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Genetic equidistance at nucleotide level

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Abstract

The genetic equidistance phenomenon shows complex taxa to be all approximately equidistant to a less complex species in amino acid percentage identity. The overlooked mystery was re-interpreted by the maximum genetic diversity hypothesis (MGD). Here, we studied 14 proteomes and their coding DNA sequences (CDS) to see if the equidistance phenomenon also holds at the CDS level. We found that the outgroup taxon was equidistant to the two more complex taxa species. When two sister taxa were compared to human as the outgroup, the more complex taxon was closer to human, confirming species complexity to be the primary determinant of MGD. Finally, we found the fraction of overlap sites to be inversely correlated with CDS conservation, indicating saturation to be more common in less conserved DNAs. These results establish the genetic equidistance phenomenon to be universal at the DNA level and provide additional evidence for the MGD theory.

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