

# **Proteomic and Carbonylation Profile Analysis at the Critical Node of Seed Ageing in *Oryza sativa***

**Guangkun Yin<sup>1+</sup>, Xia Xin<sup>1+</sup>, Shenzao Fu<sup>1,3+</sup>, Mengni An<sup>1</sup>, Shuhua Wu<sup>1</sup>, Xiaoling  
Chen<sup>1</sup>, Jinmei Zhang<sup>1</sup>, Juanjuan He<sup>1</sup>, James Whelan<sup>2\*</sup>, Xinxiong Lu<sup>1\*</sup>**

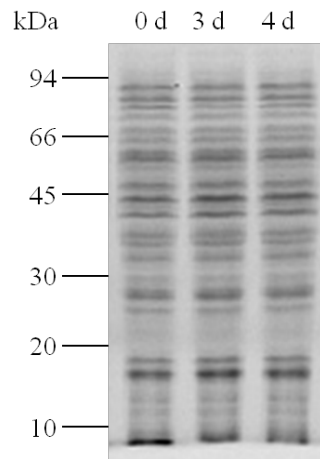
<sup>1</sup>Current Address: National Genebank, Institute of Crop Science, Chinese Academy of  
Agricultural Sciences, Beijing 100081, China

<sup>2</sup>Australian Research Council Centre of Excellence in Plant Energy Biology, School  
of Life Science, La Trobe University, Bundoora, Victoria 3083, Australia

<sup>3</sup> China National Rice Research Institute, Hangzhou 310006, China

\*Corresponding authors: E-mail: luxinxiong@caas.cn; J.Whelan@LaTrobe.edu.au.

<sup>+</sup> These authors contributed equally to this work.



**Figure S1. SDS-PAGE analysis of protein from 0 d, 3 d and 4 d aged rice seeds after imbibition for 48 h.** Total 10  $\mu\text{g}$  protein was separated by 12% sodium dodecyl sulfate polyacrylamide gel electrophoresis.

**S1 table. List of genes used in real-time PCR.**

Gene name	Accession No.	Gene description
<i>MDH1</i>	NP_001064860.1	malate dehydrogenase 1
<i>SDH1</i>	NP_001058845.1	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial
<i><math>\beta</math>ATP</i>	NP_001043900.1	ATP synthase, H <sup>+</sup> transporting, mitochondrial F <sub>1</sub> complex, beta polypeptide
<i>PDC1</i>	NC_029260.1	Pyruvate decarboxylase 1
<i>6PGD1</i>	NC_029261.1	6-phosphogluconate dehydrogenase 1
<i>APX1</i>	NP_001049769.1	L-ascorbate peroxidase 1
<i>UBQ5</i>	AK062354	Ubiquitin 5