

Poster C-9

How protein evolution measured by similarity change and stop codon incidence depends on the genetic code



Authors:

Francisco Prosdocimi (*UFMG*)

Henrique Melo (*UFMG*)

Eduardo R Capanema (*UFMG*)

J Miguel Ortega (*UFMG*)

Short Abstract: One important source for protein evolution is the successive incurrence of mutations on the coding DNA. Our results support the hypothesis that one important factor on protein evolution is the codon composition, since both similarity change and stop codon incidence seem to depend on the genetic code.

Long Abstract:

One important source for protein evolution is the successive incurrence of mutations on the coding DNA. It is conceivable that amino acids coded by one single codon such as M and W might be more suitable of contributing to changes in similarity in genes under mutation than those with two or more codons, since some mutations would turn out to be synonymous. During this mutation driven evolution, the incidence of stop codons might also straightly depend on the codon usage, since some of them may be converted to stop codons by just one mutation. We developed a model where proteins composed of 100 residues coded by a single codon were submitted to increasing rounds of random mutation. We observed that, under 150 rounds of mutation, M and W polymers showed equivalent and lowest identity to the original proteins (35%), followed by polymers coded by two codons (40%, C, D, E, F, H, K, N, Q, Y). A polymer made out of I reached 45% identity, independently of the codon used amongst 3 possible. Similar result was obtained for the four different codons of the amino acids coded by four codons (50% final identity, A, G, P, T, V). As suspected, S codons behave as a group of two and a group of four codons, showing 40% and 50% identity, than, in average, S seems to evolve as fast as I. An interesting behavior was observed for R and L that showed three groups of two codons in respect to the final identity, all of them being more resistant than all others. We then set up for determining the ratio of incidence of stop codons in diploid copies of the polymers, and observed that the slot of time without the incidence of stop codons in at least one copy, during the entire mutation period, varied from 10% up to 95%. Remarkably, M was the most prone amino acid to yield the occurrence of stop codons in both copies and W the least one. Amino acids coded by two codons yielded intermediary rates but, impressively, both codons always attained the same result. Putting the experiments together, we may raise the hypothesis that one important factor on protein evolution is the codon composition, since both similarity change and stop codon incidence seem to depend on the genetic code. We are currently applying mutation on clusters of orthologs that are either evolutionary close or distant to evaluate how codon composition may be affecting protein evolution.