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Essential amino acid usage and evolutionary nutrigenomics of eukaryotes - insights into the differential usage of amino acids in protein domains and extra-domains

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ABSTRACT. Nutrigenomics studies the effects of nutrients on the genome, transcriptome and proteome of organisms, and here an evolutionary standpoint on this new discipline is presented. It is well known that metazoan organisms are unable to synthesize all amino acids necessary to produce their proteins and that these essential amino acids (EAA) must be acquired from the diet. Here, we tested the hypothesis that conserved regions such as protein domains (DM) have different essentiality indexes and use different sets of amino acids when compared to extra-domains (ED) and proteins without mapped domains (WD). We found that auxotrophic organisms have a tendency to use less EAAs in DM than do prototrophic ones. Looking into the amino acid usage of eukaryotic proteins downloaded from KEGG and COG, we showed that WD have a usage of amino acids closer to DM, which suggests that proteins without mapped domains behave as large domains. Using an ED index that shows the proportion of prevalent amino acids in ED, a differential usage of amino acids in domains versus extra-domains was demonstrated. Protein domains were shown to be enriched with a higher number of EAA, and it may be related to the fact that these amino acids had lost their biosynthetic pathways in metazo-

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ans during a great amino acid pathway deletion, followed by a nutritional constraint that may have happened close to the conquest of the terrestrial environment. Thus, the proportion of EAA outside domains could have decreased during evolution due to nutritional constraints.

Key words: Amino acid usage; Essential amino acid; Protein domains

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