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Abstract

Have nutritional constraints been involved in protein evolution?.

Significance and context

Organisms inhabiting different environments encounter different environmental factors influencing their growth and survival. As Cornu *et al*. point out in this paper, this raises the question of whether ecological fluctuations could alter biological macromolecules. The publicly funded genome sequencing projects and the characterization of complete metabolic pathways now allow the search for such ecological imprints in the proteome. A widely accepted principle is that protein evolution is mainly determined by constraints on activity, specificity, folding and stability. But other constraints may come into play, in particular nutritional ones. The availability of the elements used in the construction of proteins is not only determined through metabolic pathways within the organism but also by the geochemical cycles operating at the Earth's surface. Many hypotheses concerning the chemical composition of proteins are based on constraints independent of element availability or metabolism, such as structure and function or molecular phylogeny. To assess the hypothesis that nutritional factors might have influenced the evolution of protein structure, Cornu *et al*. computed the atomic composition of enzymes involved in element assimilation in two model microorganisms - the bacterium *Escherichia coli* and the yeast *Saccharomyces cerevisiae*.

Key results

The authors investigated sulfur usage in proteins that are involved in sulfur assimilation in *E. coli* and *S. cerevisiae*. The protein sets used for the analyses included the transporters of inorganic sulfur and the enzymes involved in synthesis of methionine and cysteine. Comparison of the distribution of sulfur atoms in the proteins of the sulfur metabolism set to the distribution of sulfur atoms in the total protein set revealed that, in both organisms, the proteins involved in sulfur-containing amino-acid biosynthesis contain fewer sulfur atoms than does the total set of proteins. The authors postulate that a bias against sulfur-containing amino acids occurred in response to nutritional constraints such as environmental sulfur scarcity. They further tested this hypothesis by studying the proteins involved in sulfur metabolism in mammals. As mammals are unable to assimilate inorganic sulfur compounds, all the sulfur atoms in their proteins derive from methionine and cysteine. Cornu *et al*. found no relative sulfur depletion in mammalian sulfur-metabolizing enzymes. Next, Cornu *et al*. analyzed carbon usage in carbon-assimilatory proteins of both *S. cerevisiae* and *E. coli*, to determine whether metabolic imprinting of protein atomic composition is a more general phenomenon in protein evolution. They found that carbon-assimilating proteins do have fewer carbon atoms in their side chains relative to the side chains of the total protein sets. Cornu *et al*. also looked at the nitrogen content of the side chains of the nitrogen-assimilatory *S. cerevisiae* proteins involved in the conversion of ammonia, urea, allantoate and proline. They found that these nitrogen-assimilating proteins contain on average a decreased number of nitrogen atoms in their side chains, relative to the total set of yeast proteins, whereas no significant deviation in nitrogen usage was observed for the yeast sulfur-assimilatory protein set, which was used as a control.

Links

Yeast genome sequence and other information is available from the *Saccharomyces* Genome Database, and information on *E. coli* can be obtained from the Colibri web server.

Conclusions

Significant correlations between atomic composition and metabolic function were found in sulfur- and carbon-assimilatory enzymes in both *E. coli* and *S. cerevisiae*. Analysis of atomic composition reveals a systematic bias in the relevant elements in the assimilatory proteins of these two highly divergent microorganisms, suggesting that the elemental composition of biological polymers can be influenced by ecological constraints during evolution.

Reporter's comments

Cornu *et al*. have proposed an interesting hypothesis focusing on the nutritional constraints on protein evolution. Comparisons with other organisms of the same genera living in different environments should be informative, highlighting the value of sequencing the genomes of many different organisms. A comparison with archaea will definitely provide key insights into the evolution of organisms adapting to various environmental conditions.

Table of links

Science

Saccharomyces Genome Database

Colibri web server

References

1. Cornu PB, Kerjan YS, Marlière P, Thomas D: Molecular evolution of protein atomic composition. Science. 2001, 293: 297-300. 0036-8075