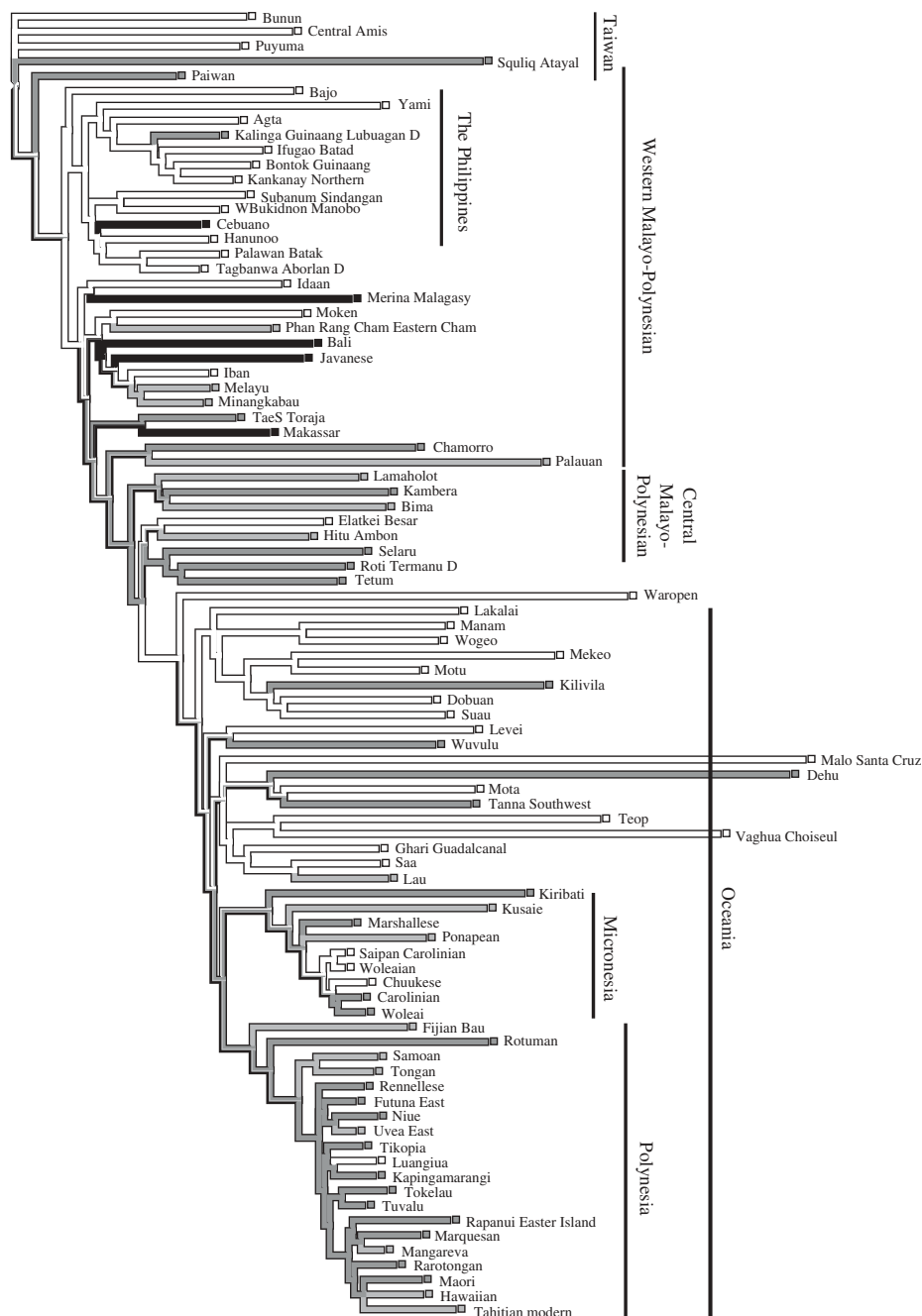
Figure 3. Stochastic character mapping for Austronesian social complexity where white represents community-level; lighter grey, petty chiefdom; darker grey, large chiefdom and black, state. Most internal nodes have uncertain reconstructions.

on the posterior distribution that is obtained by combining the prior distribution with information contained in the data using methods such as Markov chain Monte Carlo (MCMC) algorithms. The posterior probability of a tree is the probability of the tree conditional on the data and can be interpreted as the probability that the tree is correct [31]. Bayesian MCMC phylogenies based on cognates in basic vocabulary are available for both Austronesia [20] and Bantu [32,33].

We used Bayesian MCMC reconstructions performed in BayesTraits [28] and stochastic character mapping in MESQUITE software for visualizing results [34,35]. Bayesian methods have the advantage of estimating transition rates across a large number of trees. Model parameters are sampled in proportion to their likelihood, and therefore provide intuitive posterior distributions for transition rates. We sampled model parameters over 1000 Bayesian MCMC

trees. Gamma-distributed hyperpriors and a covarion model were used for all Bayesian analyses with the rate deviance set to ensure that acceptance rates were between 20 and 40 per cent. Chains were run for 20^8 generations sampling every 10^4 to reduce autocorrelation. The initial half of the run was removed to allow ample burn-in. Significance tests of transition rates in social complexity are based on likelihood-ratio tests of nested models. We systematically removed the lowest transition rate and set it to zero until the model showed a significantly worse fit to the data. The likelihood-ratio test compares the goodness-of-fit of a model to the data with that of a simpler model that lacks one or more of the parameters [28]. These nested models are evaluated with Bayes factors (estimated as twice the difference in the harmonic mean of the likelihoods), where a decrease greater than three is considered support for inclusion of the particular rate being set to zero.
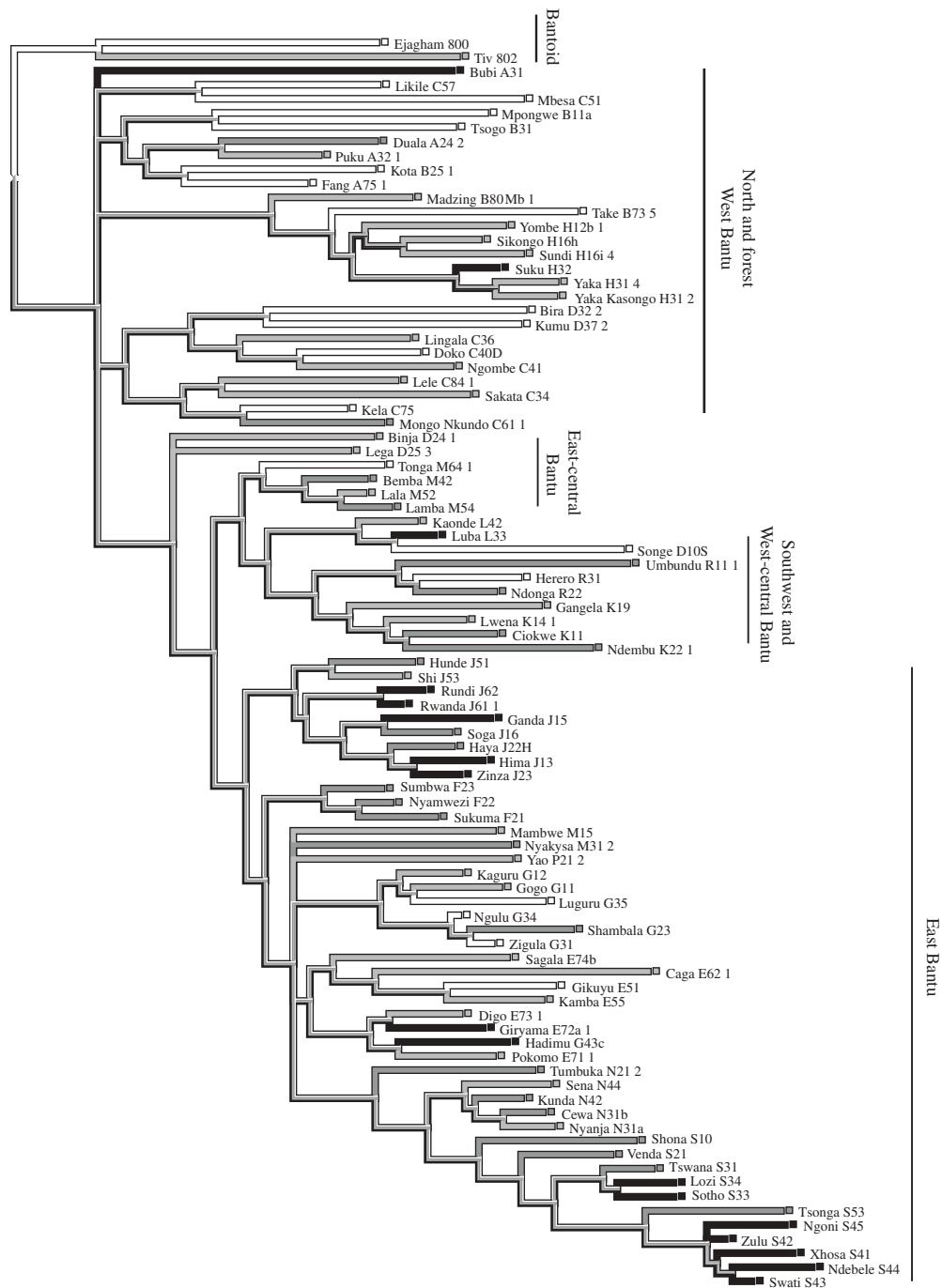
Figure 4. Stochastic character mapping for Bantu social complexity where white represents community-level; lighter grey, petty chiefdom; darker grey, large chiefdom and black, state. Most internal nodes have uncertain reconstructions.

3. RESULTS

A first step in phylogenetic analysis is to estimate the ancestral condition of the populations prior to expansion. Both Austronesian and Bantu roots may have had community-level organization, although the Bayesian reconstructions are far from certain with posterior probabilities of the four states not differing much from their prior probabilities of 25 per cent. The average posterior probability of a community-level organization in proto-Bantu is 32 per cent (compared with 25% petty chiefdom, 22% large chiefdom and 21% state; figure 3) and the posterior probability of a community-level organization for proto-Austronesia is 35 per cent (compared with 23% petty chiefdom, 21% large chiefdom and 21% state; figure 4). Bayesian analyses suggest that Bantu

petty chiefdoms may have spread across most of sub-Saharan Africa turning into states in at least four separate clades. In contrast, Austronesian expanding populations were more likely community-level organization that subsequently developed into chiefdoms in multiple clades (e.g. Micronesia and Polynesia), developing into state-level societies in perhaps four clades, and retaining community-level organization in many others (e.g. Taiwan and the Philippines). However, the uncertainty in the phylogenetic reconstructions is substantial and severely limits our ability to accurately reconstruct the social complexity in many of these prehistoric populations.

The differences in transition rates summarized in table 1 reflect important contrasts in the dynamics of social complexity between the Austronesian and Bantu

Table 1. Mean transition rates of changes from one state of social complexity to another for Austronesian and Bantu language families based on Bayesian analysis. Transition rates are means from the posterior probability distributions from the full model with all possible rates included. Significance tests are based on likelihood-ratio tests of nested models that remove the lowest rate and set it to zero. The statistically significant transition rates from the final reduced model are in parentheses. Transition rates represent the rate of change with respect to linguistic distance and can therefore be conceptualized at rates of change per unit time. Note that transition rates are comparable within language family but are not comparable between Austronesia and Bantu languages because phylogenies were based on different numbers of vocabulary words (210 and 100, respectively).

	Austronesian rate	statistically significant?	Bantu rate	statistically significant?
single ascension				
community → petty chiefdom	46 (61)	yes	80 (61)	yes
petty → large chiefdom	121 (148)	yes	66 (64)	yes
large chiefdom → state	41 (79)	yes	45 (40)	yes
multiple ascension				
community → large chiefdom	17	no	70	no
community → state	19	no	36	no
petty chiefdom → state	16	no	32	no
multiple decension				
state → community	92 (82)	yes	49	no
state → petty chiefdom	78 (63)	yes	64	no
large chiefdom → community	87 (84)	yes	59	no
single decension				
state → large chiefdom	83 (83)	yes	75 (62)	yes
large → petty chiefdom	122 (110)	yes	92 (91)	yes
petty chiefdom → community	62 (70)	yes	55 (45)	yes

expansions. These transition rates represent the rate of change with respect to linguistic distance and can therefore be conceptualized at rates of change in social complexity per unit time. Transition rates near zero represent unlikely or rare events, whereas fast rates represent common events. Our results show that multiple ascensions in both Austronesia and Bantu can be classified as rare events since these transition rates are not significantly different from zero. In other words, social complexity often tends to increase as an incremental process. However, the rates of multiple descensions in the Austronesian expansion are statistically significant indicating saw-tooth-like evolution. In contrast, the Bantu expansion exhibits primarily a wave-like pattern of evolution in social complexity where both increases and decreases in social complexity are incremental. Overall, the Bantu expansion exhibits a more even distribution of the probability of ascensions and descensions (0.44 versus 0.56, respectively) than the Austronesian tree, where the probability of descensions (0.67) is twice as large as ascensions (0.33). These results show that while both expansions exhibit underlying wave-like oscillations in social complexity over time, the Austronesian tree records a much higher multiple descension transition rate than the Bantu tree, indicating frequent and rapid declines in social complexity.

4. DISCUSSION
Our results demonstrate that the evolution of social complexity in the Austronesian and Bantu population expansions were internally dynamic. The Austronesian expansion clearly exhibited a more saw-tooth like profile in social complexity dynamics, presumably because the expansion was comprised of multiple discrete colonization events of widely dispersed island land masses, which would have led to frequent rapid reductions in social complexity.

While rapid reductions in complexity were frequent, archaeological data provide compelling evidence that rapid increases in complexity also occurred in the region [36]. In contrast, the dynamics of the Bantu expansion were more wave-like exhibiting gradual increases and decreases through time, with an overall net increase in social complexity over the expansion phase.

The marked differences in the dynamics between these expansions are probably related to the different biogeographic settings within which the expansions occurred. The Austronesian expansion involved the long-distance oceanic colonization of previously uncolonized and often small, remote island clusters, separated from neighbouring island clusters by vast distances. Such an expansion would necessarily result in frequent demographic colonization bottlenecks (and their associated founder effects), and unavoidable isolation by distance of local populations, despite the development of extensive transoceanic trade networks throughout the Pacific. As such, the colonization of Oceania was a discrete step-like process.

The Bantu expansion, on the other hand, was almost entirely a terrestrial process, where colonizing agricultural populations displaced, assimilated and converted much of the indigenous hunter–gatherer and pastoralist populations of sub-Saharan Africa to agriculture. The Bantu expansion likely involved fewer and less severe demographic bottlenecks by maintaining greater population connectivity than Austronesian populations resulting in different regional demographics.

The differing evolutionary dynamics of social complexity in these two vast regions also affected the evolution of linguistic diversity within the two language families. There are about 691 Bantoid languages and about 1257 Austronesian languages [37], an almost two-fold difference. Assuming that both expansions began

with a single language, it follows that the mean annual rate of language diversification was about twice as fast in Austronesia than Bantu (1257/5000 = 0.25, and 680/5230 = 0.13, respectively), probably reflecting the different colonization histories, and consequent population sub-structures of the two language families. These rates indicate remarkably rapid linguistic evolution with a new language originating, on average, about every 4 years in Austronesia and every 8 years in sub-Saharan Africa. While the diversification of the Austronesian language family was clearly exacerbated by the geographical structure of Oceania and the isolating mechanism of widely dispersed island clusters, it is somewhat remarkable that the terrestrial Bantu expansion also shows such rapid rates of ethnolinguistic evolution.

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