A weakly structured stem for human origins in Africa

Aaron P. Ragsdale[1], Timothy D. Weaver[2], Elizabeth G. Atkinson[3], Eileen Hoal[4], Marlo Möller[5], Brenna M. Henn[2,6,*], and Simon Gravel[7,**]

[1]FIXME: UW Madison
[2]Department of Anthropology, University of California, Davis, Davis, CA 95616, USA
[3]FIXME: DSI-NRF Centre of Excellence for Biomedical Tuberculosis Research; South African Medical Research Council Centre for Tuberculosis Research; Division of Molecular Biology and Human Genetics, Faculty of Medicine and Health Sciences, Stellenbosch University, Cape Town, South Africa
[4]FIXME
[5]FIXME
[6]UC Davis Genome Center, University of California, Davis, Davis, CA 95616, USA
[7]FIXME: McGill
[*]bmhenn@ucdavis.edu
[**]simon.gravel@mcgill.ca

January 2, 2022

Abstract

A very simple template for an article class document.

Introduction

The intro..

Results

A Late Middle Stone Age common ancestry for contemporary humans

Deep population structure but not archaic admixture within Africa

Reconciling multiple lines of genetic evidence

Discussion

The Middle Stone Age in Africa

Contrasting archaic admixture and a weakly structured stem

Methods

Kelleher et al. (2016)

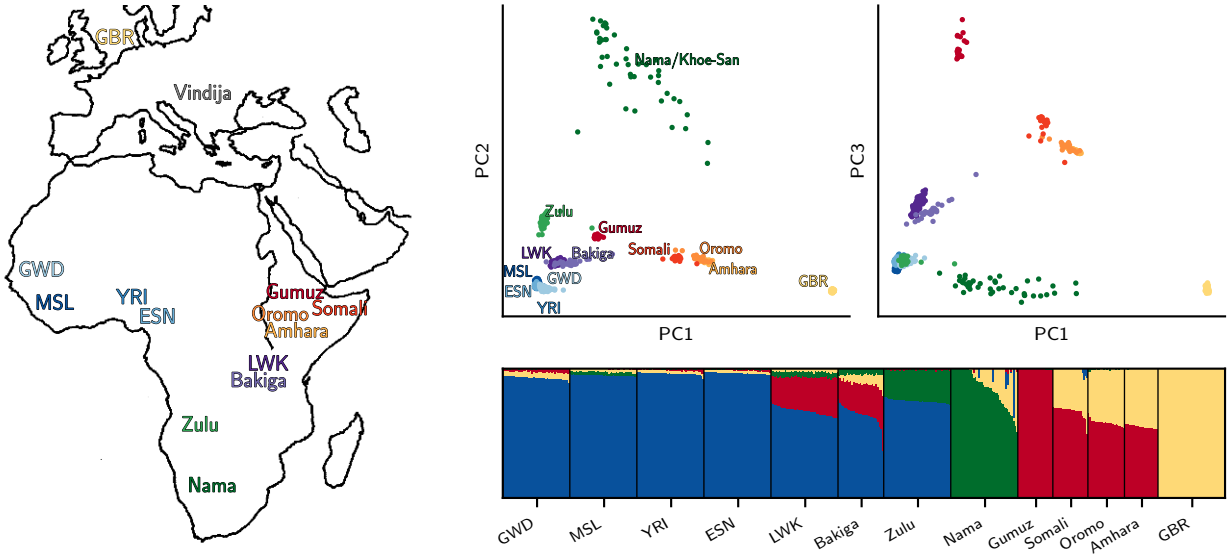

Figure 1: **The first figure**. The geographic and genetic diversity of populations across Africa.

Figure 2: **The second main figure**. A placeholder - best fit model(s).

Acknowledgements

Figure 3: **The third main figure**. A placeholder - validation (Relate and cSFS).

Figure 4: **The fourth main figure**. A placeholder - predictions (FST and/or f4).

References

Jerome Kelleher, Alison M Etheridge, and Gilean McVean. Efficient coalescent simulation and genealogical analysis for large sample sizes. *PLoS Comput. Biol.*, 12(5):e1004842, May 2016.