

Abstract

Seed dormancy and germination are important processes that influence plant growth and productivity in *Oryza*. This study aimed to investigate the factors regulating seed dormancy and germination among different *Oryza* accessions, including both cultivated and wild accessions, and to examine post-transcriptional RNA regulation during seed maturation. Germination analyses were conducted through dormancy level identification, water uptake analysis, barrier and husk-related treatments, and gibberellic acid (GA₃) induction experiments. On the other hand, post-transcriptional regulation was evaluated using a processed RNA-seq dataset of *O. sativa* seeds at 14 and 42 days after pollination (DAP). The results indicated significant variation in germination performance among *Oryza* accessions, indicating differences in dormancy regulation. Water uptake and husk-removal analyses suggested that the physical barrier imposed by the husk was not the primary factor limiting germination, while GA₃ responses indicated the involvement of hormonal regulation. Furthermore, correlation analysis between gene expression changes and poly(A) tail length changes determined no correlation, supported by a Spearman's correlation coefficient of $\rho = 0.016$. No overlap was observed between the genes exhibiting the largest expression changes and those exhibiting the largest poly(A) tail length changes. Overall, the findings suggest that seed dormancy and germination in *Oryza* are regulated by multiple physiological and hormonal factors, while transcriptional and poly(A) tail post-transcriptional regulation may operate independently during seed maturation.

Keywords: *Oryza*, germination, gene expression, poly(A) tail