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Search for coevolution in protein interaction network of translation termination factors

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Motivation and Aim: In eukaryotes, two proteins named eRF1 and eRF3 (abbreviation for Eucaryotic Release Factor) play major role in translation termination process. Aside from providing release of a nascent peptide from a ribosome, eRFs couple translation termination with other molecular pathways and therefore have a vast network of interactions with other proteins. Although these proteins are highly conservative, their sequences may vary even at low taxonomic level, thus rising a question whether such alterations reflect any degree of coevolution.
Methods and Algorithms: To look for traces of coevolution, we selected a set of proteins known to interact tightly with either eRF1 or eRF3 in the *Saccharomyces cerevisiae* yeast. These proteins are the following: Sup45 (eRF1) versus Sup35, Upf1, Rli1, Dbp5, Tif35, and Tif34; Sup35 (eRF3) versus Sup45, Upf1, Upf2, Upf3, Pab1 (yeast gene names are indicated). We focused at low taxonomic level using primarily different *Saccharomyces* yeast species. The protein sequences were obtained from Genbank and from "The 1002 Yeast Genomes Project" site (http://1002genomes.u-strasbg.fr/files/) [1]. We aligned sequences using MUSCLE and tested the resulting alignments using CAPS2 software (http://caps.tcd.ie/) [2].
Results: The proportion of variable positions varied from 1 to 10 % for different proteins within one species and from 5 to 15 % at interspecific level, with most substitutions occuring in a small number or just in a single sample. Such level of conservativeness imply that most sites within one protein or a pair of proteins might be not coevolving. Results of CAPS2 analysis supported this assumption: we found no significant correlation between amino acid substitutions in any sites. However, we are proceeding the analysis using a larger taxonomic sample.
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References

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