Detecting genomic features under weak selective pressure: the example of codon usage in animals and plants

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ABSTRACT
Large scale experiments of gene inactivation in yeast have shown that 50% of genes have no detectable impact on the phenotype, and similar observations have been made in other model organisms. This apparent paradox is probably due to the fact that many genes only have a marginal contribution to the fitness of organisms. Because of the size of populations and the number of generations that can be studied in laboratories, experimental approaches only permit to detect functional elements that have a strong phenotypic impact. Comparative sequence analysis can help to solve this problem: the analysis of sequences evolution permits to detect the action of selection, and hence to reveal functional features of genomes. This approach will be illustrated by the study of synonymous codon usage in animals and plants.