

Internal subgrouping of Northern Naga based on Bayesian phylogenetic analysis

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This paper presents the results of a large-scale study of the internal subgrouping of Northern Naga using Bayesian inference on lexical data sets. Data are analysed from approximately 140 central Sal dialects covering approximately 750 concepts. Concepts cover many of the most stable etyma (Matisoff 2009) as well as many culturally-relevant concepts such as those described in Matisoff (1978). Further concepts were incorporated based on frequency of inclusion in the literature.

The data used in the study include both published and unpublished wordlists as well as newly elicited lexical data. Efforts were made to include all extant published source material on the languages which provided sufficient lexical data, including descriptions from as far back as the early 19th century. Lexemes were then hand-coded for cognacy based on regular sound correspondences, as determined by newly done historical reconstructions at various levels in the family. As a lack of archaic written data precludes estimations of time depth, with the oldest sources still too recent for proper clock calibration, analysis was done in MRBAYE (Huelsenbeck et al 2001) using Markov Chain Monte Carlo sampling.

The resulting phylogeny confirms a clear north-south split in the family (van Dam, forthcoming), with the northern branch corresponding directly to the Tangsa-Nocte subgroup, and an additional primary split among the southern branch roughly corresponding to the political boundary between India and Myanmar. Lower level subgrouping also confirms many of the previous judgements on subgrouping found in the literature based on both lexical and non-lexical features (Morey 2015; van Dam 2018).

Keywords

Bayesian phylogeny, Tibeto-Burman, Sal, Northern Naga

References

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