Largest rice genetics study finds vast differences in rice

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Morphological diversity in seeds and whole grains of rice. This image illustrates the diversity of color, size and shape of rice seeds (with hulls intact) and corresponding grains (edible portion of the seed visible only after removal of the hull) in the rice diversity panel used for genome wide association studies. (Raluka Iorga, McCouch lab)

The largest publicly available genomewide association mapping study in rice to date has found that although the five subpopulations of Asian rice -- *indica, aus, temperate japonica, aromatic* and *tropical japonica* -- all belong to one species (*Oryza sativa*), their genetic structures are so different that, genetically speaking, they are almost like different species.

An international team led by Cornell researchers and published Sept. 13 in *Nature Communications* conducted the study based on genotyping (identifying genetic differences) more than 44,000 single nucleotide polymorphisms (SNPs) across 413 diverse *O. sativa* varieties from 82 countries. SNPs refer to genetic variation on the DNA level -- points in the genome where a base pair change makes one individual within a species different from another.

The researchers also phenotyped (measured the observable characteristics) for 34 traits related to size, shape, plant development and agronomic performance. Finally, the researchers analyzed the data to determine which particular traits are associated with which SNPs.

"Unlike maize, tomato and many other crops, Asian rice is highly differentiated into five distinct subpopulations or ecotypes," said Susan McCouch, professor of plant breeding and the paper's senior author. The genetic differences among these five rice subpopulations are greater than the differences between many cultivated crops and their wild ancestors, she added.

That's because ancient rice subpopulations have evolved separately for thousands of years as farmers migrated and selectively bred them in a wide range of different ecological and climatic conditions that collectively altered their genetic makeups, McCouch said.

Also, rice mostly self-pollinates or inbreeds, with plants recycling their

own genes, while such crops as maize and potato freely cross-pollinate, so they continuously exchange genes within their species and with their wild ancestors. And other inbreeding crops such as tomatoes, for example, were domesticated only once, narrowing the gene pool, while rice was domesticated multiple times in different places.

"You have to take all this into account when you evaluate the genetics of rice," McCouch said.

For example, when the researchers analyzed a trait such as the size of rice panicles (the branched structure holding clusters of flowers or grains), they found variation is highly partitioned by subpopulation, such that the genes that determine panicle length in each subpopulation are entirely different, providing an example of convergent evolution, where very different genetic architecture underlies the same phenotype.

Also, the group demonstrated that the same trait may be governed by different genes in different environments, as in the case of flowering time evaluated in Arkansas, Bangladesh and the United Kingdom.

By understanding which different SNPs confer specific traits, breeders can start to understand and predict how crossing between subpopulations can give rise to offspring that outperform their parents in such desired traits as yield, grain size or drought tolerance.

All the genotypic and phenotypic data and the seeds for the 413 lines of rice are publicly available, allowing geneticists and breeders to build on this work, selecting subsets of SNPs for use in local rice populations, using phenotypic data to identify lines with desired traits to cross with local varieties, and leveraging genotypic data to better understand the genetics of complex trait variation in natural populations of rice and other plant species.

"On the science side, we are taking complex traits and breaking them down into their genetic components," and then using SNP variation to begin to predict phenotypic variation, McCouch said.

Co-authors for the Nature Communications paper include researchers from Stanford University; the U.S. Department of Agriculture's Dale Bumpers National Rice Research Center in Stuttgart, Ark.; the University of Arkansas; the University of Aberdeen in the United Kingdom (UK); and the Bangladesh Agricultural University in Mymensingh, Bangladesh.

Provided by Cornell University