

Table 1 Suppl. Antioxidant and metabolite-related genes used for expression analysis in rice.

Gene	Forward Sequence (5'-3')	Reverse Sequence (5'-3')
<i>OsCATA</i>	CGGATAGACAGGAGAGGT TCA	AATCTTCACCCCCAACGACT
<i>CAT</i>	CATCTGGCTCTCCTACTGGTCT	CAGGAGAAACGTGTCTTCAGGT
<i>MnSOD</i>	GGAAACAACCTGCTAACCAGGAC	GCAATGTACACAAGGTCCAGAA
<i>Cu/ZnSOD</i>	CAATGCTGAAGGTGTAGCTGAG	GCGAAATCCATGTGAAGCTGAG
<i>Cytosolic APX</i>	AGTACATTGCCCCGTGGTACTCT	CGCATTTACAAACACATCT
<i>OsAPX1</i>	CCAAGGGTTACCACCTA	CAAGGTCCCTCAAAACCAGA
<i>GPOD</i>	ACCGTGAGCGAGGACTACCT	AGCGTCAAGTGAGCCTTAGC
<i>GABA-T</i>	CTGAATTCGCAGACAACAAATC	TTATCATCGTCATCGTCGTCTC
<i>P5CS</i>	CAAATGCTCCTTTTAGCCTGTT	GCGTTGGTACACAAGTTCTCAG

Note: The genes are involved in antioxidant defense (e.g., SOD and APX) and stress related metabolite biosynthesis (e.g *P5CS* and *GABA-T*).

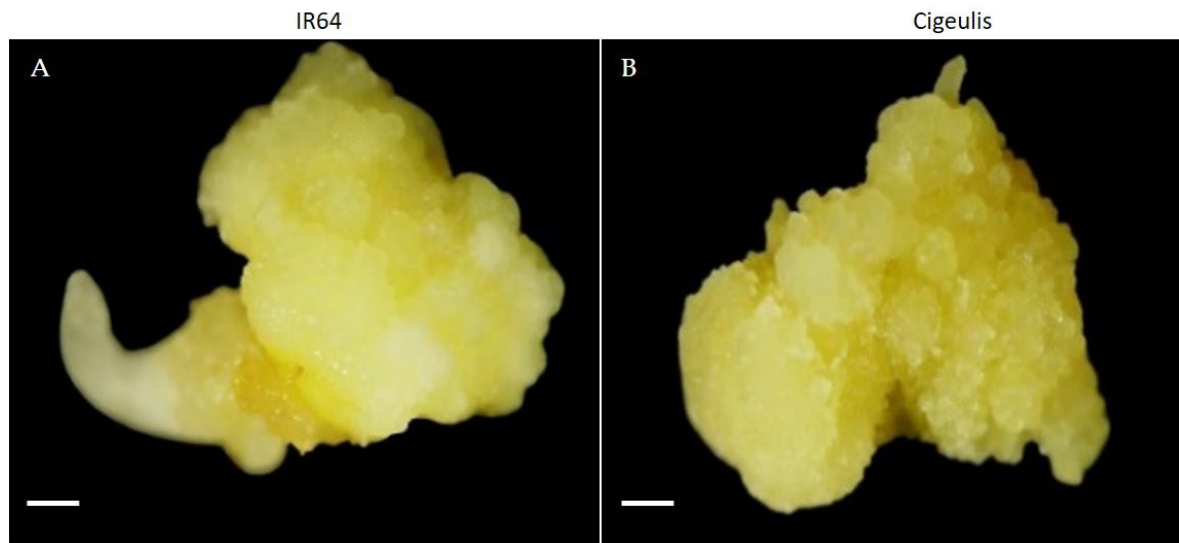


Fig. 1 Suppl. Morphological characteristics of callus induction in rice varieties (A) IR64 and (B) Cigeulis after 2 weeks on callus induction medium (scale bars = 1 mm).