Locomotor adaptation in *Australopithecus afarensis*, ZERESENAY ALEMSEGED (California Academy of Sciences, Department of Anthropology, San Francisco, CA; zeray@calacademy.org).

Since its discovery in the 1970s, the species *Australopithecus afarensis* played a pivotal role in our understanding of early hominin adaptation and evolution. It lived between ca. 4 and 3 million years ago, occupied a wide range of environments across Africa and was the first to venture into more open habitats containing C4 grasses. The species is currently one of the best-documented early hominin and its paleobiology is relatively better understood. Yet, many issues pertaining to its locomotor adaptation continue to be source of heated debated. One of these issues is whether the species engaged in arboreal lifestyle. In this presentation I provide data showing that the species did climb trees while being fully upright on the ground. This has implication for our understanding of the species’ place in the paleolandscape and its behavior.

Standing on the Shoulders of Apes: Development and the Evolution of Hominin Postcrania, NATHAN M. YOUNG (University of California San Francisco, Department of Orthopaedic Surgery, 2550 23rd Street, San Francisco CA 94110; nathan.m.young@gmail.com).

Understanding the forces that have influenced the evolution of the human appendicular skeleton, including both limbs and girdles, has played an important part in paleoanthropology. In the human lineage, evolutionary shifts in shoulder and limb morphology are associated with some of the most important behavioral changes in hominins, such as reduced arboreality, sophisticated tool use, increased manual dexterity, and accurate throwing. The unique features of the human shoulder, consisting of the scapula and proximal humerus, evolved from an ancestral hominoid pattern presumably found in the last common ancestor (LCA) of humans and chimpanzees, and the starting point from which the hominin lineage evolved. However, interpretation of recent hominin fossils cast doubt as to whether the morphotype was chimpanzee-like, suggesting instead that many features of the human postcranium evolved from a more primitive condition found in early apes. In this talk I present a novel integrated approach combining comparative evidence from living and fossil apes and humans, developmental biology of the shoulder, and functional studies, to test the likelihoods for these alternative models of the human-chimpanzee LCA. I argue that the total evidence is consistent with evolution from a suspensory and knuckle-walking chimpanzee-like LCA.

Developmental Insights to Modularity, Integration and Evolvability of the Hominin Skull, JENNIFER L. FISH1*, BRIAN A. VILLMOARE2, MICHAEL J. DEPEW3, and RALPH S. MARCUCIO3

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Morphological differences among fossil skulls provide key evidence for diversity in hominin adaptation and evolutionary history, and often are critical to species identification. Since genetic analyses are not possible for most hominin fossil samples, genetic differences are inferred to be causal to morphological differences. However, it is still largely unknown how well variation in skull morphology reflects genetic distance. A major complication affecting these studies is that fact that the skull is a very complex structure composed of multiple, integrated components that also may be modular, or relatively independent, during development. Using insights gained from studies in comparative vertebrate morphology and development, we investigated modularity and integration of the skull with the aim of understanding its morphological evolution in the hominin lineage. We are particularly interested in mechanisms regulating jaw length and robusticity, especially as they relate to robust vs. gracile hominin phenotypes. Based on a broad range of comparative and experimental data, we identified patterns of character co-variation that might have led to distinct hominin phenotypes and tested these hypotheses using data collected from murine and primate crania. Our data suggest that selection on jaw size, predominantly driven by different dietary adaptations, may have been a primary factor driving hominin craniofacial...
evolution. Further, the patterns of cranial integration and modularity identified in our study support monophyly of a robust hominin clade may have other implications for hominin phylogenetic studies.

Ancient Admixture between ‘Archaic’ and Modern Human Groups, JEFF WALL (Institute for Human Genetics, 513 Parnassus Avenue S965, University of California San Francisco, San Francisco, CA 94143; wallj@humgen.ucsf.edu).

As modern humans expanded out of Africa, they encountered various ‘archaic’ human groups such as Neanderthals, Denisovans and Homo erectus. We present new methods for identifying regions in contemporary genomes that were inherited from these archaic human groups, and quantify the amount of Neanderthal and Denisovan ancestry across a wide range of human populations. Our results suggest that the highest proportion of archaic human ancestry is found in Melanesians, and support the idea that there were at least two major waves of migration of modern humans out of Africa and into Eurasia.

Many Human Accelerated Regions are Developmental Enhancers

Many Human Accelerated Regions are Developmental Enhancers, KATHERINE S. POLLARD (Gladstone Institutes, University of California San Francisco, 11650 Owens Street, San Francisco, CA 94158; kpollard@gladstone.ucsf.edu).

Despite a wide variety of molecular and clinical data suggesting that disease can be caused by mutations in gene regulatory enhancers and that phenotypic differences between closely related species are frequently driven by changes in developmental gene expression, only a few mutations that alter enhancer function have been identified thus far. Human Accelerated Regions (HARs), the fastest evolving regions of the human genome, are mostly uncharacterized non-coding sequences. Because HAR sequences are highly conserved across mammals, the human-specific mutations in them are excellent candidates for regulatory mutations with functional effects. To test this hypothesis, we developed computational tools to predict gene regulatory enhancers and their targets and to test if mutations in regulatory sequences significantly alter their transcription factor binding site content. We and others then used transient transgenic reporter gene assays in mouse embryos to validate over 60 HARs that function as developmental enhancers, several of which show differences in expression patterns between human and chimpanzee sequences. Because this approach to characterizing regulatory mutations is costly and slow, we are now using massively parallel reporter assays (MPRAs) coupled with stem cell techniques to functionally screen all HARs for enhancer activity in developing human and chimp neuronal cells (early initiation, neural progenitor, glial progenitor) and to characterize the effects of nucleotide variants on their enhancer activity. This approach could easily be adapted to pinpoint causative regulatory variants in the many disease-associated genomic loci that lack an obvious coding mutation.