Genes underlying the key domestication process in sorghum and other cereals

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A study by a team of university and government scientists led by a Kansas State University researcher, indicates that genes responsible for seed shattering -- the process by which grasses disseminate their seeds -- were under parallel selection during sorghum, rice and maize domestication.

The study, "Parallel domestication of the Shattering1 genes in cereals," was published May 13 in the online version of the journal, *Nature Genetics*. In order to identify the molecular basis underlying seed shattering in sorghum, which is the world's fifth major crop, the researchers conducted map-based cloning and diversity mapping in sorghum first, and then examined the identified gene in other cereals. Cereal crops, including sorghum, rice and maize were domesticated from their early wild progenitors by humans thousands of years ago, because of their importance as a food source, said Jianming Yu, associate professor of agronomy at Kansas State University. Although these crops were domesticated by human groups in different geographical regions, they all underwent systemic and parallel changes during the domestication process.

"Once we better understand seed shattering in sorghum, the better we will understand seed shattering and domestication in other cereal crops," Yu said. "Moreover, as the demands for food, feed and fiber increase, domesticating other grasses into crops would also benefit from the current research findings."

The implications for sorghum alone are huge, because of sorghum's emerging applications in bioenergy and stress management, as well as its long-time importance as a food and feed source, he said. A better understanding about the origins of sorghum, a very diverse species, helps in terms of preserving natural resources for breeding use, classifying germplasm, and facilitating the process of bringing useful genes from wild relatives to crops.

Seeds on wild grasses shed naturally when they mature, which ensures their natural propagation, Yu said. When humans began cultivating those crops, however, seed shattering would have caused inefficient harvesting and large losses in grain yield, because some of the seeds which were to be harvested, would have already disbursed naturally.

"Selection for non-shattering crop plants would have greatly facilitated harvesting and improved production," said Zhongwei Lin, research associate in agronomy at Kansas State and the first author of the publication. He noted that several other genes have been identified as being responsible for seed shattering in rice and wheat. Prior to this current study, however, no systematic findings have been made on whether other cereals share the same molecular genetic basis for shattering, although such hypothesis was proposed more than a decade ago. The highly similar genomes of these cereals and the critical role of non-shattering in their domestication make this speculation plausible.

The researchers found that seed shattering in sorghum is controlled by a single gene, Sh1. That finding, paired with findings of conserved collinearity -- genes and their orders are similar on corresponding chromosome segments from different species -- of genomic regions containing the Sh1 orthologs (genes can be traced back to the same ancestral copy) across several cereals, the identification of the rice OsSh1 and the structural variation and quantitative trait locus analyses of the two maize orthologs (ZMSH1-1 and ZMSh1-5.1+ZmSh1-5.2) suggest that the Sh1 genes for seed shattering have undergone parallel selection during domestication in multiple cereals.

"It is great to have this team of scientists with complementary expertise in different species to work on this project," said Frank White, professor of plant pathology at Kansas State University.

To identify the molecular basis underlying seed shattering in sorghum, the team constructed a large population from a cross between a wild sorghum with complete seed shattering, Sorghum virgatum (SV), and a non-shattering domesticated sorghum line, Tx430. Once the gene was pinpointed, they moved on to a diverse set of sorghum lines and landraces to examine how many different version of domesticate copy of Sh1 exist. Not surprising, they found three different ones, which corroborated the earlier inference of multiple origins of sorghum in different parts of the African continent from morphology characteristics.

Provided by Kansas State University

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