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Role of Circulating Amino Acids and Gut Microbiota in Health and Healthy Ageing

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Extended Abstract

Amino acids circulate abundantly in the blood, acting as essential mediators across all organ systems. Variations in these circulating amino acids significantly impact physiological processes, playing critical roles in the onset and progression of various diseases [1]. Studies suggest that amino acid profiles can serve as biomarkers for disease prediction, diagnosis, and response to therapies. However, findings on the roles of circulating amino acids in disease are often inconsistent, highlighting the need for further research.

Gut microbiota regulates vital health functions, including metabolism, digestion, and immune modulation. Dysbiosis—an imbalance in the gut microbiota—is associated with a wide range of health disorders, including metabolic, cardiovascular, and neurological diseases. Recent studies emphasize complex interactions between amino acids and gut microbiota, indicating a symbiotic relationship. We propose that interventions such as exercise and diet may beneficially modulate gut microbiota and amino acid profiles, supporting disease prevention and promoting healthy aging.

Our research, involving approximately 9,000 participants across various age groups, aimed to clarify associations between circulating amino acids and diseases such as diabetes, hypertension, and metabolic syndrome, which are becoming increasingly prevalent. In a recently completed cohort study, we attempted to explore potential links between gut microbiota, amino acids, and changes in physical, physiological and neurological functions among elderly individuals. To measure, plasma free amino acid (PFAA) levels, we used high-performance liquid chromatography coupled with electrospray ionization-mass spectrometry. Gut microbiota was analyzed through shotgun metagenome sequencing of collected stool samples.

Our findings (Fig. 1) indicate that specific profiles of plasma-free amino acids (PFAAs) are associated with lifestyle-related diseases (LSRDs) [2]. We identified distinct patterns of PFAA alterations linked to hyperuricemia within LSRDs, which we refer to as the 'amino-uric interaction.' Additionally, we observed positive associations between branched-chain amino acids (BCAAs) and hypertension [3], as well as significant correlations of isoleucine, leucine, and phenylalanine with reduced kidney function [4]. Data analysis from our cohort study is ongoing, and we anticipate sharing the results at JBRP 2024. This research could offer valuable insights into the interplay between gut microbiota, amino acids, and healthy aging, potentially informing the usefulness of new interventions to enhance health and promote longevity.

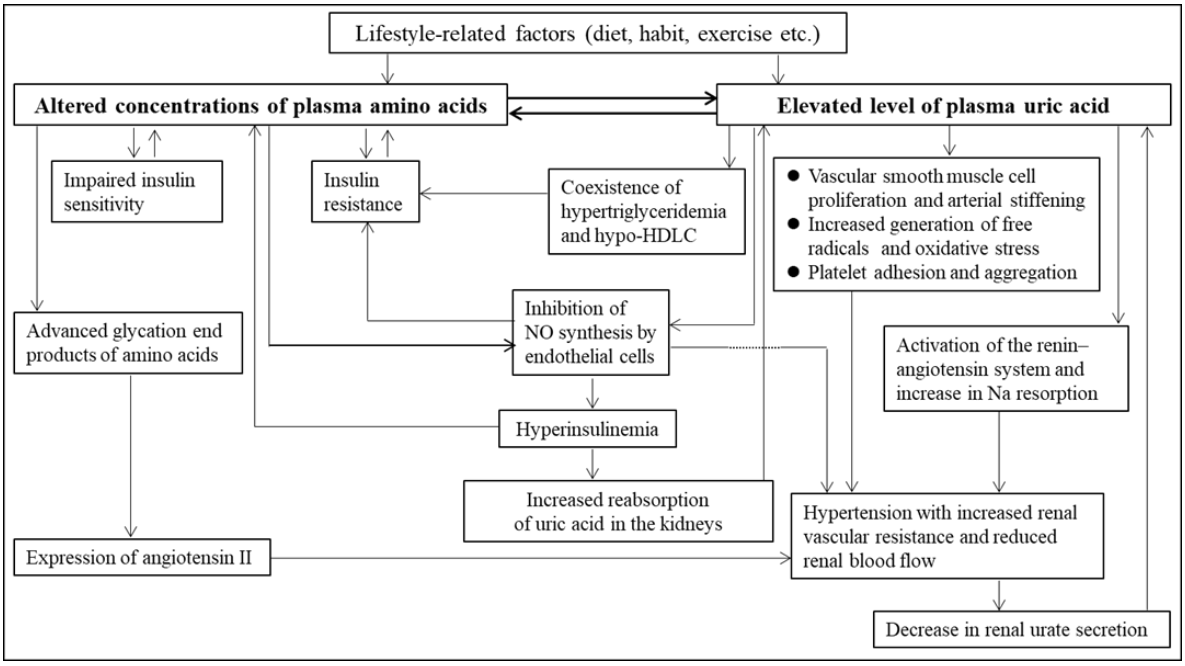

Figure 1: Schematic diagram of probable causes and consequences of altered plasma levels of amino acids and uric acids [2].

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