

## ABSTRACTS

### An fMRI investigation into the neurocognitive bases of stone tool manufacture

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Recent investigations into lithic technology have considered whether activation of language networks in the brain during stone tool manufacture supports hypotheses about the possible co-evolution of language and stone tool technology. Our team launched a naturalistic fMRI study in order to investigate the cognitive underpinnings of Oldowan, Acheulean, and Levallois technologies, focusing on their activation of language networks. Our subjects, including expert stone toolmakers and naïve participants with no prior stone tool training, watched naturalistic videos of three Paleolithic technologies being made by an expert toolmaker while being scanned. Subjects were asked to imagine themselves performing the same actions as the toolmaker in the video. We performed event-related GLM analyses on the subjects' fMRI data, focusing on activation during observation and flaking events. Across all technologies, our team found activation in networks involved in language production and comprehension, including BA 44/45/47 (IFG), BA 6 (vPMC and dPMC), BA 7 (SPL), BA 40 (IPL), and BA 22 (PMTG). Flaking events engaged language networks more reliably than observation. Previous neurocognitive work on toolmaking suggested that increased stone tool complexity yields increased activation. While this pattern applied to a comparison between the Oldowan and Acheulean technologies, we found greater activation for the Acheulean than the Levallois. Once subject expertise was factored in, however, we found the expected increases in activation from Oldowan (lowest), through Acheulean (intermediate), to Levallois toolmaking. This study is the first neuroimaging analysis of the Levallois technology, providing insight into the extent to which Levallois comprehension requires expertise.

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### Population-genetic and functional investigation of high altitude adaptation in the Himalayan populations

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The Himalayas provide a diversity of environments for humans, some of which have required substantial genetic adaptation. We have used a combination of SNP-chip data, genome sequences and functional studies to explore the demographic history, genetic structure and signatures of adaptation in the Himalayan populations. We previously genotyped ~600,000 genome-wide SNPs in 883 Himalayan individuals from 49 different autochthonous groups from Nepal, Bhutan, North India and the Tibetan Plateau in China, and have now generated whole-genome sequences of 100 individuals from a subset of these populations plus four additional ones. We find that the Himalayan populations share a genetic component derived from a common ancestral population, followed by the development of local fine structure correlating with language and geographical distribution, with variable gene flow from neighbouring populations. High-altitude adaptation seems to have originated in a single ancestral population and spread widely across the Himalayas: We find a major demographic expansion taking place only 3,000-4,000 years ago, coinciding with the archaeological evidence of permanent settlements above 2,500 m. We find signatures of adaptation to high altitude in *EPAS1* and other genes involved in the hypoxic response. We performed *in vitro* functional validation of variants in the *EPAS1* region that have been previously reported to result from introgression of DNA from the Denisovans using cell lines with and without the adaptive haplotype. We find that *EPAS1* expression in normoxia or hypoxia remains constant in cultured cells with the Denisovan introgressed haplotype, unlike cells with the lowland haplotype where it increases in hypoxia.

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### Phylogenetic analysis of extant colobine monkeys using craniodental data

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The colobines are a widespread and successful radiation represented by two extant groups, the Asian Presbytina and the African Colobina, and a relatively diverse fossil record across Africa and Eurasia. However, traditional views hold that little phylogenetic signal is contained in their craniodental morphology, and few published studies have used morphological data to estimate colobine phylogeny. This study uses craniodental characters and updated methodology to estimate phylogenetic relationships among extant colobines. 270 (127 qualitative, 143 quantitative) characters were coded for males and females separately in 19 colobine species representing all ten colobine genera, plus three outgroups (*Victoriapithecus macinnesi*, *Allenopithecus nigroviridis*, and *Macaca fascicularis*). Size-adjusted quantitative characters were corrected for allometry when highly correlated with size ( $r > 0.5$ ), and otherwise coded using gap-weighted coding. The matrix was analyzed using parsimony in TNT, and recovered a single most parsimonious tree. The Colobina form a monophyletic group with well-supported genus arrangements congruent with molecular analyses, and multiple well-supported molecular clades are recovered among the Presbytina as well. However, Presbytina are recovered as paraphyletic, with the odd-nosed colobine clade diverging first, followed by *Semnopithecus*, then a clade with *Trachypithecus* and *Presbytis* sister to the African colobines. Mapping synapomorphies on the tree demonstrates Asian colobines are generally primitive relative to African colobines, consistent with previous studies of colobine comparative morphology. These results demonstrate a phylogenetic signal in the craniodental morphology of the Colobinae, and future inclusion of fossil taxa may provide better polarity for extant species and allow exploration of their potential evolutionary relationships.

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### Genomic insights into the human population history of Northwestern Amazonia

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