Secondary structure changes according to evolutionary age

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The origin of new genes is an important factor for innovation in all organisms. For a long time was thought that all modern genes forms were derived from other genes through the processes of duplication-divergence and horizontal gene transfer. Today, several other mechanisms are known to be involved in gene origin, such as exon shuffling, retroposition, mobile elements, lateral transfer and *de novo* origination. The *de novo* origin term refers to when a non-coding region start to code a new gene. This concept of "orphan genes" is based on comparative genomics findings showing that about 10-30% of all genes in a species show no similarity to existing proteins. In this study we analyzed 66 reference proteomes managed by the Quest for Orthologs (QfO) consortium and, estimating their age through orthology inference algorithms, we analyzed the differences of structural distributions between these groups. We tried to answer the question: Sequence independent properties are different depending on the evolutionary age of the proteins? Using information of secondary structure prediction, we noticed the presence of less structured sequences in eukaryotes than in prokaryotes. Furthermore, we found a decrease of structure in newer sequences in eukaryotes, while the orthologous proteins in prokaryotes have similar distribution parameters. We also explored the secondary structure of noncoding sequences and found that the source of new genes is compatible with the readily achieved by translation of these sequences. Perhaps the origin of secondary structures is the simple reflection of the individual potential contribution of each type of residue. Thus, the secondary structure content achieved by translation or intergenic antisense sequences is compatible with that present in said orphan genes or *de novo*.