research highlights

REVERSE GENETICS Wheat solution

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Various mutant libraries have facilitated functional genetic studies in diploid plants, such as rice and Arabidopsis. For polyploidy species, a comprehensive mutant library can effectively facilitate the characterization of recessive hidden variations masked by redundant homeologues. However, in polyploid crops, such reverse genetic resources are often lacking, hindering gene function analyses and breeding. Ksenia V. Krasileva, from the Earlham Institute, and colleagues, from the John Innes Centre, Rothamsted Research and the University of California, Davis, have now developed an exome capture platform to characterize the mutations in two ethyl methanesulfonate (EMS) mutagenized populations of wheat.

Using the exome capture assay, which was jointly developed with NimbleGen, the researchers captured and sequenced the coding regions of 1,535 EMS mutants from a tetraploid variety and 1,200 EMS mutants from a hexaploid variety. From



these, 4.15 million and 6.42 million high-quality induced mutations were characterized, respectively. The mutations exhibited a uniform distribution along the coding regions.

More than 90% of the captured genes contained deleterious mutations, with an average of 23–24 truncation and missense mutations per gene. The fast identification of mutations in the wheat genes provides a valuable genetic database that enables rapid generation of null mutants to expedite gene function studies or to uncover previously hidden variation. These mutants can be applied directly in breeding for various agronomic traits as they are not subject to regulation.

The researchers have developed a public database (www.wheat-tilling.com) and search tools to share and visualize the mutation information and facilitate its usage. Scientists and breeders can request the mutant seeds from the University of California, Davis or the UK Germplasm Resources Unit.

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