

## W10

### Contrasting rice sub-populations to tocopherols ratio associated with seed longevity

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#### Abstract

Understanding the mechanism(s) to overcome or prevent seed ageing deterioration during storage is of fundamental interest to seed physiologists. Vitamin E (tocopherols) is known as a key metabolite to efficiently scavenge lipid peroxy radicals which cause membrane breakdown resulting in seed ageing. However, in rice research this hypothesis has been tested for very few lines only without considering intraspecific variation in genomic structure. Here, we present a correlation study between tocopherols and seed longevity using a diverse rice panel. Seeds of 20 rice accessions held in the International Rice Genebank at the International Rice Research Institute, representing *aus*, *indica*, *temperate japonica* and *tropical japonica* subpopulations, were used for tocopherols analysis (quantification of  $\alpha$ -,  $\beta$ -,  $\gamma$ -,  $\delta$ - tocopherol/tocotrienol by ultra performance liquid chromatography) and storage experiments at 45°C and 10.9% seed moisture content (sample taken for germination testing every 3 days up to 60 days). To examine interactions between DNA sequences and phenotype, the 700k high-density single-nucleotide polymorphism marker data-set was utilized. Both seed longevity (time for viability to fall to 50%;  $p_{50}$ ) and tocopherols content varied across subpopulations due to heterogeneity in the genetic architecture. Among eight types of tocopherol homologues,  $\alpha$ -tocopherol and  $\gamma$ -tocotrienol were significantly correlated with  $p_{50}$  (negatively and positively, respectively). While *temperate japonica* varieties were most abundant in  $\alpha$ -tocopherol, *indica* varieties recorded 1.3 to 1.7-fold higher  $\gamma$ -tocotrienol than those of other subpopulations. It was highlighted that specific ratio of tocopherol homologues rather than total tocopherols content plays an important role in the seed longevity mechanism.

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