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IMPROVING RICE PRODUCTION

Rice is one of our most important food crops and provides an essential part of the daily dietary intake for nearly half of the world's population. However, rice production worldwide is affected by various biotic and environmental stresses. Among all biotic stresses, pathogen infections are considered as major constraints for rice production as 10 to 30 per cent of the annual rice harvest is lost due to disease infection. Of many different infections, a common and severe disease in rice is **sheath blight**. Rice sheath blight disease is caused by *Rhizoctonia solani* and has led to large scale crop losses, especially in Japan. *Rhizoctonia solani* is a fungus that can affect rice production by reducing crop production through the **inhibition of germination**.

However, **genetic breeding** has successfully introduced species resistant varieties. Infection resistance strains (32R) have shown different physiological responses than infection susceptible rice lines (29S). Several key enzymes and metabolites in the phenylpropanoid phenylalanine ammonia lyase enzyme and shikimate pathways are observed to have increased after *R. solani* infection. Phenylpropanoid, amino acid and shikimate pathways are involved in plant **defense mechanisms** during pathogen infection. Plant metabolites, especially amino acids and phenols that are involved in plant defense to *R. solani* infection include glutamate, GABA, glycine, histidine, phenylalanine, serine, tryptophan, tyrosine, and pipecolic acid that are abundant in 29S (susceptible) species and influenced by the presence of *R. solani*. The enhancement of specific amino



acids in 29S may increase the plant susceptibility as host response to necrotrophic pathogens. On the other side, **chlorogenic acid** was primarily higher in 32R (resistant) strains. These metabolomic results suggest that the accumulation of chlorogenic acid could be related to the resistance to pathogen as Chlorogenic acid levels are maintained high in 32R resistant strains perhaps to prepare for defense against a pathogen infection in advance (Figure A: Chlorogenic pathway).

FLAVOR AND AROMA

The **flavor of rice** differs by type of rice and depends on if it has been polished (i.e. brown or white rice) and, of course, cooking methods. Those considerations are obvious to most of us. But flavor may also vary by genetics, the growing environment, type of fertilizer and cultural practices, the timing of draining and harvesting the field, harvest moisture content, rough rice drying conditions, final moisture content, storage conditions, degree of milling, and also finally also washing and soaking practices and serving temperature of the cooked rice. There are over a dozen **different aromas and flavors** in rice. Analyses have found

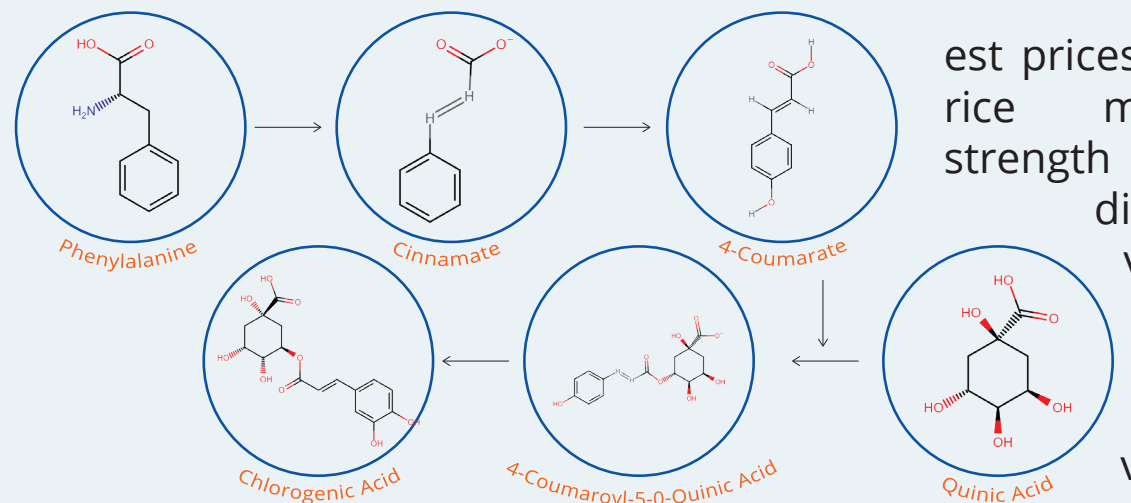


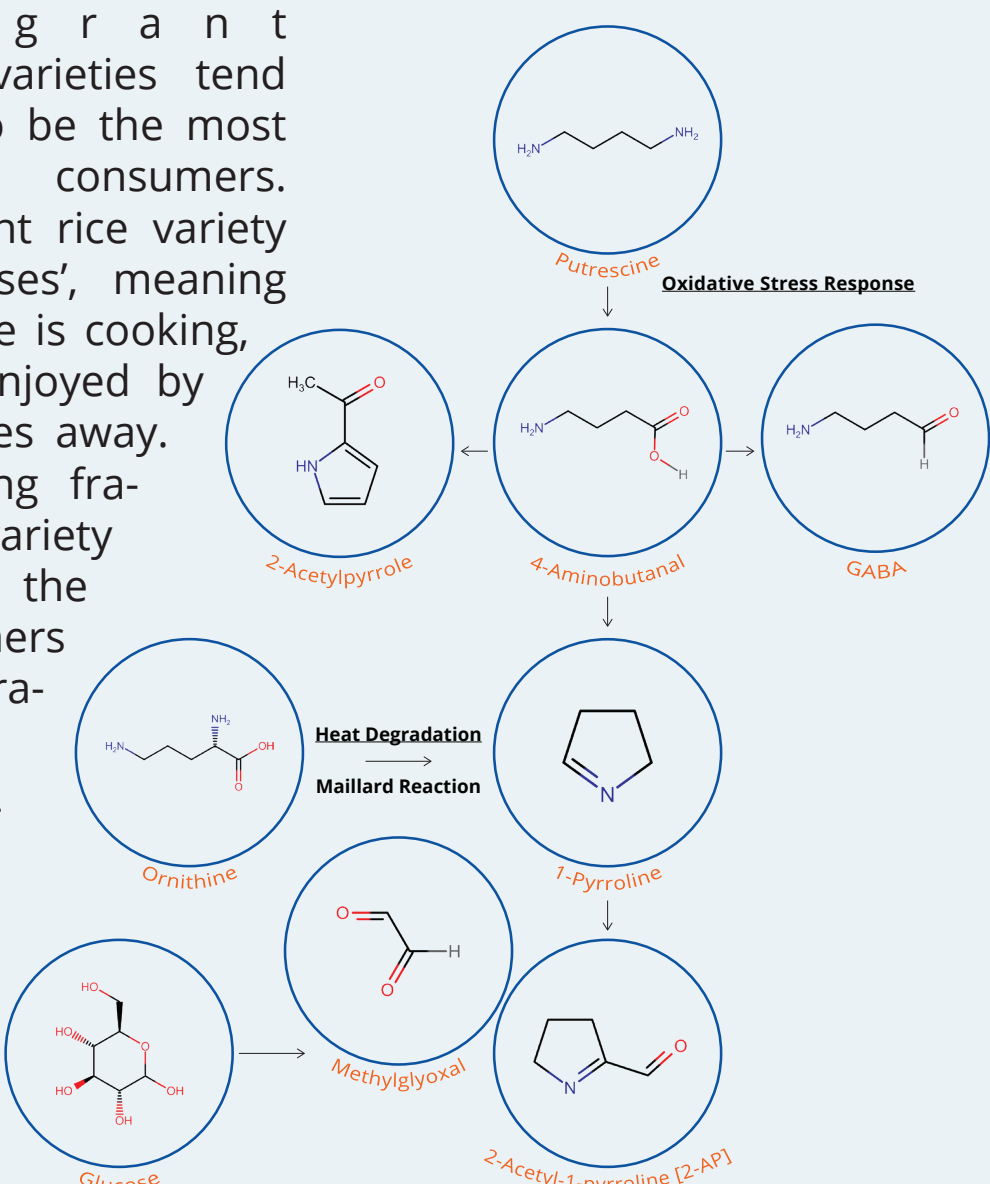
Figure A: Chlorogenic acid is biosynthesized from the amino acid Phenylalanine and maybe a chemical that provides pathogen resistance to riceplants.

over 200 volatile compounds present in rice. However, after over 30 years of research, little is known about the relationships between the numerous volatile compounds and aroma/flavor. Fragrant (or aromatic) rice commands the high-

est prices in the global rice market. The strength of fragrance differs between varieties and the most highly fragrant varieties tend to be the most popular among consumers. There is a fragrant rice variety called 'Four Houses', meaning that when this rice is cooking, its fragrance is enjoyed by people four houses away. Emphasizing strong fragrance through variety naming indicates the value that consumers place on highly fragrant rice.

2-acetyl-1-pyrroline (2AP) is the most

important aroma compound in rice. However, three other amine heterocycles: 2-acetylpyrrole, pyrrole and 1-pyrroline also correlate strongly with the production of aromaticity and related through biochemical



The aroma of rice can originate from a major metabolite, 2-AP, that is biosynthesized from polyamines by oxidative stress or through sugar (glucose) or amino acid (ornithine) by heat degradation. Other chemical intermediates including 2-acetylpyrrole and 1-pyrroline may contribute to odor.

pathways. Oxidative stress transforms putrescine to 4-aminobutanal (4-ABA), 4-ABA can then further convert to γ-aminobutyric acid (GABA), 2-acetylpyrrole or 1-pyrroline. GABA is a signaling metabolite while 2-acetylpyrrole can contribute to aroma. 1-pyrroline can combine with methylglyoxal to form 2-AP. In addition, 1-pyrroline can be formed from the heat denaturation by a maillard reaction from amino acids proline and ornithine. Methylglyoxal can be formed from the heat decomposition of glucose. Together, these metabolomic pathways provide new insights into the production of 2AP, and evidence for understanding the pathways leading to the accumulation of aroma in fragrant rice.

POLAR METABOLITES

The metabolites in rice can be categorized into two groups, primary and secondary. Primary metabolites include polar metabolites, glucose, sugars, lipids, vitamins, free amino acids and free fatty acids, those needed to provide fuel and energy for cellular growth, while secondary metabolites include complex metabolites that include flavonoids and terpenes that adjust to environmental stress (water, salt, temperature), as well as, providing additional health benefits for human consumption. Among these primary metabolites, the concentrations of certain **free amino acids** (FAA) have been linked directly to the taste scores of rice. This apparent relationship between the palatability of cooked rice and the FAA profile of rice grains has generated a growing interest in research on the physiological basis of FAA accumulation in rice grains. FAAs contribute significantly to the overall acceptability of rice grains by serving as sensory active flavor agents in cooked rice. FAA accumulation is a complicated process involving a complex of biochemical networks and control mechanisms. Metabolites existing in glycolysis, the tricarboxylic acid cycle, the pentose phosphate pathway (oxidative and reductive), photorespiration, and amino acid biosynthesis, can be classified into four groups. Group A contained amino acids, amines,



and purine bases; group B included organic acids and sugar phosphates; group C included nucleotides and coenzymes; and group D containing neutral sugars (Chart A: Prominent Concentrations of Polar Metabolites nmol/g (wt)).

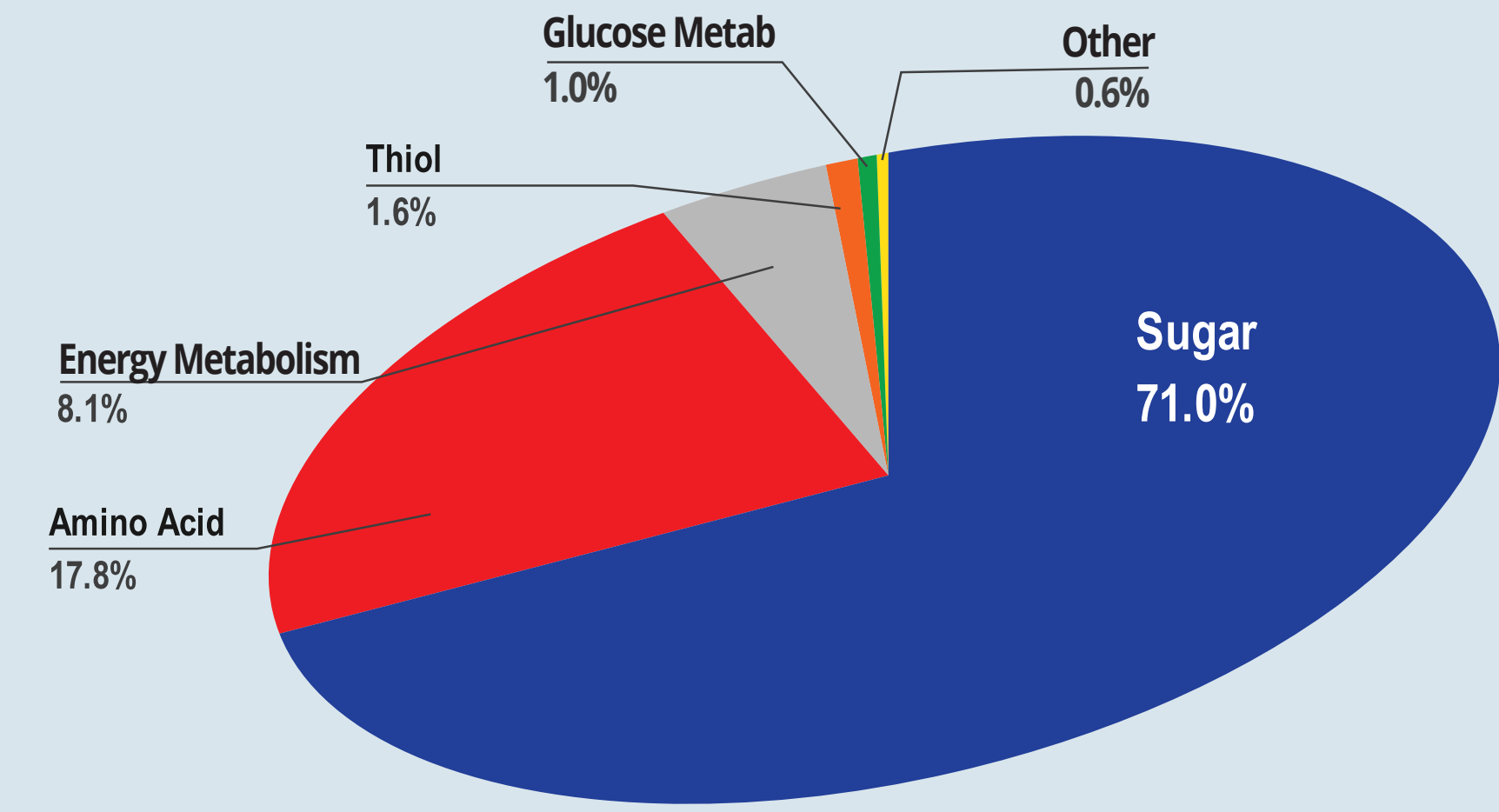
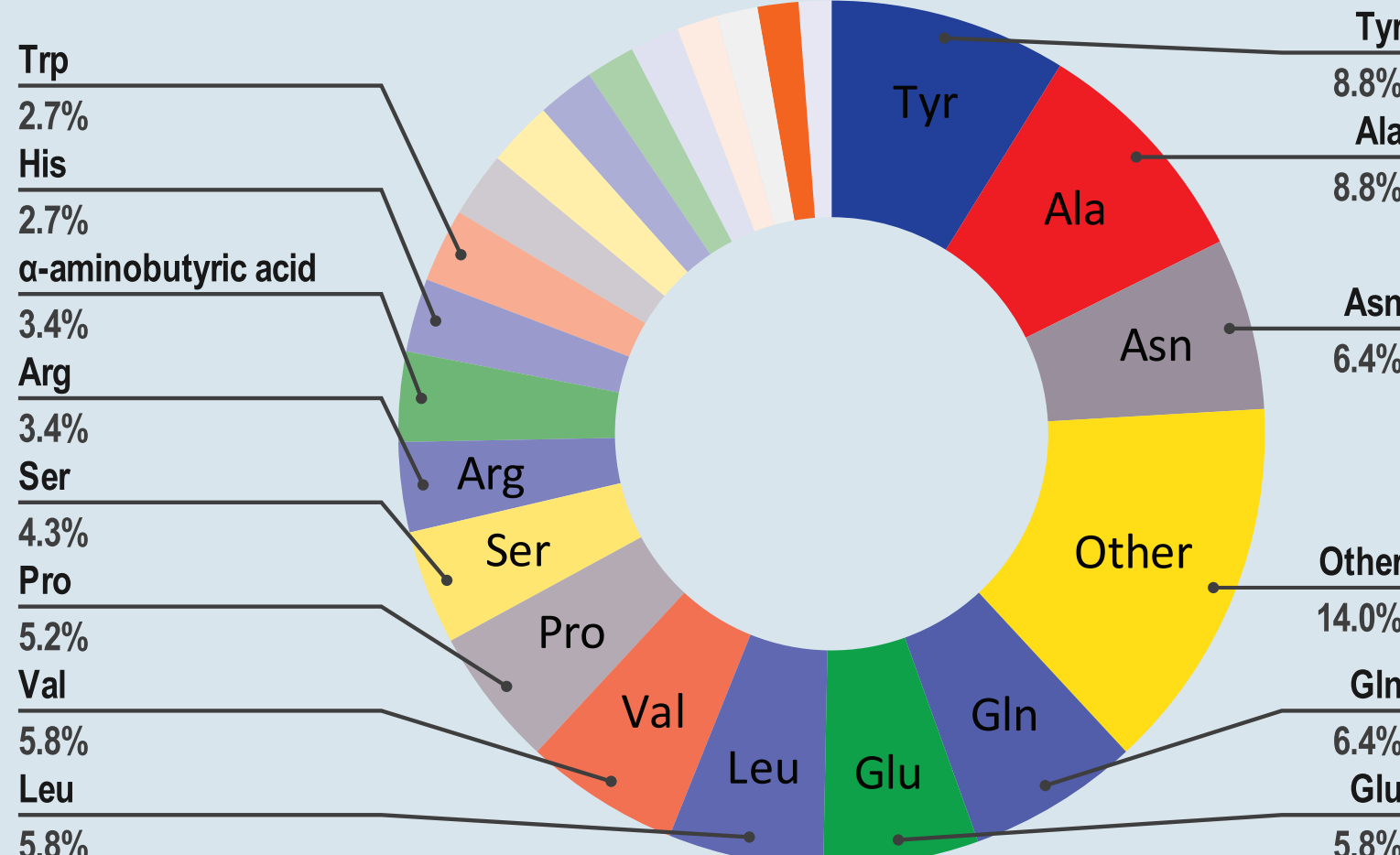
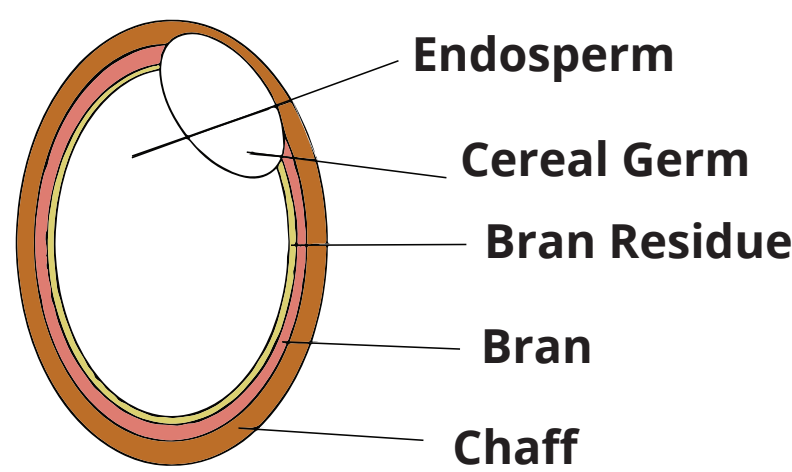


Chart A: Prominent Concentrations of Polar Metabolites nmol/g (wt)

CROSS SECTION RICE GRAIN



Graph B: Dry Weight Japonica Rice (mg/100g)

DID YOU KNOW? (STATISTA.COM, RICEPEDIA.ORG)

- Japan is 100% self-sufficient in rice, but only 14% wheat and 8% beans.
- 85% of the 2.3 million farmers in Japan produce rice.
- The average rice farmer works only 1.65 acres.

REFERENCES

Simultaneous Determination of the Main Metabolites in Rice Leaves Using Capillary Electrophoresis Mass Spectrometry and Capillary Electrophoresis Diode Array Detection. The Plant Journal 44(1) 151-163 (2004), S. Sato, T. Soga, T. Nishioka and M. Tomita (Keio University, Japan).

Metabolome Analysis of Rice Using Liquid Chromatography-Mass Spectrometry for Characterizing Organ Specificity of Flavonoids with Anti-inflammatory and Anti-Oxidant Activity. Chem. Pharm. Bull. 64(7) 952-956 (2016), Z. Yang, R. Nakabayashi, T. Mori, S. Takamatsu, S. Kitanaka and K. Saito (RIKEN Center for Sustainable Resource Science, Japan).

Variation in Free Amino Acid Profile Among Some Rice Cultivars. Breeding Science 60: 46-54 (2010), J. Kamara, S. Konishi, T. Sasanuma and T. Abe (Yamagata University).

Metabolomics and Genomics Combine to Unravel the Pathway for the Presence of Fragrance in Rice. Sci Rep. 7(1) 8767 (2017), V.D. Daygon, M. Calingacion, L.C. Forster, et al. (The University of Queensland, Australia).

Metabolite profiling of sheath blight disease resistance in rice: in the case of positive ion mode analysis by CE/TOF-MS. Plant Production Science 19:2, 279-290 (2016) W.-S. Suharti, A. Nose and S.-H. Zheng (Saga University, Japan).

Rice Sheath Blight: Major Disease in Rice. Int. J. Curr. Microbiol. App. Sci. Special Issue 7: 976-988 (2018), V. Turaidar, M. Reddy, R. Anantapur, K. N. Krupa, N. Dalawai, C. A. Deepak and K. M. H. Kumar (University of Agricultural Sciences, India).

*Capillary-Electrophoresis Mass Spectrometry Based Metabolomics