

Bc. Klára Kopicová

**Phylogeny of human populations in Papua New Guinea,
a genetic and linguistic diversity hotspot**

M.Sc. project, supervisor's opinion

Klára Kopicová has worked on the project for two years, although in an intermittent way. She expressed interest in Papua New Guinea and its populations, and we together designed a project for her. The project was focused on re-analysis of a major genetic dataset published in 2017. Human genetic history is best approximated as a graph including population divergence and admixture events or continuous “gene flows”. Nevertheless, most archaeogenetic studies including those devoted to Papua New Guinea avoid using graph-based methods altogether, or build simplistic graph models, or build complex models using non-optimal statistical significance metrics and thresholds. Nowadays nearly all work in my group is focused on rectifying this situation and developing a robust protocol for phylogenetics of human populations (here I use the word “phylogenetics” in a broad sense). That is why we kept updating our graph-construction protocols during Klára’s project, and that is one of the reasons why the project and the thesis turned out to be far from ideal. Nevertheless the aim of the project, namely constructing a graph for major ethno-linguistic groups in Papua New Guinea, has been fully accomplished, and that represents a major advance, in my opinion.

Klára has shown a genuine interest in biology in general and in human genetic history in particular. She has also mastered a complex statistical method that many scientists in the field are simply afraid to use. However, Klára has demonstrated little independence, has worked only once in a while, and failed to write a structured scientific text. Despite these reservations, I believe that Klára has fulfilled the requirements for the Master of Science degree.

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