

Chapter 1

Introduction

1.1 Background

Oryza, also known as rice, is one of the world's major staple crops, used for food and related products, including medicines and cosmetics, and also as an important model for cereal genomics due to its rich genetic resources and genomic synteny with other cereals (Panesar & Kaur, 2016). As the model plant, seed-related traits in *Oryza*, particularly seed maturation and dormancy, play critical roles in ensuring the successful establishment of the next generation and maintaining agricultural productivity. During seed maturation, embryo growth terminates while storage compounds accumulate, the seed coat develops, and desiccation tolerance is established. These processes are tightly regulated by hormonal, transcriptional, and metabolic networks that ultimately induce seed dormancy (Feurtado, 2017; Wang & Komatsu, 2017).

On the other hand, seed dormancy prevents germination under unfavorable environmental conditions, ensuring proper timing and leading to a high survival rate in the plant (Khalid et al., 2023). In *Oryza*, seed dormancy is regulated by the hormones abscisic acid (ABA) and gibberellin (GA), as well as by external factors such as light, temperature, and soil conditions (Xu et al., 2025). In addition to hormonal regulation, the rice husk also plays an important role in controlling dormancy and germination.

As a protective outer layer composed mainly of cellulose, lignin, and silica, the husk can influence water uptake, gas exchange, and mechanical restriction of embryo growth (AboDalam et al., 2022). Although the physiological and hormonal mechanisms regulating seed maturation and dormancy have been extensively studied, these processes are ultimately controlled through gene expression. Therefore, understanding how ribonucleic acid (RNA) molecules are regulated during seed

development may provide additional insights into the molecular mechanisms underlying seed maturation, dormancy establishment, and germination.

Post-transcriptional processes play important roles in regulating gene expression during plant development (Tognacca & Botto, 2021). One important mechanism of post-transcriptional regulation involves modification of the poly(A) tail located at the 3' end of messenger RNA (mRNA) molecules. The poly(A) tail consists of a stretch of adenine nucleotides added during mRNA processing and contributes to mRNA stability, protection from degradation, and efficient translation. These functions are particularly important during seed maturation, when transcriptional activity gradually decreases and seeds rely on stored mRNAs to support subsequent germination (Passmore & Coller, 2021). Despite increasing interest in poly(A) tail dynamics and post-transcriptional regulation in seed biology, the relationship between changes in gene expression and poly(A) tail length during *Oryza* seed maturation remains poorly understood (Cai et al., 2025).

Therefore, this study aimed to investigate post-transcriptional mechanisms during *Oryza* seed maturation and dormancy, as well as factors influencing germination regulation. Germination analyses under different seed conditions, together with gene expression and poly(A) tail length analyses, were conducted to analyze the relationship between physiological and post-transcriptional regulatory processes during seed maturation. The findings of this study were expected to provide further insights into the molecular mechanisms underlying seed maturation, dormancy establishment, and germination regulation in *Oryza*.

1.2 Objectives

This study aimed to investigate the factors regulating seed dormancy and germination in different *Oryza* accessions through the analysis of germination performance, water uptake, structural constraints, and the effect of gibberellic acid (GA₃) induction on husk-mediated germination

inhibition. In addition, this study aimed to analyze post-transcriptional regulation during *Oryza* seed maturation through the analysis of gene expression and poly(A) tail length regulations. Specifically, the study evaluated the correlation between changes in gene expression and poly(A) tail length and explored their potential contribution to seed maturation and dormancy regulation.

1.3 Hypothesis

Hypothesis Set 1: Germination Analysis

Null hypothesis (H_{01}): Seed dormancy and germination did not differ among *Oryza* accessions and were not significantly affected by water uptake, husk-related factors, or GA₃ induction.

Alternative hypothesis 1 (H_{11}): Seed dormancy and germination differed among *Oryza* accessions and were significantly affected by water uptake, husk-related factors, and/or GA₃ induction.

Hypothesis Set 2: Post-transcriptional Analysis

Null hypothesis (H_{02}): Changes in gene expression during *Oryza* seed maturation were not correlated with changes in poly(A) tail length.

Alternative hypothesis 1 (H_{12}): Changes in gene expression during *Oryza* seed maturation were correlated with changes in poly(A) tail length.