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Seed longevity, the time a seedlot can be kept at the dry state without loss of viability, is key in agriculture as it directly ensures field establishment and thus yields, in addition to its main role in biodiversity preservation. Acquisition of seed longevity is tightly regulated at molecular level during seed development. A role of DELAY OF GERMINATION1 (DOG1) in positively regulating seed longevity in *Arabidopsis thaliana* has been previously characterized[1]. In addition, further research has revealed that BRAHMA (BRM), an SNF2 (Sucrose NonFermenting) – type ATPase from SWI/SNF (SWItch/Sucrose Non-Fermentable) chromatin remodelling complex – shows a 3′ localized pattern of binding at 1759 genes, including *DOG1*[2]. Here, we investigated the role of BRM in relation with DOG1 in seed longevity. Using physiological assessments, RNAseq analysis, and untargeted metabolomics approach, we conducted a deep analysis of the *brm-3*, *dog1-4* and double *dog1-4xbrm-3* mutants. Our results indicate that BRM negatively regulates seed longevity. In order to identify putative pathways involved in the regulation of seed longevity by BRM, we analyzed both RNAseq and metabolomics data of the mutants. Our findings indicate a role of BRM in balancing redox status by negatively regulating antioxidants pathways at gene expression level as well as by inhibiting glutathione accumulation in seeds, an important antioxidant in seed longevity[3]. Finally, our results show also a role of BRM in other agronomical traits of interest such as yield and nutritional quality by regulating seed size, weight and lipid accumulation.

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[2] Archacki R, et al. Nucleic Acids Res (2016) 45: 3116-3129.
[3] Kranner, Ilse, et al. Free Radical Biology and Medicine (2006): 2155-2165.

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Topic: From genes to seed biology, novel issues in molecular mechanisms and beyond
Oral application