**Enhancing Rice Grain Yield through Functional Genomics and Advanced Breeding Techniques**

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KeyWords: grain yield; mutation breeding; drought tolerance; gene editing

The continuous improvement of grain yield in rice varieties is crucial to meet the demands of the growing global population. This presentation will demonstrate how functional genomics data has been leveraged to enhance the yield of a hybrid parent under both normal and drought conditions. Rice grain yield is a complex trait influenced by three key components: the number of panicles, the number of grains per panicle, and grain weight. Numerous genes associated with these traits and drought have been identified by the rice research community and our internal research. This rich source was used to compile a high-quality list of candidate genes.

KeyPoint® Breeding, a high-throughput mutation and polymorphism discovery technique based on massive parallel sequencing of target genes amplified from thousands of mutants in a bulked-M2 population, has been employed to identify novel alleles. Comprehensive field testing has been carried out to assess grain yield and its component traits. Several mutant alleles have shown significant improvements in yield and specific component traits, while others have demonstrated increased tolerance to drought stress during panicle development. Testing of these alleles in multiple hybrids is underway.