Proceedings of the Joint Meeting AGI-SIBV-SIGA
Assisi, Italy – 19/22 September, 2011
ISBN **978-88-904570-2-9**

Poster Communication Abstract – 9.52

STRUCTURAL VARIABILITY IN GENE PROMOTER

BUIATTI M.*, LIVI R.**, CALISTRI E.*,**

*) Dipartimento di Biologia Evoluzionistica, Università degli Studi di Firenze, Via Romana 19, 50125 Firenze (Italy)
**) CSDC - Dipartimento di Fisica, Università degli Studi di Firenze, INFN - Firenze,
Via G. Sansone 1, 50019 Sesto Fiorentino (Italy)

Gene promoters, phylogensis, Shannon entropy, base composition

In a previous paper (Calistri et al., 2011), we analysed GC/AT ratios along the 1000 nucleotide sequences upstream of the TSS in wide sets of promoters belonging to organisms ranging from bacteria to pluricellular eukaryotes and showed very clear phylogenetic trends throughout evolution of promoter sequence base distributions. We are now interested to search a putative correlation between the increase in organismal complexity observed during phylogenesis and the increase of variability in their promoter structures. To test this hypothesis we have introduced a suitable spatial entropy indicator (Positional Shannon Entropy), which allow the measure of the variability content in promoters sets. Every species examined shows its own specific entropy along the sequences and shows regions with different levels of information. By selecting our sequences according to the presence/absence of the TATA-box or comparing housekeeping versus tissue specific or single versus alternative promoters, we obtain, in higher vertebrates, structurally different classes of sequences.

Thus, promoter functional differences correlate with structural differences, which can also be appreciated through the analysis of the base distributions along promoters, by which we manage to identify different structural categories, the composition profiles allowing a division between genes with a small density gradient and others with a straight one.

This would be in accordance with the progressively more elaborate regulation of gene expression systems that seem to account for organism's complexity and the widening of the functional variability spectrum. We show an increase in intraspecific structural diversification among promoters during evolution: more complex organisms, that is the ones with a higher number of differentiated tissues or stages of development, possess more diversified promoters. We hypothesize that heterogeneity in structure may correspond to functional variability, which has an adaptive value, as variable gene expression helps to cope with variable environments and/or changes during development and might also favour adaptation during evolution.