

Inheritance and convergence in Bantu lexicon and morphosyntax: A new phylogenetic study

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With about 350-400 languages the Bantu family is an ideal testing ground for the study of language relationship and micro-variation. Traditionally, research in comparative Bantu has focused on the study of innovation and divergence, with a view to developing a genetic sub-classification of Bantu languages (e.g. Heine et al. 1977, Ehret 1999, Nurse and Philippson 2002). Recent work by Grollemund et al. (2015) has proposed a genetic sub-classification of Bantu based on a phylogenetic study of a comparative word list of 100 lexical items, which is then correlated with historical and archaeological data.

However, convergence effects in Bantu have also been noted (e.g. Möhlig 1981, 1983, Marten et al. 2007), and have been related to the dynamics of multilingual language ecologies and language contact. Focussing on convergence effects, rather than on shared innovations, may result in a different picture of the relationship between Bantu languages.

In this talk we further develop the idea that different structural relations obtain between the Bantu languages. We employ phylogenetic methods to compare lexical and morphosyntactic data of the same languages and show that they result in different groupings. Taking the lexical classification proposed by Grollemund et al. (2015) as a starting point, we develop a phylogenetic analysis of 39 Bantu languages based on 136 morphosyntactic features (Guérois et al. 2017) from data in the Bantu Morphosyntax Variation database (Marten et al. 2019).

The results of the study indicate a difference between lexical and morphosyntactic groupings:

- The main division of the lexical classification can be related to geographic distribution – roughly, East vs. West
- In contrast, the main division of the morphosyntactic classification can more easily be related to a division between four different convergence areas: Northwest, Northeast, Centre and South

We propose that the lexical results reflect genetic relations and long-term history, while the morphosyntactic results reflect convergence effects through language contact and more recent history. Interestingly, the three of the four convergence groups map well into wider African linguistic areas which have been identified previously (see Heine and Nurse 2007) – the northwest area as part of the Macro-Sudan belt, the northeast as part of the Rift Valley, and the South as part of the Kalahari Basin – all of which are characterised by diffusion of features across genetic boundaries. Furthermore, we propose that the Central area likewise results from diffusion, but in this case within the overall Bantu family, a process identified as centripetal convergence (Marten et al. 2016, Gibson and Marten 2019).

The analysis is further supported by a comparison of the rate of change of the two feature sets, which shows that morphosyntactic features evolve faster than lexical ones.

The talk shows the value of morphosyntactic data for comparative Bantu, but also the value of the use of quantitative methods for the study of morphosyntactic variation, both in Bantu and more broadly. It provides novel, quantitative evidence for the relation between language change and language contact, for the conception of linguistic areas, and the difference in diachronic processes affecting lexical and morphosyntactic features.

Keywords

Bantu languages, convergence, phylogenetic methods, language contact, linguistic areas

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