The FOXP2 gene supports Neandertals being fully human

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Speech enables humans to communicate effectively and is probably the most prominent trait which distinguishes people from other creatures. However, some people are born with an impaired ability for language and speech development, a syndrome known as *specific language impairment* (SLI). Children with SLI lag behind their peers in language development and comprehension, which contributes to learning and reading disabilities in school. Recently, a defective gene in a three-generation family that had the SLI speech disorder was identified as the *FOXP2* gene. The *FOXP2* gene was also defective in a non-relative who suffered from the same disorder.[1,2] Those with a defective FOXP2 are more prone to display SLI difficulties, but the same mutational variants do not always result in this disorder, reflecting the complexity of the genetics of speech.[3]

The entire DNA sequence of the human *FOXP2* gene is known, and the genetic homologues in chimpanzee, gorilla, orangutan, rhesus monkey and mouse have recently become available. The FOXP2 proteins are identical in chimp, gorilla and rhesus monkey. Orangutan and mouse differ by only two amino acids outside the Q regions (The Q regions are not taken into account, since they are subject to rapid mutations (due to slippery DNA polymerases)). In contrast to these five sequences, the human version differs at two positions. Depicted in figure 1, amino acid residue 304 has 'N' for humans, 'T' for the other five organisms; amino acid residue 326 has 'S' for humans, 'N' for the other five organism.[2] The two amino acid variations are present in all 226 examined human samples and typify the human *FOXP2* gene sequence. The *FOXP2* genes and proteins can thus be used as an *indicator gene*, a genetic tool to distinguish between humans, primates and other species (figure 1).

The recent DNA analysis of the Neandertaler, who according to evolutionary timescales evolved around 400 thousand years ago, showed they carried the exact same FOXP2 protein (deduced from the DNA sequence) as modern humans,

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                1          11         21         31         41         51         61         71         81         91

Human           MMQESATETI SNSSMNQNGM STLSSQLDAG SRDGRSSGDT SSEVSTVELL HLQQQQALQA ARQLLLQQQT SGLKSPKSSD KQRPLQVPVS VAMMTPQVIT
Chimp           .......... .......... .......... .......... .......... .......... .......... .......... .......... ..........
Gorilla         .......... .......... .......... .......... .......... .......... .......... .......... .......... ..........
Orangutan       .....V.... .......... .......... .......... .......... .......... .......... .......... .......... ..........
Rhesus          .......... .......... .......... .......... .......... .......... .......... .......... .......... ..........
Mouse           .......... .......... .......... .......... .......... .......... .......... .........E .......... ..........


                101        111        121        131        141        151        161        171        181        191

Human           PQQMQQILQQ QVLSPQQLQA LLQQQQAVML QQQQLQEFYK KQQEQLHLQL LQQQQQQQQQ QQQQQQQQQQ QQQQ-QQQQQ QQQQQQQQQQ QQHPGKQAKE
Chimp           .......... .......... .......... .......... .......... .......... .......... ....Q..... .......... ..........
Gorilla         .......... .......... .......... .......... .......... ....-..... .......... ...--..... .......... ..........
Orangutan       .......... .......... .......... .......... .......... ....-..... .......... ....-..... .......... ..........
Rhesus          .......... .......... .......... .......... .......... ....-..... .......... ....-..... .......... ..........
Mouse           .......... .......... .......... .......... .......... ....-..... .......... ....Q..... .......... ..........


                201        211        221        231        241        251        261        271        281        291

Human           QQQQQQQQQQ LAAQQLVFQQ QLLQMQQLQQ QQHLLSLQRQ GLISIPPGQA ALPVQSLPQA GLSPAAIQQL WKEVTGVHSM EDNGIKHGGL DLTTNNSSST
Chimp           .......... .......... .......... .......... .......... .......... .......... .......... .......... ..........
Gorilla         .......... .......... .......... .......... .......... .......... .......... .......... .......... ..........
Orangutan       ......-... .......... .......... .......... .......... .......... .......... .......... .......... ..........
Rhesus          .......... .......... .......... .......... .......... .......... .......... .......... .......... ..........
Mouse           .......-.. .......... .......... .......... .......... .......... .......... .......... .......... ..........


                301        311        321

Human           TSSNTSKASP PITHHSIVNG QSSVLSARRD
Chimp           ...T...... .......... .....N....
Gorilla         ...T...... .......... .....N....
Orangutan       ...T...... .......... .....N....
Rhesus          ...T...... .......... .....N....
Mouse           ...T...... .......... .....N....
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Figure 1. The letters indicate the leading 330 amino acids of FOXP2 protein of human, chimpanzee, gorilla, orangutan, rhesus monkey and mouse. The amino acid sequences show two poly-glutamin stretches (indicated in bold) and the two specific mutations (indicated by arrows) which set the human sequence apart from the rest of the presented mammals (the N on position 304 and the S on position 326). The terminal 386 amino acids of FOXP2 are identical in all species and are not shown here. Sequences are as reported in Enard *et al*.[2]

including the N and S at position 304 and 326, respectively.[4] In addition to morphological and physiological evidence for the vocal tract, including the modern hyoid bone,[5] molecular biology is now providing support that Neandertals were fully equipped for speaking complex languages. The *FOXP2* genes found in Neandertals therefore show that they were *Homo sapiens*. These findings are entirely in accord with the creationist's stance that Neandertals were fully human (post-Flood) inhabitants of Europe and Asia.

References

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Mud experiments overturn long-held geological beliefs

Tas Walker

New research presented in *Science* documents how, contrary to conventional wisdom, mud can be deposited from rapidly flowing water.[1] These findings cut across beliefs held by geologists for over a century and signal that 'mudstone science is poised for a paradigm shift.'[2]

Using specially designed laboratory equipment, Juergen Schieber, John Southard and Kevin Thaisen have shown that mud-sized material will deposit under much higher current velocities than previously thought.

How to move mud

Schieber, the lead researcher, said it should have been obvious that mud can settle from flowing water.

> 'All you have to do is look around. After the creek on our university's campus floods, you can see ripples on the sidewalks once the waters have subsided. Closely examined, these ripples consist of mud. Sedimentary geologists have assumed up until now that only sand can form ripples and that mud particles are too small and settle too slowly to do the same thing.'[3]

With graduate student Kevin Thaisen, Schieber designed and built a 'mud flume' that looks a bit like an oval race track. They installed a motorized belt with paddles to keep the muddy water moving at a constant speed.

For mud they used extremely fine clays, calcium montmorillonite and kaolinite, as well as natural lake muds. According to conventional geological wisdom, talc-sized clay material would not settle from rapidly moving water. However, after only a short time the mud was moving along the bottom of the flume. According to Schieber, 'They accumulated at flow velocities that are much higher than anyone would have expected.'[4] They report that flow rates sufficient to move sand will still allow the deposition of clay sized fractions.

Mudslinging the Bible

For more than a hundred years, geoscientists have *assumed* that long periods of quiet water conditions are required for the deposition of mud. Based on that belief, whenever geologists have encountered mud deposits in the sedimentary record they have interpreted them as forming in a tranquil deposition environment.

Long-age scientists have long attacked the idea that Noah's Flood was a real, historical event, and disparaged the claim by young-earth creationists that the year-long Flood can account for most of the geological deposits exposed on the earth today. One of their major arguments concerns this widely held but erroneous belief.

For example, Alan Hayward uses the Haymond rock formation in the USA for this purpose, describing it as almost a mile (1.6 km) thick, extending over a large area and containing more than 30,000 alternating layers of shale and sandstone.[5]

Hayward assumed the conventional geological beliefs about the deposition of mud as fact:

> 'Shale is made of compacted clay. As most readers will have noticed, clay consists of exceedingly fine particles which take a long time to settle in water. Turbulence keeps them in suspension and consequently clay will only settle in calm water.'

He then uses these erroneous ideas to disparage the biblical account of the global Flood: 'How did the Flood bring in a thin layer of sand and deposit it over a large area, then bring in a thin layer of clay and all this to settle quietly—all in a matter of minutes? And then repeat the whole performance fifteen thousand times?'

He then mocks the scientific standing of Flood geologists: 'It seems rather obvious that there is only one way in which a series of events could possibly occur. God would have to