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Molecular evidence for a multiregional development of the human lineage: A response to C. Stringer

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ABSTRACT

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In a recent review, Chris Stringer presents his interpretation of the unexpected findings of ancient DNA sequences in modern humans and argues against the multiregional model of human evolution (Stringer 2014). He acknowledges, however, that the mainstream view was multiregional as recently as 1970, with Neanderthals representing just a stage of human evolution (Weidenreich 1943). By the 1990s, the recent African origin (RAO) model prevailed due to fossil and DNA findings. Stringer concludes that the RAO model is still valid in combination with multiregional admixtures. So, according to him, the molecular data point to either the RAO+hybridization or the assimilation model, both of which are based on interbreeding between ancient and modern humans (Stringer 2014).

Let us have a closer look at the new molecular findings in order to be able to validate any interbreeding claims: Vernot and Akey discovered over 15 Gb of introgressed Neanderthal sequence in modern humans, but on average, only 23 Mb of introgressed sequence was found per individual (Vernot and Akey 2014). The authors realized that they had to explain why "inferior" genes showed up in the "superior" *Homo sapiens*, so they hypothesized that certain Neanderthal gene variants provided a selective advantage. If this scenario is correct, why does every modern human population seem to have inherited different pieces of Neanderthal DNA (15Gb versus 23 Mb (Vernot and Akey 2014)) and why are modern human genomes lacking any signs of adaptations to new environments (= strong selective sweeps) (Alves et al. 2012)?

It is even more surprising that no modern human sequences have yet been found in the genome drafts of Neanderthals, despite the claim of multiple hybridizations (Green et al. 2010, Wills 2011, Prufer et al. 2014), as well as the so-called "genetic superiority" of *Homo sapiens*. It remains to be seen if additional sequencing projects can solve this mystery in the future and deliver more convincing scenarios other than the scenario of Neanderthal men raping modern human women.

In my view, the new molecular findings do not support admixtures between Neanderthals and modern humans, and rather point to the original multiregional model with local Neanderthals directly transforming into modern humans worldwide (Weidenreich 1943). This would be in line with the extreme variation of inherited Neanderthal sequences in modern human populations, as well as with the absence of any modern human genetic sequence in Neanderthal DNA. It would also provide an alternative explanation for the unexpected rapid elimination of much of the Neanderthal DNA in modern humans (Stringer 2014), which has been proposed based on similar Neanderthal DNA portions

found in the 40,000 year-old Tianyuan sample (Fu et al. 2013).

Sometimes, existing scientific knowledge can be a burden rather than a benefit. If we did not have this dominant model of human evolution (RAO), would the interpretations of the new molecular findings be the same? Is it possible that there is a tendency within the scientific establishment to interpret the evidence in a way that shows that we were right and have not wasted our time on incorrect models? Wouldn't it be nice to go back in time before the globalization of scientific thought and return to the era of diversity in scientific research? I will give it a try and present here my alternative interpretation of the scientific facts.

There is a reason why multiregional origins of modern humans are a no-go for molecular biologists: the lack of any molecular mechanism capable of producing such a scenario. A multiregional transformation of ancient humans into modern humans would require some kind of trigger and a non-random mechanism of genomic change.

The Nobel laureate Barbara McClintock discovered both. She knew that broken chromosome ends (eroded telomeres) lead to chromosomal instability and activate transposable elements (McClintock 1984) that can rewire the genome (Kunarso et al. 2010). Telomeres erode in somatic tissues (actually, in tissue stem cells) during aging, but are supposed to remain stable in the germ line of a species. However, the results of a large multigenerational study on healthy subjects published in *PNAS* (Eisenberg, Hayes, and Kuzawa 2012) are indicative of telomere erosion in the human lineage (Stindl 2014).

Transgenerational telomere erosion has been hypothesized to be the biological clock (Stindl 2014) that the early proponents of Darwinian evolution could not possibly imagine. According to the telomeric sync model of speciation, transgenerational telomere erosion is the trigger for the repatterning of the genome by transposable elements, which facilitate the phenotypic change (Stindl 2014). Equipped with these biological mechanisms, the old European mainstream model of saltatory evolution of nonadaptive characters is waiting to be resurrected and might better fit the molecular data on human evolution (Stindl 2014).

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APPENDIX

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