EFFECTS OF GERMINATION AND DEBRANNING ON AMINO ACID PROFILE OF DIFFERENT RICE GENOTYPES

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ABSTRACT: In this work, the impact of germination and debranning on the total (TAA) and free (FAA) amino acid in four rice cultivars were evaluated. The rice genotypes were germinated, polished and analyzed by the content of TAA and FAA. In comparison to non-germinated rice, 4 h of soaking and 24 h of germination increased the level of TAA and FAA, especially γ-aminobutyric acid (GABA). Debranning decreased the content of TAA and FAA. But, even after this reduction, the polished germinated samples showed higher levels of TAA and FAA than the polished non-germinated.The significant impact on the amino acid composition was caused mainly by genotype than the process used. These results could help the food industry to produce germinated rice enriched with high amino acid levels including GABA based on the choice of rice genotype.

Keywords: Germination, debranning, umami amino acid, γ-aminobutiric acid

INTRODUCTION

Rice is a staple food and concerning the global 2022/23 rice market, the production is projected at a record of 515.35 million tons (USDA, 2022). Germination is a economic, simple, efficient and environmental-friendly technique used to improve the nutrional, technological and sensory quality of rice (CHO; LIM, 2016). Rice is a important source of hypoallergenic protein and the study of the composition of TAA and FAA is relevant to determine the protein quality of rice (VIMARSHI et al., 2021).

During germination process the action of protease and synthesis of new enzymes, which help to liberate TAA and FAA (MOONGNGARM; SAETUNG, 2010) especially GABA, a non proteinogenic amino acid which has has been described in the literature as of having hypotensive effect (NISHIMURA et al., 2014), the sleep improvement (EHIRI, 2020) and the insomnia reduction (YU et al., 2020). Brown rice (BR) has a greater supply of nutrients than polished rice (PR), but its consumption is very small due to its taste, hardness and longer cooking time(VAN DAM, 2020). There is a lack of information about amino acid profiles in relation to BR and

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germinated brown rice (GBR), particularly after debranning process that produce polished forms which are the most preferable choice of consumption. Therefore, the present study evaluates the impact of germination associated with the debranning process on the amino acid profiles.

MATERIALS AND METHODS

Materials

Four rice (*Oryza sativa* L.) genotypes were selected from Active Germplasm Bank of *Embrapa Rice and Beans* (Santo Antônio de Goiás-GO, Brazil): BRS Formoso (F), Guaporé (G), Empasc_104 (E) and Mochi (M). All genotypes were multiplied in the 2018/2019 harvest using a flood-irrigated system in the farm experimental field of *Embrapa Rice and Beans* (6° 29' 8" S, 49° 18' 32" W).

Methods

Germination process

Germination was performed according to the methodology described by ZHANG et al. (2014) with some modifications (4 h of soaking and 24 h of germination). The germinated brown rice grains were dried in a circulated air oven at 50 ℃ overnight, then pericarp were removed of a rice polisher machine model MT-97 n° 3788-5 (Suzuki,Santa Cruz do Rio Pardo, Brazil) for 2 min and then ground in an M 3100 hammer mill (Perten Instruments AB, Huddinge, Sweden) fitted with a 0.8 mm sieve aperture obtaining a flour that was stored in a freezer until further analyses.

Amino acid composition analysis of rice

The separation and quantification of the TAA were performed according to methodology described by Pacheco (2014) and acid hydrolysis step according to method 994.12 (AOAC, 2000). In relation to FAA and GABA quantifications, an acid extraction step and subsequent derivatization with 6-aminoquinolyl-succimidyl-carbamate (AQC) were conducted (Waters Corporation, Milford, USA).
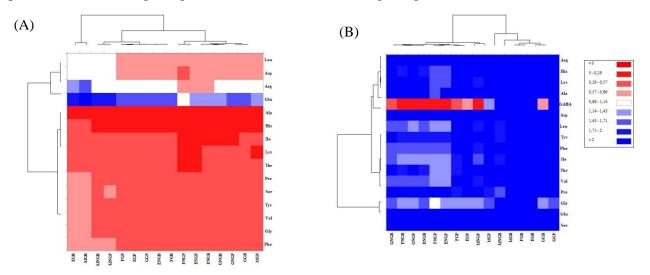
RESULTS AND DISCUSSION

Heat map analysis was used for clustering rice samples based on similarities of TAA (Figure 1A) and FAA (Figure 1B) concentrations for each genotype after germination and debranning. There was no

statistical difference ($p \leq 0.05$) in the TAA content between non-germinated and germinated samples. And, debranning did not cause a decrease in TAA, except for the Mochi genotype.Mochi was the cultivar that presented the highest levels of all TAA. The type of genotype, differences in the environmental conditions such as rainfall, temperature and water could be influence on the synthesis of amino acid (LIYANAARACHCHI et al., 2021).

Figure 1 – Heat map analysis by clustering groups of amino acid and GABA based on amino acid profiles of (A) total (g/100g) and (B) free amino acids (mg/100g).

Where: F= BRS Formoso; G= Guaporé; E= Empasc 104; M= Mochi; NG = non-germinated; G = germinated; B= brown rice; P=polished rice.

Concerning FAA, there was a significant ($p \leq 0.05$) increase in all amino acid except for Mochi cultivar. Mochi-GBR showed a great increase in proline (58%). Pro an precursor for the synthesis of 2-acetyl pyrroline that provide popcorn aroma in *Jasmine* or *Thai* rices (BUTTERY et al., 1983). GABA levels increased after germination in all cultivars, but debranning cause a great decrease in non-germinated (94% of reduction) and germinated samples (96 % of reduction), more pronounced in the Mochi rice (*O. sativa sups. Japonica*). Lower values of FAA in polished rice could be due to the removal of significant amounts of amino acids present in the pericarp during debranning (LIYANAARACHCHI et al., 2020). Although this reduction occurred, the non-germinated samples appear to be larger than germinated FAA.

CONCLUSION

Germination has a significant influence on the amino acid composition of rice. However, the change in levels of TAA and FAA significantly depended on the rice cultivars. In comparison to

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the non-germinated rice, germination caused an increase in GABA levels in rice Debranning caused a decrease in TAA and FAA, but the levels in GPR was higher than NGPR.

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