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Of clothes, clocks and lice

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We humans are the only species who wear clothes. And, it is obvious that we are obsessed with clothes – about the designing, making and procuring of clothes and materials that are used to make clothes. As the ‘Page 3’ would testify, we are fascinated about who wears what, and also who did not wear what!!

But, how did it all come about? What were the first ‘baby’ steps? When did we start wearing clothes?

The trouble with this kind of investigation is the paucity of ‘hard’ evidence. Clothes, unlike bones, do not fossilize, and unlike stone and metal, they perish fast. Thus, except under special environmental conditions in which some paleo-humans (such as iceman Ötzi) have been unearthed, the direct evidence of prehistoric clothing is scanty and so the origins of clothes have been lost in the mists of Time.

But, as always, there is evidence – it is only about properly looking for it. In this case, the evidence lies in the well-known pest – *the human louse*.

THE PEST FAMILY

Almost all mammalian and avian species are host to various species of lice. But, humans are among the few species that are host to, not one, but 3 species (or subspecies) of lice! The human head louse (*Pediculus humanus capitis*), the body louse (*P. humanus corporis*, also considered *P. humanus humanus*) and the pubic louse (*Phthirus pubis*) are obligate ectoparasites (Figure 1) to the human body and cannot survive on other species, including pets. Head louse are slightly smaller in size than body louse and usually have a darker pigmentation. There are subtle differences in the lengths and widths of the antennae and the front legs. But, not surprisingly, the head louse and body louse have considerable morphological similarity. Their main difference lies in the choice of habitat.



Figure 1: Lice that parasitize humans. (A) head louse, (B) body louse, (C) pubic louse (credit: Wikimedia Commons)

The head louse is a blood-sucking insect that lives *only on the head scalp* and lays eggs only on scalp hair. The body louse, in contrast, doesn't venture towards the head. It feeds from the skin and notably, *it lives and lays eggs in human clothing*. The head louse and the body louse are fastidious about their habitats – neither encroaches into the other's 'territory' (in fact, the head louse cannot live on clothes). And, neither species can survive away from a human host for long – the head louse perishes within 24 hours, while the body louse (which reside on clothing) can live without human contact for about a week. Noted biologist Mark Stoneking (Figure 2) – who had already made a name for himself by studies on the 'mitochondrial Eve' – got interested to study the migration of these obligate parasites across the globe hoping that would lead to insights about human migrations. Stoneking hypothesized that the head louse was the ancestral species and body louse have evolved from head louse *only when a new ecological niche got available – in the folds and creases of human clothes*. When did this happen? – the most likely answer is when humans started regular wearing of clothes. This leads to the intriguing possibility that finding out the time when the body louse evolved from head louse would (by inference) correspond to the beginning of extensive use of clothing by ancestral human populations. The answer, as was elegantly shown, lay in using a *molecular clock* approach to calculate the origin of body louse.



Figure 2: Mark Stoneking, faculty at the Max Planck Institute for Evolutionary Anthropology.
(credit: Eugene Dubois Foundation, The Netherlands)

BOX: What is a molecular clock?

The molecular clock is a method to determine when 2 species/ sequences diverged from a common ancestor. It is based on the principle that, as time passes, random errors/substitutions take place during DNA replication and get transmitted down the generations. More the time since the 2 sequences diverged greater the number of differences between them (as substitutions happen independently). Thus, if the 'number of substitutions per million years' is known, it is possible to estimate how many years have passed since the 2 sequences had a common ancestor. This calibration can be done by knowing the number of substitutions that have accumulated in 2 DNA sequences whose divergence-time is actually well-established from other lines of evidence, for eg, fossil record. Assuming the error rate stays constant across time and in different species, this allows to calculate the unknown time points (Figure 3).

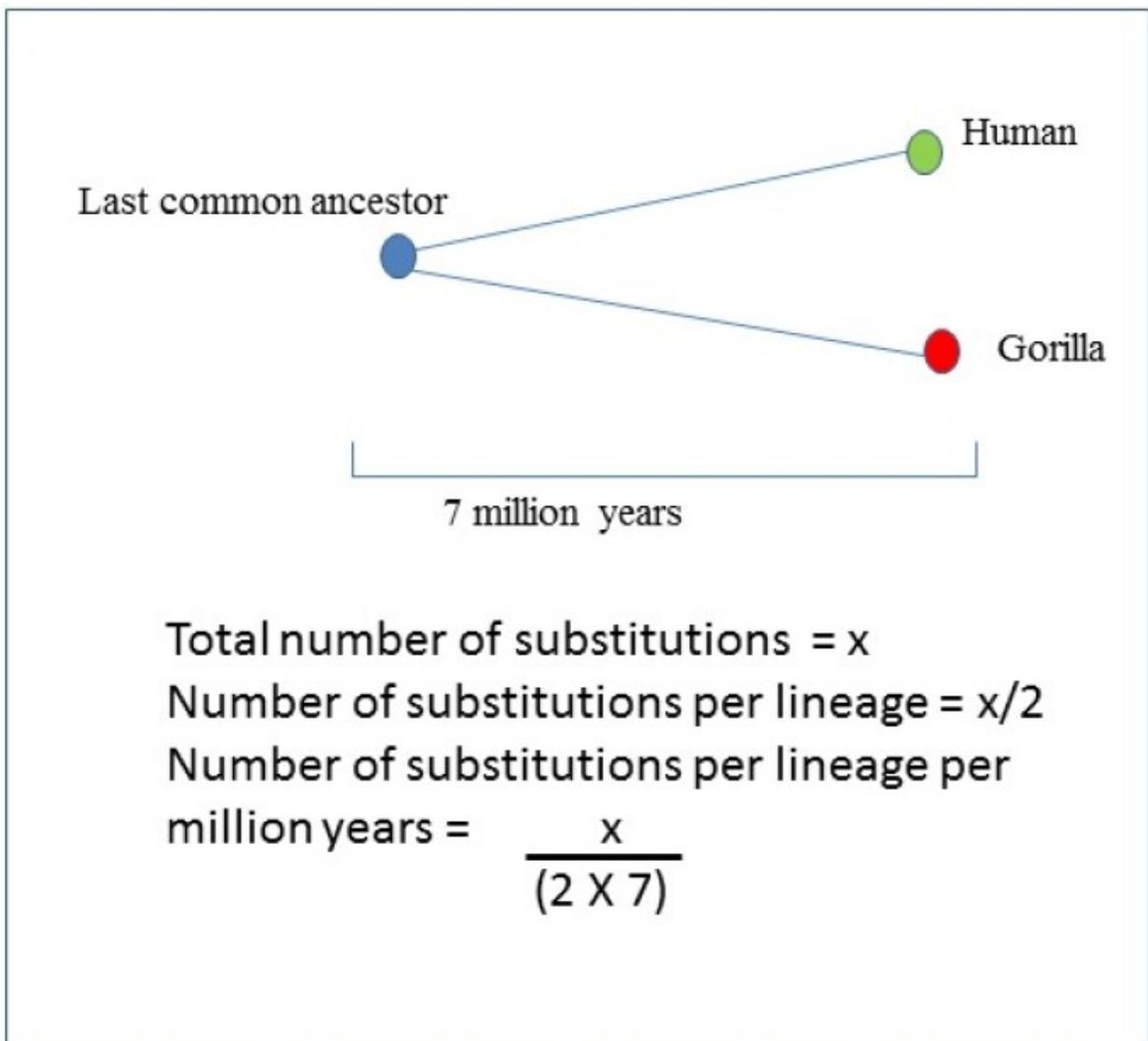


Figure 3: Calibrating the human molecular clock

THE GENETIC TALES OF THE LICE...

The molecular clock for dating the evolution of lice was built by using 2 mitochondrial DNA and 2 nuclear DNA segments. To avoid any bias in their investigation, the scientists collected lice from 12 geographical regions – Ethiopia, Panama, Germany, Philippines, Iran, Ecuador, Laos, Papua New Guinea, Florida (USA), Taiwan, Nepal and the United Kingdom – and extracted nuclear and mitochondrial DNA. They also collected DNA from chimpanzee head louse. Since it is well known that hosts and their parasites often co-evolve, it was assumed that the chimpanzee louse (*Pediculus schaeffi*) and *P. humanus* must have co-speciated with their respective hosts, and this must have happened at around 5.5 MYA – the scientifically-established period when humans and chimps diverged. Thus, the differences between DNA sequences of chimp louse and human head louse must have accumulated over 5.5 million years. Using this specific time period as a calibration point for the clock, the time when head louse and body louse diverged could be estimated.

For the sequence analysis, Stoneking's group first analysed segments of the genes ND4 and CYTB present in mitochondrial DNA of the louse. They followed it up with comparative sequence analysis of 2 bits of nuclear sequence – from the important genes of elongation factor EF-1 α and RNA polymerase II subunit RPII. The size of fragments ranged between 400-600bp. The results obtained were fascinating to say the least.

The first result (Table 1) showed that genetic diversity of the African louse (although collected only from Ethiopia) is significantly greater than the global samples of non-African louse. The finding mirrored the greater genetic diversity of humans seen in Africa compared to that in other continents. Since greater genetic diversity almost invariably occurs at the source, the results indicate, as in the case of humans, the African origin of the human louse.

Table 1: Comparing genetic diversity of African versus Non-African lice (adapted from data present in Kittler et al (2003))

Genetic Diversity		
	African louse	Non-African louse
mtDNA	3.31	1.76
EF-1 α	0.29	0.10
RPII	0.94	0.56

The next set of results (Table 2) similarly showed that human head louse was far more genetically diverse compared to its cousin, the body louse – proving that the head louse was the ancestral species.

Table 2: Comparing genetic diversity of Head louse and Body louse (adapted from data present in Kittler et al (2003))

Genetic diversity

	Head louse	Body louse
mtDNA	3.42	0.19
EF-1 α	0.23	0.18
RPII	0.93	0.61

(BOX: A few definitions: **Phylogenetic tree**: a tree-like diagrammatic representation that describes the evolutionary relationships between the organisms/sequences being studied (Figure 4).

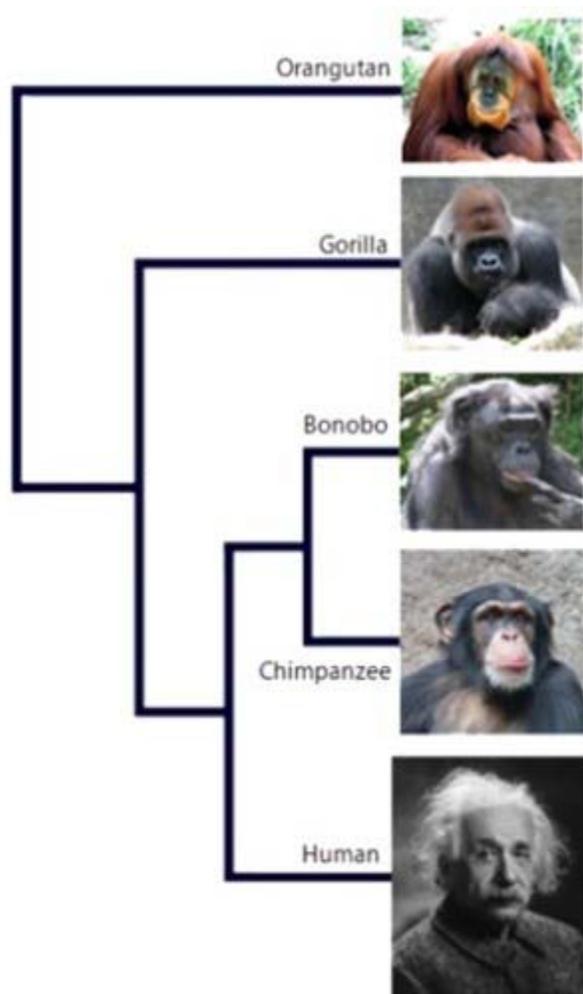


Figure 4: Phylogenetic tree showing the divergence of the apes and their evolutionary relationship (credit: Wikimedia Commons)

Monophyletic sequences: Two or more DNA sequences that have evolved from a common ancestral DNA sequence.

Clade: A group of monophyletic sequences that consists of all the sequences included in the analysis that are descended from the ancestral sequence at the root of the clade.

Outgroup: a homologous sequence that has originated from a common ancestor as the sequences under investigation, but is not as closely related to the being-studied sequences as they are to each other. In this case, the DNA from chimp louse serves as an outgroup and helps to locate the root of the tree)

THE FINGERPRINTS ON THE TREE...

Next, a phylogenetic tree was constructed using all these mitochondrial sequences of human lice (Figure 5). The tree showed presence of number of *clades*. The deepest clades contained only head louse sequences, confirming that body louse had originated from head louse. Notably, one particular clade contained *all body louse and 16 head louse sequences* and included samples from all over the world. The molecular clock, calculated using the sequences from the chimp louse as an outgroup, showed that this clade is 72000 +/- 42000 years old. Since it contained all body louse sequences, the estimated age of this clade has to be the upper limit for the time since body louse originated. And, since body louse exclusively inhabits human clothing, this must be the time period when modern humans started regular use of clothes.

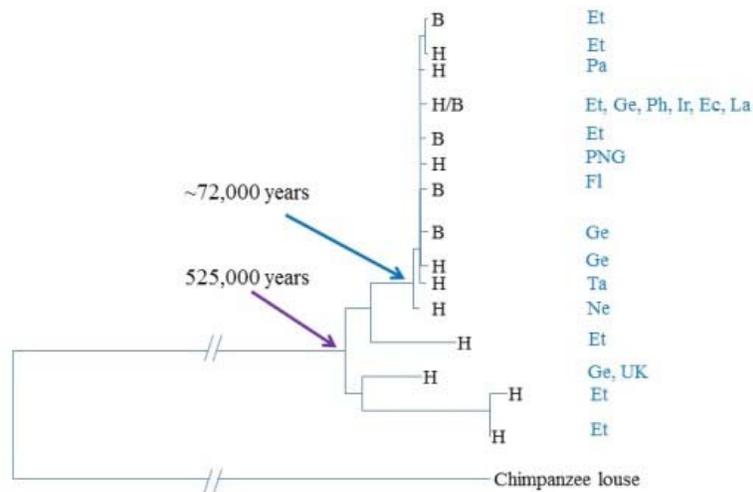


Figure 5: Phylogenetic tree based on mitochondrial DNA sequences, showing divergence of head louse (H) and body louse (B). The arrows indicate the estimated ages of the clades. Note that one clade, aged ~72000 years, houses all body louse sequences and some head louse sequences. The geographic origin of the lice are in abbreviations. Et: Ethiopia, Pa: Panama, Ge: Germany, Ph: Philipines, Ir: Iran, Ec: Equador, Ne: Nepal, PNG: Papua New Guinea, Fl: Florida, La: Laos, UK: United Kingdom, Ta: Taiwan. The tree was rooted with the corresponding sequences from chimpanzee louse. (adapted from Kittler et al (2003) *Curr. Biol.* 13, 1414-1417)

Very similar results were obtained from studying the nuclear sequences, in spite of the fact that DNA recombination can make such analysis difficult compared to that for mitochondrial DNA. As a final piece of evidence, Stoneking's team also analysed parts of the Cytochrome oxidase (COX) gene, also present in mitochondrial DNA and showed that the results were in agreement with that obtained from ND4-CYTB i.e. *anatomically modern humans, residents of Africa, started wearing clothes around 70,000 years ago.*

In a latter study, David Reed's group from the University of Florida carried out a more robust analysis using a *Multilocus Bayesian isolation-with-migration coalescent method* and concluded that body louse had diverged around 170,000 years ago, and certainly not after 83,000 years ago. The difference between the two sets of data is not surprising given the different methodologies used (moreover, Reed et al also used 18S ribosomal RNA from louse nuclear genome for their analysis), but they are in broad agreement. Importantly, both conclude that the body louse evolved in presence of anatomically modern humans in Africa because of the availability of a new ecological niche – clothes.

But, what if clothing originated much earlier, and louse colonized this ecological niche later? This is an intriguing possibility and cannot be discounted entirely. Stoneking et al believe that, since a new ecological niche is colonized fairly rapidly, it is unlikely that clothing could have existed for thousands of years before body louse occupied it. Indeed, the molecular data also corresponds well with the archaeological finding that the earliest eyed needles – the only prehistoric tools that can be definitely associated with clothing – are ~ 40000 years old, and they have been found only in settlements of modern humans and not archaic humans like Neanderthals.

TO SUMMARIZE,

The genetic and archaeological data converge on the conclusion that the chimp louse and the human head louse are close cousins who must have originated from a common ancestor. The human head louse got confined to one relatively small habitat (i. e. scalp) when ancestral humans lost significant amount of body hair/fur ~1.2 million years ago. However, sometime between 70,000-170,000 years ago, anatomically modern humans started stitching and wearing clothes and the lice could now colonize a new niche. Indeed, it is quite possible that clothing protected the modern humans against the vagaries of environment and allowed them to explore the world out of Africa ~50000-80000 years ago – a time period that has been validated by the latest studies. And, along with humans and their clothes, the human lice have spread across the globe.

POSTSCRIPT:

Not surprisingly, this is not the end of 'louse research'. Lice found in 1000 year-old Peruvian mummies have subsequently given insights into how and when humans migrated to the New World.....just imagine the unearthed treasury if we could genetically score for lice present in the various populations of the Indian subcontinent.

ACKNOWLEDGMENTS:

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