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Biodiversity Use for Food Security

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The origin and survival of our civilization depends upon agricultural biodiversity. We are the guests of green plant on this planet. I fondly remember a sticker on the bumper of a car that I once read, "Have you thanked the green plants today?" Approximately 250,000 plant species have been identified and described to date. More than 30,000 are edible and 7000 have been used as food. More than 300 are cultivated for food and feed at present.

The grass family, Poaceae is the most important source of food for feeding the world. Its three species, namely rice, wheat and maize provide 50% of the calories consumed by world population. Rice is the staple food of half of the world population. Genus *Oryza* to which cultivated rice belongs is distributed in four continents, e.g. Asia, Africa, Australia and Latin America. It has two cultivated and 20 wild species. Asian cultivated rice, *O. sativa* is grown on all continents. African cultivated rice, *O. glaberrima* is grown on limited areas in the West Africa.

Genetic relationships between *O. sativa* and wild species have been investigated thoroughly and various genomes have been designated based on crossability and chromosome pairing in F_1 hybrids. Thus, both cultivated and six wild species have AA genomes. Wild species with AA genomes are easy to cross with cultivated rice and useful genes for disease and insect resistance have been transferred to cultivated rice. Species with BB, CC, BBCC, CCDD, EE and FF genomes can be crossed with cultivated rice and F_1 hybrids can only be obtained through embryo rescue. Very useful genes for disease and insect resistance have been transferred to cultivated rice from these species. These include resistance to brown plant hopper, white backed plant hopper, blast and bacterial blight. Some of the progenies from the cross *of O. sativa* and *O. officinalis,* with resistance to brown planthopper were released as varieties in Vietnam. Monosomic alien addiction lines (MAALs) having full chromosome complement of cultivated rice and one chromosome of a wild species have been selected from these interspecific crosses. These MAALs are very useful source of variation for rice improvement.

Asian cultivated rice *O. sativa* is very diverse species. It is grown from below sea level in Kerala to seven thousand feet above sea level in Nepal and between 47^0 north latitude in China and 35^o south latitude in Australia and Chile. Moreover, it is adapted to growing under diverse ecologies, from deep-water to uplands. Perhaps more than 250,000 rice varieties exist that have been preserved in the world's gene banks. Three of the largest collections are in genes banks of IRRI Philippines, India and China. Almost all other rice-growing countries have rice gene banks.

Kato *et al*. (1928) recognised two varietal groups of rice i.e. indica and japonica. This classification agreed with empirical distinction Chinese people had recognized since ancient times between two types of rices called 'Hsien' and 'Keng' that correspond to indica and japonica respectively. Matsuo (1952) classified rice into three groups later referred to as indica, japonica and javanica. Oka (1958) suggested that japonica and javanica should be considered as temperate and tropical ecotypes of single group. Glaszman (1987) studied allelic variation at 15 polymorphic loci coding for eight enzymes in 1,688 traditional rice cultivars from Asia. He divided the varieties into 6 groups on the basis of multivariate analysis of data. Group 1 varieties found throughout tropical Asia are typical indica types. Group II includes short duration varieties of Eastern India and Bangladesh locally called aus. Groups III and IV include photoperiod-insensitive and photoperiod-sensitive deep-water rices of Bangladesh respectively. Aromatic rices of Indian subcontinent belong to group V. Group VI has temperate japonicas of Northern China, Japan, Korea and tropical japonicas distributed along with indicas in Thailand, Vietnam, Philippines and Indonesia (Table 1).

During green revolution, there has been massive exchange of germplasm internationally. Rice varieties

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Table 1. Distribution of rice varietal groups

Varietal group	Distribution
Group I Indica	Tropical Asia
Group II Aus	Eastern India, Bangladesh
Group III Photoperiod insensitive	DW Bangladesh
Group IV Photoperiod sensitive	DW Bangladesh
Group V Aromatic	Indian subcontinent
Group VI Temperate Japonica	North China, Japan, Korea
Tropical Japonica	Thailand, Philippines, Indonesia

belonging to different groups have been used in varietal improvement programmes. As an example IR 36 has 10 parents; eight indica, one tropical japonica and one wild species. Similarly IR 64 has 20 parents, 16 indica, one temperate japonica, two tropical japonica and one wild species. Two widely used genes for bacterial blight resistant–*Xa5* and *Xa21* were derived from an aus variety DZ192 and wild species *O. longistaminata,* respectively. Thus traits from different varietal groups and wild species have been combined to develop high yielding varieties with disease and insect resistance, improved grain quality and adapted to diverse growing conditions. Improved varieties have also been developed from crosses of two cultivated species of *Oryza*, e.g. NERICA rices in Africa. These modern varieties are now grown on 90% of world's riceland. Wide scale adoption of these varieties has led to unprecedented increases in rice production and world food security. For example, world rice production increased from 200 million tons in 1960 to 720 million tons in 2015 and price of rice is 50% lower than what it was during 1960s. Poor people who spend 50-60% of their income on food have greatly benefited from low price of rice. Thus, genus *Oryza* is an excellent example of use of biodiversity for the world food security.

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