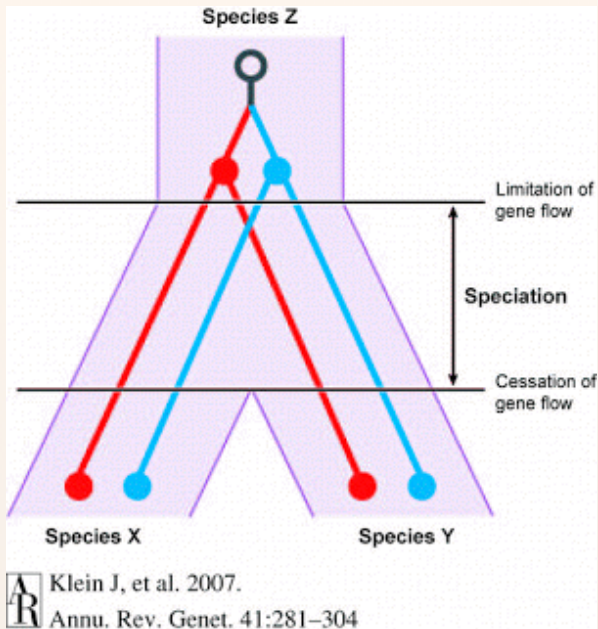


Evo and Proud

Peter Frost's anthropology blog, with special reference to sexual selection and the evolution of skin, hair, and eye pigmentation

→→→ SATURDAY, SEPTEMBER 29, 2012

Trans-species polymorphisms



A trans-species polymorphism. Some genetic polymorphisms are found in distantly related species, having persisted across multiple speciation events. ([source](#))

It is widely known that considerable genetic overlap exists between human populations, even those that are geographically distant from each other and quite different physically. You probably learned in BIO101 that genetic variation is much greater within than between human populations.

It is less widely known that this high degree of genetic overlap also exists between many species that are nonetheless distinct morphologically, physiologically, and behaviorally (Frost, 2011). This is especially so with young sibling species. Such species differ only over a small fraction of the genome—at those genes where a certain variant is adaptive in one species but not in the other. Elsewhere, over most of the genome, the same variant works just fine in both species, either because the gene itself is of little or no value or because certain body functions are pretty much the same in a wide range of organisms.

With time, and reproductive isolation, two sibling species will gradually lose this genetic overlap, as a result of random mutations here and there over the entire genome. The two

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<https://twitter.com/frost61h> (click on image)

L'homme n'est ni ange ni bête, et le malheur veut que qui veut faire l'ange fait la bête — Pascal

Welcome to my blog! For the most part, this page will be an extension of [my website](#), with comments relating to my research. But it will also branch out into more general discussions of human evolution.

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species will be less and less alike even at “junk genes” of little value.

Even so, some overlap will remain. It’s not just that we see the same gene in distantly related species. We also see the same gene with the same set of alleles—a trans-species polymorphism (Klein et al., 1998). A good example is the ABO blood group system. On the basis of that gene marker, I probably have more in common with certain apes than I do with some of my readers. Such polymorphisms have in fact persisted for millions of years across multiple speciation events.

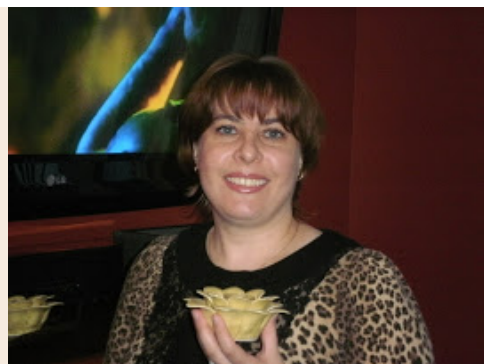
Until recently, it was believed that trans-species polymorphisms were no more than an oddity. Now, it looks like they may be more common than previously thought:

[...] we searched for trans-species polymorphisms between humans and chimpanzees using genome-wide resequencing data for 10 western chimpanzees from the PanMap project and 179 humans from the 1000 Genomes Pilot 1 data. [...] In addition to the MHC region, we identified over 100 cases, a set significantly enriched for transmembrane glycoproteins, which are often involved in interactions with pathogens. To further rule out the possibility of deep coalescent events by chance, we examined patterns of variation in seven samples of Gorilla gorilla. We discovered 25 cases shared among all three species, which we verified by Sanger sequencing. In a subset, within species diversity levels were unusually high and the tree of haplotypes clustered by allelic type rather than by species, providing definitive evidence for trans-species polymorphisms. ([Segurel et al, 2012](#))

At such genes, variation within species exceeds variation between species ... and even between genera.

So just what, then, makes a species a species? The traditional answer is reproductive isolation, and the resulting accumulation of genetic differences over time. Yet this answer seems increasingly problematic. On the one hand, we have cases of living fossils that remain essentially the same over eons of time. Analysis of “junk DNA” would show a steady accumulation of genetic change over those eons, although nothing has changed in appearance or behavior. A coelacanth today is still a coelacanth after millions and millions of years.

On the other hand, we have cases of sibling species that have emerged in recent times and have become quite different from each other both anatomically and behaviorally.



Mon amour, Irina

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About Me

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Yet genetic analysis of such species often shows considerable genetic overlap. If we use any of the usual genetic markers (blood groups, enzymes, etc), individuals may not be assignable to a single species with reasonable certainty.

So if genes in general don't matter, what exactly does? What matters is what matters. Genes for highly adaptive traits matter. Differences you can see matter. Therefore, reproductive isolation in itself is not what makes two populations different; it's the different ways in which they adapt to different environments.

If a population splits in two with one group moving into one environment and the other moving into another, the two groups will nonetheless continue to look and act similarly as long as their respective environments remain similar (of course, if the two groups are human societies, one of them might create a radically different cultural environment). It is the difference in selection pressures, as a result of differing environments, that will drive them apart ... and such differentiation will proceed even if reproductive isolation is still incomplete:

Judging from the number of studies devoted to it, the nature of a reproductive barrier is currently central to the interests of researchers working on speciation. It seems to us, however, that the process of adaptation to the environment is a much more important and interesting part of speciation. The erection of the reproductive barrier may mark the end of speciation, but it tells us little about the process that makes the species differ from one to another, the process that creates biological diversity. ([Klein et al., 2007](#))

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Anthropologist. I've published mainly on sexual dimorphism in human skin color and on the evolutionary origin of European hair and eye colors.

 [View my complete profile](#)

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Posted by [Peter Frost](#) at [12:02 PM](#)

Labels: [balanced polymorphism](#) [trans-species polymorphism](#)

13 comments:



[Chris Crawford](#) said...

" I probably have more in common with certain apes than I do with some of my readers."

I can't resist it: "Would that be through your grandfather or your grandmother?" ;-)

[September 29, 2012 at 4:57:00 PM EDT](#)

Ben10 said...

You're right, interspecies fertility means nothing, which could support the idea that human ethnic groups qualify as sub-species.

But may I add some philosophical considerations?

During my master in the 90's, i was schocked when i had to trigger the ovulation of the female Xenopus, a modest amphibian not famous for its cognitive performances, with an extract from the urine of a supposedly much more advanced organism... a pregnant woman. Apparently, the biological nature of 'love' hasn't change much between a toad and a pretty girl, despite 400 millions years of evolution.

I ironised with my buddies that perhaps the girl of our dreams could, inversely, fall in love with us with an elixer containing the urine extract of a toad. Suddenly those fairy tales of princess falling for a frog looked different to me. Think about that when Halloween comes and show some respect for the 'love-potions' of the witches.

Recently i had this other thought, could we, if we had at our disposition 100% of the DNA sequence of a given organism but in absence of any knowledge from this organism and all other organisms, i.e, a dead world, reconstitute the said organism de novo?

No, because the information carried is context-dependant.

For example, having the entire DNA of one h. sapiens alone, but without any clue of all the other animals, does not carry enough information to reconstitute this h. sapiens completely de novo. We would need the DNA of all the ancestral species of homo, down to the root of the Tree of Life, to recover all the necessary information and make sense of the particular human dna. And side species too, as the information in the bee's dna, for example, doesn't make any sense without the information carried in the flower's DNA.

The chain goes ad finitum and theoritically, all the information carried by ALL the living world on Earth would be necessary, although a good approximation could be made with fewer

well chosen species.

Said otherwise, resurrecting a human being from the deads is not limited to 170lb of mixture mostly composed of dirt + water + information, it implies recapitulating the information flow of 4 billions years of 'evolution' and, since information is not free, this flow has been driven by the cumulated solar output for this duration, so that's a lot of energy to consider.

September 30, 2012 at 12:07:00 PM EDT

Sean said...

How would this affect the case for Neanderthal genes being found in modern humans?

For what it's worth I don't like think the site 'Occidentalist'. I find it rather confusing. The author seems unaware of various ways that pupils are removed from statistics, or the very high proportion of 'black' children in the UK that have a white parent. Or that it has been true for over a decade that most cohabiting black men in the Britain are doing so with a white woman. I think you should link to Ron Unz too.

October 1, 2012 at 5:35:00 PM EDT

Kiwiguy said...

On the issue of differentiation, I see there is a new Lynn paper looking at an aspect of Rushton's rule of 3.

It has been reported in the Daily Telegraph. [here](#) in quite an amusing manner.

Lynn's full paper is [here](#). I saw Jelte Wicherts tweeted that it relied on anonymous survey data so perhaps isn't overly reliable.

October 1, 2012 at 6:32:00 PM EDT

Peter Fros_ said...

Chris,

Perhaps my paternal grandfather. He was a "rake," having married two women and cohabited with at least two others.

Ben,

Actually, an American research team was able to create a synthetic virus, using laboratory chemicals.

http://usatoday30.usatoday.com/news/science/2003-11-13-new-life-usat_x.htm

Sean,

Originally, species were defined primarily in terms of anatomical differences and secondarily in terms of ability to cross-breed. Over the past forty years, this definition has

been stood on its head. We now define a species as a population that is reproductively isolated and unable to cross-breed. By that definition, many currently defined species aren't really species.

This is incidentally the argument that is being used to downgrade Neanderthals to subspecies status. They interbred with us; therefore they aren't a species. Since viral genes have been inserted into the human genome, does it follow that humans and viruses form a single species?

Occidentalist is good with statistics but he needs to develop a critical sense with respect to the sources of his statistics.

Kiwiguy,

Yes, I've read that paper. I don't disagree with its conclusions, but a lot of the sources are very questionable (or nonexistent). The tables also make it difficult to look up the sources.

October 1, 2012 at 7:21:00 PM EDT
<https://www.rx247.net/> said...

Dictionaries define genetic polymorphism as the presence, in appreciable frequencies, of two or more alleles at a locus in a species. Hence H2 polymorphism was expected to have arisen by an unusually high mutation (evolutionary) rate in the house mouse after its divergence from its nearest relative. There was, however no indication that this was the case. On the contrary, Klein and his co-workers found, by the methods then available, indistinguishable alleles in the two European house mouse species, *Mus domesticus* and *M. musculus*, which diverged from each other some 1–2 million years (my) ago. Similarly, in *M. domesticus* populations, whose divergence times could be dated, they found no new variants. Klein's group could also not find any new Mhc (HLA) variants in isolated human populations such as those of the South American Indians and the indigenous populations of Siberia. These and other observations led Klein to the formulation of the trans-species polymorphism (TSP) hypothesis positing that the divergence of similar Mhc alleles predates the divergence of the species in which they occur. The original detection of trans-species polymorphism relied on serological (antibody-based) identification of antigenic molecules. Later, however, the identity of alleles in different species could be confirmed by peptide-mapping analysis of the antigenic proteins. Ultimately, DNA-sequencing not only confirmed the results obtained with the earlier methods, but also introduced a new dimension into the TSP studies. The tests revealed that closely related species such as *M. domesticus* and *M. musculus*, the many haplochromine fish species in East African lakes and rivers, or Darwin's finches on the Galapagos Islands, shared many alleles at not only the Mhc, but also at some of the non-Mhc loci. In more distantly related species, such as human and chimpanzee or the house

mouse and the Norwegian rat, sharing of identical alleles could no longer be demonstrated, but shared related alleles were clearly in evidence. This finding led to the concept of allelic lineages, in which members of a given lineage in one species were more similar to members of the same lineage in another species than they were to other alleles in either of the two species, TSP of Mhc and other loci has since been documented in many species and found applications to a variety of issues in evolutionary biology.

October 2, 2012 at 12:54:00 PM EDT

Mitch said...

So then you would posit that different domestic dog varieties are in fact all different species?

October 2, 2012 at 2:50:00 PM EDT

Sean said...

If I follow, trans-species polymorphisms may mean the argument of **Richard Lewontin** can't easily be defeated by using more loci? I was wondering if Klein's work on the MCH cast doubt on the supposedly Neanderthal introgression into the modern human MHC region.

Lynn's paper cites Baker's tome 'Race' but ignores what it contains about the tiny endowment of Bushmen (Bushman are never gay, make of that what you will). Bushmen females have sexually selected characteristics: big behinds, genitalia. Penis size is irrelevant, it's an aid to impregnating only when the **female has multiple partners** immediately before or after (consensually or otherwise). In chimps the alpha roughs up the female and makes her have sex with him and his pals. Chimps have big testes, but small penes. Black Africans have smaller testes and more effective sperm. I would say that if anything the evidence is for African males being adapted to sperm competition (they're also rated as better looking). The trouble with Rushton is that he ignores the reproduction of females; European women are more fertile than Black African women.

October 2, 2012 at 3:25:00 PM EDT

Peter Fros_ said...

Http,

Amazing, a spammer who actually read and understood my post!

Mitch,

I'm saying we should give more weight to anatomical criteria, and less to reproductive isolation, when defining species. Of course, there is no perfect definition because these two sets of criteria are often at cross-purposes.

Dog breeds are a good example. Their morphological differences are like what we see between different genera.

Yet dogs can interbreed, and the genetic data show massive overlap among breeds.

Sean,

If we use more loci, the picture will remain fundamentally the same: more variation within than between human populations. The problem is that we misunderstand the picture. Not all variability is of equal value, and the variability we see between populations (which reflects differences in selection pressures) differs qualitatively from the variability we see within populations (where variability tends to be insensitive to the leveling effect of similar selection pressures, i.e., junk variability or balanced polymorphisms).

I agree with your second point. Large penises are an adaptation to high levels of polygyny (and sperm competition).

October 3, 2012 at 3:07:00 PM EDT

Ben10 said...

Since archaic humans have interbred with pre-moderns in africa or elsewhere, couldn't they also interbreed with chimps and gorillas?

I mean even indirectly, like Erectus interbred with Australopithecine which in turns interbred with Gorillas or chimps.

October 5, 2012 at 11:58:00 AM EDT

Anonymous said...

"On the issue of differentiation, I see there is a new Lynn paper looking at an aspect of Rushton's rule of 3.

It has been reported in the Daily Telegraph. here in quite an amusing manner.

Lynn's full paper is here. I saw Jelte Wicherts tweeted that it relied on anonymous survey data so perhaps isn't overly reliable.

NE Asians having basically chimpanzee sized genitals (which are half the size of humans) sounds a bit dodgy.

Perhaps the NE Asian tendency to vacillate between authoritarian paterfamilias and humble servant has had some effect.. (given that it's all self report)?

October 5, 2012 at 3:40:00 PM EDT

James A. Donald said...

There has been a lot of work on speciation in three spined fresh water sticklebacks.

I would interpret the results as follows:

About ten thousand years ago, salt water three spined

sticklebacks entered numerous separate fresh water rivers, and evolved independently into various kinds of fresh water three spined stickleback.

In many cases, they evolved into the same species of fresh water three spined stickleback despite the fact that there was absolute geographic separation - the rivers were separate.

In other cases, they evolved into two species in the same river, limphetic and benthic, despite extensive interbreeding between the two species that continues to this day:

So geographic separation and independent evolution did not produce separate species, and lack of geographic separation and frequent interbreeding did not prevent the evolution of distinct and separate species.

The benthic and limphetic kinds had evolved apart in the face of massive gene flow, and formed meaningfully and importantly different separate kinds despite thousands of years of massive interbreeding, despite total and extreme failure to comply with the biological species concept, while the allopatric river of origin kinds had failed to drift apart despite perfect and complete separation for vast periods, and therefore were not meaningfully separate species, despite perfect compliance with the biological species concept.

The implication of this experiment is that prolonged and total separation failed to result in the evolution of separate species, while massive and continuing interbreeding failed to prevent or reverse the evolution of separate species.

October 10, 2012 at 4:16:00 AM EDT



Rev. Right said...

A coelacanth today is still a coelacanth after millions and millions of years.

They may look similar, but wouldn't millions of years of reproduction make that impossible? The modern coelacanth must have many 'improvements' that don't necessarily show up in gross morphology, such as organ functioning or the efficiency of cellular processes. Right?

Do you think you could (theoretically) successfully mate a modern coelacanth with one from 60 million years ago?

October 26, 2012 at 1:55:00 PM EDT

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