

Review of: "Why We Stop Synthesizing Essential Amino Acids: The Extracellular Protein Hypothesis"

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Potential competing interests: No potential competing interests to declare.

The nature of and reasons for the commonality of "essential amino acids" in many eukaryotes has not been explained. This author examines the need for essential amino acids across the domain Eukarya, which is capable of protein ingestion. The essential amino acids are highly similar throughout the domain (from humans to slime moulds). The author notes that the (loss of) essential amino acid synthesis enzymes is similar and arises from mutation. These losses are absent from the plant kingdom. His analysis shows that there is a clear composition boundary between intracellular (cell metabolic) and extracellular (majorly structural) protein amino acid compositions. In animals, the extracellular matrix protein - high in non-essential Pro, Gly, and Ala especially - makes up a high proportion of protein mass. Crucial cell metabolism relies heavily on recycling intracellular proteins, which contain a higher proportion of the essential amino acids that have to be derived from ingestion.

The author presents an "Extracellular Protein Hypothesis" which explains that the need to synthesize non-essential amino acids for extracellular proteins has counter-intuitively led to the common "essential amino acids" found in eukaryotic organisms that have acquired the ability to ingest. Cost-benefit analysis (of enzymic synthesis vs. external acquisition) is one of a number of variables considered numerically.

This article is very clearly written and well argued, with analyses of literature data. It must have a contribution to make to nutrition and to tackling deficiencies and is worthy of publication.

One suggestion by this reviewer is that the author looks at insectivorous plants, which throughout evolution have been capable of ingesting (and using) animal protein, to see if there has been a loss of any amino acid synthesis capabilities through genetic shift, drift, and mutation.