

Role of NAGPA, GNPTAB and GNPTG genes in the development of speech and language in *Homo sapiens*

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The genetic architecture that underlies complex traits, such as speech and language in humans, makes it extremely unlikely that one single gene has been selected in the evolution of our language capabilities. Hence the purpose of this research was to compare the sequences of NAGPA, GNPTAB and GNPTG, genes whose mutations are linked to stuttering in humans [1], among species for which the nucleotide sequences of the entire genome are known, and are relevant to human evolution, that is: *Homo sapiens*, *Pan troglodytes*, *Pongo abelii*, *Macaca mulatta*, *Mus musculus*, *Equus caballus*, *Gallus domesticus*, *Taeniopygia guttata* and *Danio rerio*. In this way, through the study of homologies and divergences at the level of the encoded proteins, we aim to achieve greater knowledge about the genetic control of the organization of brain areas that are involved in the function and evolution of human language. With an extensive bioinformatics analysis regarding expression of GNPTAB, GNPTG, and NAGPA genes, we have found one amino-acid substitution between *Homo sapiens* and *Pan troglodytes* in each of these three genes. All substitutions have a high functional value. Therefore, it is reasonable to infer that NAGPA, GNPTAB and GNPTG genes have had a crucial role in the evolution of human language.

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References

- [1] Kang and Drayna (2011) Genetics of speech and language disorders. *Annu Rev Genomics Hum Genet* 12: 145-64.

Key words

Human language, speech disorders, stuttering, evolution.