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Category	: International Rice Research Conference
Select Theme	: Systems physiology
Keyword 1	: Phenomics
Endorsement email	:
Keyword 2	: Yield potential
Keyword 3	:
Title of Entry	: Gaining insights and improvement in cold tolerance in rice
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Abstract : A major constraint facing the temperate rice industry both nationally and internationally, is the occurrence of low temperature (15-19oC) events particularly during the reproductive stage (booting and flowering), leading to reduced fertility and yield. Our aim was to improve understanding of cold tolerance in terms of underlying physiological mechanisms and the molecular basis of traits involved in cold tolerance. A two-set phenotyping system was developed and a series of experiments have been conducted to evaluate the cold tolerance at the booting and flowering stages (14 days @ 21/15oC day/night temperature) of current Australian varieties and 5 populations. Significant genotypic variation for spikelet sterility was identified with lines identified in all populations that had greater tolerance than currently available commercial varieties. Our research has identified key floral traits: number of dehisced anthers (NDA) and dehiscence length; pollen number in anther; pollen number on stigma and their associations with spikelet fertility within a population of lines. Pollen number in anther, which ranged from 0 to 1903 pollen grains per anther when exposed to cold at booting in a population (120 lines), accounted for 53% of variation in spikelet sterility (SS). NDA accounted for 58-69% of the variation in SS at booting stage cold under flooded conditions and 42% under aerobic conditions. While at flowering stage cold, NDA accounted for 29-44% of the variation in SS. Thus, anther dehiscence is critical at both reproductive stages but explained more variation in SS at booting under flooded conditions. Under aerobic conditions at booting and at the flowering stage cold, other floral mechanisms appeared contributing to cold tolerance. GWAS analysis utilising DArTseq, a genotype by sequencing system for high resolution mapping, identified SNPs in two unrelated populations with 6 and 5 loci that were identified associated with spikelet

fertility when exposed to cold temperatures at booting. Furthermore, all loci identified for SS had co-locating loci with at least one floral trait, in particular NDA (5 out of 6 loci). The use of putative markers in combination with improved understanding of underlying floral traits will lead to increased efficiency in breeding for cold tolerance in rice.

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