

A combined comparative and phylogenetic analysis of the Bosavi and East Strickland languages.

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Trans-New Guinea, one of the world's largest language families, has long been a challenge for historical linguistics. Originally proposed in the 1970s on the basis of the first large-scale documentation and comparison of Papuan languages of the New Guinea region (Wurm 1975), there is still relatively little known about the family's origins and evolution. This talk aims to expand our understanding of the history of Trans-New Guinea by using both traditional methods of historical linguistics and Bayesian phylogenetic approaches to reconstruct linguistic and sociolinguistic histories for small groups of Trans-New Guinea languages.

The languages of the Mount Bosavi region straddle the boundary between the Southern Highlands and Western Provinces of Papua New Guinea, and are generally taken to be part of the Trans-New Guinea language family – although this is not universally accepted (Hammarström et al. 2016). If the Bosavi languages do belong to Trans-New Guinea, it is either as a small subgroup within a much bigger grouping that includes languages further south and west (McElhanon and Voorhoeve 1970) or as two primary subgroups and an isolate language within the family (Ross 2005). Traditionally, people in this region lived in scattered longhouse communities that were connected through marriage alliances and trading routes, and which are described by Shaw (1973, 1986) in terms of three linguistically- and culturally-defined groups: (i) the Strickland Plain or East Strickland languages spoken along the eastern bank of the Strickland River; (ii) the Papuan Plateau languages spoken to the north and west of Mount Bosavi; and (iii) the Bosavi Watershed languages spoken to the south of Mount Bosavi.

In this talk we explore the evidence that the languages of the Mount Bosavi region form a single subgroup of Trans-New Guinea, as well as investigate the internal relations of these languages. Since there is more lexical than phonological diversity across these languages, Bayesian phylogenies add an extra dimension to more traditional approaches to reconstructing linguistic history, and allow us to quantify patterns of shared lexical innovations, and reveal the deeper relationships between these languages.

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