GGSB PRELIM QUESTION # 6

The Recent African-Origin model of human evolution holds that humans emerged as a species in Africa and subsequently colonized Eurasia, Australia, Oceania, and the Americas. Strict forms of the model suppose there was no subsequent interbreeding with existing archaic humans outside of Africa, and this model has been the standard model for human origins for nearly two decades. Recently,
ancient DNA has helped build evidence for some small amount of admixture with archaic humans outside of Africa.

a) Describe what patterns are observable in contemporary human DNA that suggest admixture with archaic humans (To be clear: lines of evidence not based on ancient DNA).

b) Describe specific lines of evidence from the ancient DNA literature that have been used to argue for admixture between modern and archaic humans.

c) Early mtDNA studies of Neanderthal DNA show human mtDNA and Neanderthal mtDNA as reciprocally monophyletic, suggesting no admixture. How can this be reconciled with the more recent results based on nuclear genomic sequencing?

c) Discuss how 'archaic introgression (genetic) maps' are reconstructed and provide critical perspectives on what has been inferred about the distribution of archaic tracts across the modern human genome and the role of natural selection in shaping these distribution patterns.

(d) Describe at least 3 examples to support the claim that functionally important and plausibly adaptive variation has introgressed from archaic humans into moderns. Provide a critical perspective on each example.

e) Form an opinion/perspective on whether archaic admixture is a major factor in shaping genetic diversity in humans or whether it is simply historically interesting but of limited importance for studying contemporary diversity. Couch your answer separately for relevance to each of: adaptive trait evolution, disease trait architecture, and overall patterns of human diversity.

References

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4. Green et al (2010) A draft sequence of the Neanderthal Genome. Science 328:710-722.

5. Reich et al (2010). Genetic history of an archaic hominin group from Denisova Cave in Siberia. Nature 468:1053-60.

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