**A novel RNA binding protein enhances drought resistance by promoting stress mRNA stability via protein phase separation in rice**

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**Abstract**

Drought stress poses a significant threat to global rice production, underscoring the urgent need to decipher the genetic components of drought resistance in rice. Through a genome-wide association study of leaf-rolling trait measured by UAV-based in-field phenotyping technique, genetic basis of drought response was dissected in rice. We further revealed that natural variations in *DROUGHT RESISTANCE GENE 9* (*DRG9*), encoding a double-stranded RNA binding protein, contribute to drought resistance in rice. Under drought stress, DRG9 condensed into stress granules (SGs) through liquid-liquid phase separation, via an α-helix embedded within a largely intrinsically disordered region. DRG9 binds to *OsNCED4* mRNAs, a key gene for the biosynthesis of abscisic acid, and recruits them into SGs to protect them from degradation. In drought-resistant *DRG9* allele, natural variations in the coding region, causing an amino acid substitution within the zinc finger domain, increased the DRG9 binding ability to *OsNCED4* mRNA and enhanced drought resistance. Introgression of the drought-resistant *DRG9* allele into the elite rice Huanghuazhan led to significant increase of drought resistance in the field. Thus, we identified a dsRNA-binding protein that positively regulates drought resistance by stabilizing *OsNCED4* mRNAs via protein phase separation, and substantiated the promising value of the drought-resistant *DRG9* allele in breeding drought-resistant rice.