COMPARATIVE ANTHROPOGENY: FROM MOLECULES TO SOCIEITIES

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ABSTRACTS

LINE1 Retrotransposons

Carol Marchetto, UC San Diego

Identifying cellular and molecular differences between human and non-human primates is essential to the basic understanding of the evolution and diversity of our own species. Preserved tissues are the main source for most comparative studies between humans, chimpanzees (Pan troglodytes) and bonobos (Pan paniscus). However, these tissue samples do not fairly represent the distinctive traits of live cell behavior and are not amenable to genetic manipulation. We propose that induced pluripotent stem cells are a unique biological resource to study relevant differences between human and non-human primates, and that those differences could have potential adaptation and speciation value. To test this hypothesis, we generated induced pluripotent stem cells from chimpanzees and bonobos as new tools to explore factors that may have contributed to great ape evolution. Comparative gene expression analysis of human and non-human primate cells revealed differences in the regulation of a class of transposable elements (Long Interspersed Nuclear Element 1 or LINE1 retrotransposons) between species. Transposable elements, also known as “jumping genes”, are DNA sequences that move from one location on the genome to another via a copy and paste mechanism. A force of change in mammalian evolution, these elements have remained active during primate evolution. We revealed increased copy numbers of species-specific transposable elements in the genome of chimpanzees compared to humans, supporting the idea that there is increased transposon mobility (DNA jumping) in non-human primates in comparison to human. We propose that differences in transposon elements mobility may have differentially shaped the genomes of humans and non-human primates and could have continuing adaptive significance.

ABO Blood Groups

Pascal Gagneux, UC San Diego

ABO Blood groups represent the first described human molecular polymorphism. The ABO gene encodes variants of a protein (a glycosyltransferase) that produces the short sugar chains on glycoproteins and glycolipids that define the A, B, or O antigens. These antigens are found on red blood cells, plasma glycoproteins, and other cell types in various tissues. Individual humans can have one of four blood types based on the two alleles inherited from both parents at the ABO locus: blood type A, B, AB, or O. We still lack a definitive explanation of why humans individually differ in the molecular composition of their blood and combine the absence of particular ABO antigens with circulating antibodies against the missing molecule(s). Several lines of evidence indicate that this system evolved to protect populations from parasites and pathogens that use these ABO sugar chains for invasion of the human host. Furthermore, infections by enveloped viruses can be considered “nanotransplantations”: the viruses are covered with the ABO antigens acquired from the previous host and can be targeted by circulating anti-ABO antibodies when infecting new individuals of different blood types. The same antibodies underlie crucial importance of ABO blood typing for transfusion and transplantation medicine. Recent comparative genome studies

ABO Blood Groups [CONTINUED]

Pascal Gagneux, UC San Diego

have revealed that this polymorphic system is ancient and shared between humans and non-human primates, this despite the fact that none of the great ape species carries all four ABO blood types. Historically, ABO allele frequencies across human populations have been used for pseudoscientific claims of superiority of certain regional populations and similar pseudoscience perpetuates claims for ABO blood group-based diets and/or personality types.

Phytanic Acid Metabolism

Joseph Hacia, University of Southern California, Keck School of Medicine

Diet has played a major role in the evolution of human and non-human primate digestive systems. Phytanic acid is a potentially toxic branched chain fatty acid that can be acquired in humans by ingesting plant and/or animal products. In ruminants, the fermentation of ingested plant materials by gut microbes can liberate phytol, a constituent of chlorophyll, which can be rapidly metabolized to phytanic acid and stored in fats. Members of the marine food chain can accumulate phytanic acid by ingesting zooplankton and/or krill, sources of phytol and chlorophyll-related precursors. Although humans can convert free phytol into phytanic acid, they do not derive appreciable amounts of phytanic acid from chlorophyll in plant materials. Humans with impaired phytanic acid metabolism can accumulate toxic stores of phytanic acid that have deleterious effects on multiple organ systems. Although it was established that humans cannot derive phytanic acid from chlorophyll and instead normally obtain it only from meat, dairy, and fish products, less was known about the capacity of non-human primate with proportionally larger hindguts to obtain phytanic acid from plant materials. We discuss studies profiling phytanic acid levels in red blood cells obtained from humans and captive non-human primates all on low phytanic acid diets. Therein, captive apes and Old World and New World monkeys displayed significantly higher red blood cell phytanic acid levels relative to humans. Furthermore, a small-scale gene expression profiling study indicated that genes relevant to phytanic acid metabolism were more highly expressed in the liver, heart, and testes of humans relative to chimpanzees. The favored hypothesis is that, unlike humans, the non-human primates surveyed can derive significant amounts of phytanic acid from the degradation of ingested chlorophyll through gut fermentation. This raises the possibility that red blood cell phytanic acid levels could serve as a biomarker for evaluating the digestive health of captive NHPs.

Siglec-11 Expression in the Brain

Ajit Varki, UC San Diego

Sialic acid-recognizing immunoglobulin-type lectins (Siglecs) are a family of cell surface proteins prominently expressed on immune cells in mammals. The extracellular N-terminus of Siglecs has an Ig-like V-set domain involved in sialic acid recognition, followed by a variable number of C2-set domains; and intracellular domains with inhibitory or activating signaling that regulate intracellular responses. Sialic acids are nine-carbon backbone acidic monosaccharides found primarily in animals of the “Deuterosome” lineage (vertebrates and higher invertebrates) but are sometimes found on specific bacterial pathogens that invade the Deuterosomes. One of the major roles of the inhibitory Siglecs is to recognize endogenous sialic acids as “Self-Associated Molecular Patterns” (SAMPs) and dampen innate immune responses. Siglec-11 is an example of an inhibitory Siglec. It was the first protein in the brain found to be “human-specific”: non-human primates express Siglec-11 in other tissues but not in the central nervous system. Siglec-11 exists as a paired-receptor with Siglec-16, which shares a very high sequence identity in the extracellular N-terminus. Genome evolution and chromosomal analyses suggest that gene conversion events over the last 1-1.2 million years gave rise to the present pair of receptors. Despite their high sequence homology in the sialic acid-binding domain, when activated, Siglec-11 and Siglec-16 lead to opposing inflammatory responses: Siglec-11 dampens inflammation, and Siglec-16 heightens it. When immune cells are exposed to E. coli K1, one of the human-specific pathogens coated in polysialic acids, Siglec-11 leads to decreased bacteria-killing while Siglec-16 expression leads to increased killing. Like Siglec-11, Siglec-16 also has several uniquely human features, including its expression in the central nervous system, but an additional feature is that most of the human population have the SIGLEC16P Pseudogene genotype which does not allow protein expression of the full receptor.

Siglec-11 Expression in the Brain [CONTINUED]

Ajit Varki, UC San Diego

In summary, Siglec-11 and Siglec-16 are paired receptors with homologous ligand-binding domains but opposing intracellular signaling when activated by polysialic acid. These paired receptors do not have orthologs in all mammals, play significant roles in regulating inflammation, and have several uniquely human features including expression in brain, endogenous ligands in the developing human brain, a unique form in microglia with one less C2-set domain, that can be secreted as exosomes (therefore potentially influencing functions at a distance); interactions with the human-specific pathogen E. coli K1, loss of Siglec-16 in many humans, and is also expressed in other unusual sites in human-specific manner e.g., the columnar epithelium of the uterine cervix. Further studies are needed to understand the significance of the “human-specific” features of these molecules.

Human Arcuate Fasciculus

James Rilling, Emory University

Language is a human cognitive specialization, and as such, is expected to be supported by human neurological specializations. The arcuate fasciculus is a white matter fiber tract that connects Wernicke’s and Broca’s language areas in the human brain, and also connects the homologues of Wernicke’s and Broca’s areas in non-human primate brains. Damage to the human arcuate fasciculus is implicated in multiple linguistic functions. In contrast to chimpanzees and macaques, the human arcuate fasciculus is larger and extends well beyond classic Wernicke’s area into lateral temporal cortex involved with syntax and semantics. Expansion of this language circuit appears to have displaced adjacent visual pathways in a ventral and posterior direction in the human brain. This specialization of the arcuate fasciculus may help to explain why only humans have language in the complete sense.

Incidence of Carcinomas

Nissi Varki, UC San Diego

During embryogenesis, the three germ layers (endoderm, ectoderm, mesoderm) differentiate into epithelial and non-epithelial cells, which eventually form differentiated tissues and organs. Epithelial cells arise from stem cells and often line body surfaces that interact directly with the environment. The type of epithelium reflects location and function. Epithelial cells are typically attached to underlying connective tissue by a basement membrane, and the underlying stroma includes blood vessels, lymphatic vessels, hematopoietic cells, stromal fibroblasts, extracellular matrix, neuronal structures, smooth muscle and adipose tissue. Neoplasia is the term given to the new growth of cells proliferating without regard to stop signals, with attendant new blood vessels, forming a tumor mass (neoplasm). If the growing neoplasm within an epithelial layer stays restricted by a basement membrane and does not invade that barrier, it is designated as a benign tumor. However, once tumor cells undergo multiple genetic changes and breach and infiltrate through the basement membrane, the neoplasm becomes invasive and malignant, and the cells use proteases and glycosidases, which allow breakdown of the extracellular matrix, reaching and invading blood vessels. Abundant data now indicates that we humans are very closely related to other hominids including chimpanzees, bonobos, gorillas, and orangutans (the so-called "great apes", hereafter called non-human hominids, or NHHs. There has been a considerable body of published information regarding their disease profiles, particularly from primate facilities in the USA. Surprisingly, surveys of this existing information suggest that several common human diseases may be partially or completely unique to our species, and that captive chimpanzee population may suffer from different profiles of pathology. Among these apparent differences in disease incidence, one that has been emphasized in multiple reports is the rarity of occurrence of common human carcinomas in captive chimpanzees.We conclude that while relative carcinoma risk is a likely difference between humans and chimpanzees (and possibly other “great apes”), a more systematic survey of available data is required for validation of this claim.

The Impact of Intergroup Social Ties on Coalitionary Aggression

Pauline Wiessner, Arizona State University & University of Utah

Intergroup coalitionary aggression is a vast and sensitive topic. Here I will limit the discussion to the impact of mutually supportive intergroup ties on aggression in small scale societies. Unlike our closest primate relatives, chimpanzees and bonobos, humans form strong intergroup ties which can mitigate coalitionary aggression and make peace possible. However, such bonds can also be used to build to larger alliances that take such conflicts to a new level of magnitude, supported by cultural and linguistic proficiencies. First, I will compare intergroup ties between humans, chimpanzees and bonobos and explore some of the possible evolutionary developments that contributed to the human disposition to form mutually supportive external bonds. Then I will discuss the impact of social ties on coalitionary action. Intergroup ties can reduce coalitionary aggression of the nature proposed in the 'imbalance of power hypothesis' used to account for chimpanzee intergroup attacks, as well as human motivations such as marriage by capture and revenge. However, when social ties are expanded into institutions to bind and motivate larger coalitions into communities or tribes, new incentives enter the picture that ramp up coalitionary competition: These include rallies to dehumanize the enemy, adoption of sacrosanct values, concern with honor, reputation and balance of power, as well as coalitionary action to unite groups against a common enemy. Fortunately, intergroup social ties can also provide a basis to restore peace.

Food Sharing

James O'Connell, University of Utah

Humans are unusual in that we depend on shared foods. We also differ from other great apes in our early ages at weaning, late ages at maturity, short birth intervals and survivorship decades past menopause. Emergence of these patterns, probably in tandem, was crucial to early human evolution. Explanations focus on an ancestral shift to sharable but difficult-to-acquire foods not previously taken by hominins. I evaluate two alternatives in light of observations among modern East African hunter-gatherers. The hunting hypothesis focuses on big game meat and marrow that males acquired to provision mates and offspring, reducing female workloads, enhancing their fertilities and favoring the later ages at maturity needed to learn and perfect essential skills. But modern data show that large animal prey would not have provided the reliable energy stream the argument requires. The grandmother hypothesis identifies certain kinds of savanna plant foods that set up the forager interdependence which propelled all aspects of the life history change. But if so, why did big game hunting and scavenging, dangerous practices in the carnivore-rich environments of the day, yet clearly demonstrated in the archaeological record and provocative with respect to the hunting hypothesis, become established when they did, several hundred thousand years after the start of the shift toward modern human life histories? Greater longevity was crucial. As longevities increased, the growing proportions of post-menopausal females and senior but still fertile males shifted the mating sex ratio from female- to male-biased. While that male bias favored mate guarding, success in that strategy depended on others' deference to their propriety claims. Agonistic encounters with large predators demonstrated by the archaeology showcased exactly the competitive capabilities that earned such deference.

Technology

Dietrich Stout, Emory University

Technology is clearly central to human life and evolution but remains hard to define and study. This talk is an evolutionarily motivated definition of technology that highlights three key features: material production, social collaboration, and cultural reproduction. The broad scope encompassed by this definition respects the complexity of the subject but poses a challenge for theoretical unification. Addressing this challenge requires a comparative approach to reduce the diversity of real-world technological cognition to a smaller number of recurring processes and relationships. To this end, a synthetic Perceptual Motor Hypothesis for the evolutionary-developmental-cultural construction of technological cognition is advanced as a target for further investigation. This perspective has important implications for the way we conceptualize and study the origins and evolution of human technologies.

Quantity and Number

Rafael Núñez, UC San Diego

Humans and many other species have biologically endowed abilities for discriminating “quantities” to some degree (e.g., subitizing), but only humans, via the distinct capacity of “symbolic reference” exhibit “number” — i.e., exact symbolic quantification. To compare human and non-human animal data in some meaningful way, a crucial distinction between “quantical” (e.g., quantity discrimination) and “numerical” (exact, symbolic) cognition is needed: quantical cognition provides biologically evolved preconditions for numerical cognition but it does not scale up to “number” and “arithmetic”, which require conventionalized cultural mediation and (biological) enculturation. Indeed, human data from non-industrialized cultures show that “number”, although distinctively human and ubiquitous in the modern industrialized world, is not (and has not been) universal. “Number” — exact symbolic quantification — appears to be a cultural trait, not a (human) species-specific biologically determined trait, driven and materialized by cultural preoccupations and practices (e.g., management of stocks, precise measurements) that are supported by language and symbolic reference — crucial dimensions that lie largely outside natural selection. Language, with its symbolic properties although present in all human cultures, is a necessary condition for “number” but it is not a sufficient condition for it. The comparative analysis of “quantity” and “number” has implications for debates about the origins of other human special capacities such as geometry, music, and art.