**Genetic markers and transcriptome studies during grain-filling of caryopsis tissue reveal that rice chalky grain growth is controlled by numerous regulatory pathways at high night temperature**

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The rice yield and quality have been reduced due to the rise in temperature resulting from substantial climate change. High temperatures during flowering limit spikelet fertility, impeding sugar energy transport from the flag leaf to the developing caryopsis tissue, causing chalky grains, which affect grain quality. Enhancing the quality and appearance of rice is crucial for achieving approval from the marketplace. The development of efficient methods in rice breeding has been the primary focus of mining potential grain quality-related genes. Although grain chalkiness is a complex, quantitative genetic trait, the molecular mechanisms underlying its formation are poorly understood. In this study, genome-wide association (GWAS) and linkage studies were conducted in a diverse and mapping population to identify loci associated with grain quality-related traits in control and high night temperatures. An in-depth analysis of the transcriptome and post-transcriptional regulation revealed differential gene expression patterns between chalk and non-chalk genotypes under both conditions, particularly genes related to sucrose and starch metabolism. Overexpression of the HYR gene led to increased expression levels of genes involved in oxidoreductive homeostasis in growing caryopsis tissue. This indicates that ROS and water deficits in starch granules may play in grain chalkiness. The knockout of SCl26, a negative splicing regulator, resulted in a reduction in chalk formation and drought and heat tolerance. This integrated approach provides novel insight to mitigate the high-night temperature effect on starch metabolism for grain quality improvement.

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