

QUALITATIVE ANALYSIS OF THE NITROGEN METABOLISM NETWORK

Montagna, E.; Torres, B.B.

Depto. de Bioquímica, IQ-USP, C.P. 260077 - 05508-900, São Paulo, SP.

A classical biochemical concept states that metazoans may use NH_4^+ as nitrogen source. Data from primary literature do not support this assumption. The aim of the present work was to establish a relationship between NH_4^+ , the origin of nitrogen present as α -amino group in metazoans and the supply of these compounds by nitrogen-fixing organisms. In order to trace this nitrogen flux, a deep revision of asystematic data found in literature and data banks was performed. The pathways involved were analyzed through enzymes' structure, function, final product, position in metabolic network, and their relationship with the organisms' physiology, environment and evolutionary history. Data analysis shows that nitrogen uptake in metazoans occurs mainly as α -amino acid and that they are unable to carry out net synthesis of amino acids from any inorganic nitrogen source. Nitrogen assimilation occurs mainly via glutamate dehydrogenase and transaminations, using α -amino acids provided by plants and prokaryotes from NH_4^+ , nitrite and nitrate, as well as by prokaryotes that are able to fix atmospheric molecular nitrogen. Nitrogen fixation is most more widespread in nature than stated by most biochemistry textbooks, going beyond the rhizosphere, reaching extreme environments made possible by physiological features that support the viability of the process in unfavorable conditions. The nitrogenase complex is very conserved among different organisms, revealing its ancient origin, representing a strong morphofunctional restriction to the nitrogen flux, even without symbiosis.