

Poster H-39

Comparative structure-based analysis of amino acid composition in proteins adapted to cold and hot environments



Authors:

Gisle Sælensminde (*University of Bergen*)

Inge Jonassen (*University of Bergen*)

Short Abstract: We present a methodology for performing comparative analysis of amino acid composition of homologous proteins in species adapted to different temperatures. It allows inclusion of structural information enabling differentiation between protein core and surface. We present an analysis showing clear trends in proteins adapted to cold environments.

Long Abstract:

Species adapted to extreme environments with respect to temperature are known as thermophiles if the species are adapted to temperatures above 60 degrees centigrades, and psychrophiles if adapted to temperatures below 20 degrees

We studied the occurrence frequencies of amino acids in aligned positions between close homologs from species living in environments separated by at least 20 degrees in temperature. We performed separate analyses of prokaryotes and of vertebrate eukaryotes for which we could obtain temperature information. Sequence data was extracted from the UniProt database, and pairwise alignments between close homologs were constructed. When possible, the sequences were mapped to experimentally determined structures from the PDB, allowing classification of individual residues as buried or exposed in the protein structure.

We found that the changes occurring on the surface and in the core of the proteins often have opposite effect, canceling each other. This was particularly the case for cold-adapted prokaryotes, where there have been reported no overall difference in amino acid composition as compared to mesophilic prokaryotes, but the difference between the surface and core were clear both for thermophilic prokaryotes as well as eukaryotes.

The most notable effect we found was that charged amino acids are more frequent on the surface of proteins adapted to a warmer environment, while they are less common in the core of the same proteins. Another trend is that there is less small amino and more long-chained, non-aromatic amino acids on the surface of proteins adapted to the warmer environment. The tendency for the core and surface of the proteins to change oppositely in psychrophiles vs mesophiles may explain why fewer differences have been reported for psychrophiles vs mesophiles as compared to mesophiles vs thermophiles.

Another finding is the proteins from eukaryotes apparently have adapted to cold environments in a different way from prokaryotes. Cold-adapted prokaryotes mainly has more charged and

polar amino acids in the core, and less charged and longchained on the surface. The cold-adapted eukaryots has unlike the cold-adapted prokaryots, less proline and more aliphatic residues on the surface, and less aliphatic residues in the core. This indicates that eukaryotic proteins adapts to cold environments in a different way from prokaryots, which leads us to speculate that there may be many ways for a protein to adapt to a cold environment.