## Comparative studies for evolutionary and linguistic analyses of mitochondrial Chordata and Invertebrata genomes

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Mithochondrial genes and genomes have long been a major focus in molecular evolution, and these genomes are an excellent candidate for working out the details demonstrating the power of evolutionary genomics. Mithochondrial genomes also have a strong advantage over nuclear genes in that they are unlikely to have experienced intraspecific recombination events.

In the present contribution, we will focus on the complete mitochondrial genomes of Chordata and Invertebrata, available through the MitBASE databases (1,2). At present the mitochondrial genomes of 74 chordata and 45 invertebrata have been sequenced and published. These genomes have been analysed in order

\* to compare the genome organisation inter- and intra- taxonomic groups

\* to infer phylogenetic relationships

\* to compare the genomic language within the different taxonomic groups. References

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2 Lanave C, Licciulli F, Liuni S, Attimonelli M."Update of AMmtDB: a database of multi-aligned metazoa mitochondrial DNA sequences." 2000, Nucleic Acids Res. 28:153-154