

附表

表 1 *CCX2* 基因定位部分引物
Table 1 Primers for *CCX2* gene mapping

标记	正向引物	反向引物
Marker	Forward primer(5'-3')	Reverse primer(5'-3')
RM15567	TGCATCGATCCTTTCTTTGTCC	CCGGGACGCTATATGTTCTTCC
RM6468	CTTGTGGCCGAGGACATG	AGAGAAGCAGAGGCCCTGAC
CM02	CCCTTTGAGCGATTGTGAT	GTGAGCTCTAATCGCGAAGG
CM03	CCATCCGTTGAGCAATTCTT	CAAGAATTTCCTGCTTTCAA

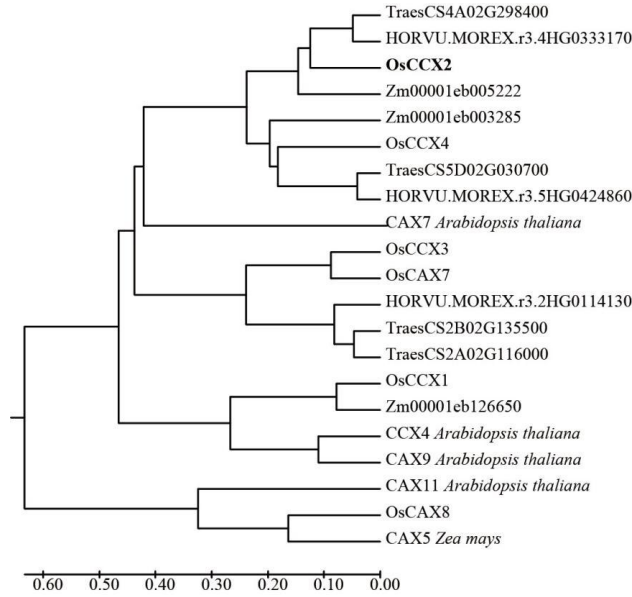
表 2 *CCX2* 基因的遗传分析
Table 2 Genetic analysis of the *CCX2* gene

杂交亲本	正常植株	突变植株	总数	$\chi^2(1:3)$
Cross Parents	Normal Plants	Mutant Plants	Total	
<i>ccx2</i> /WYJ7	327	108	435	0.33

表 3 分子定位区间内注释基因
Table 3 Annotated genes within the molecular localization interval

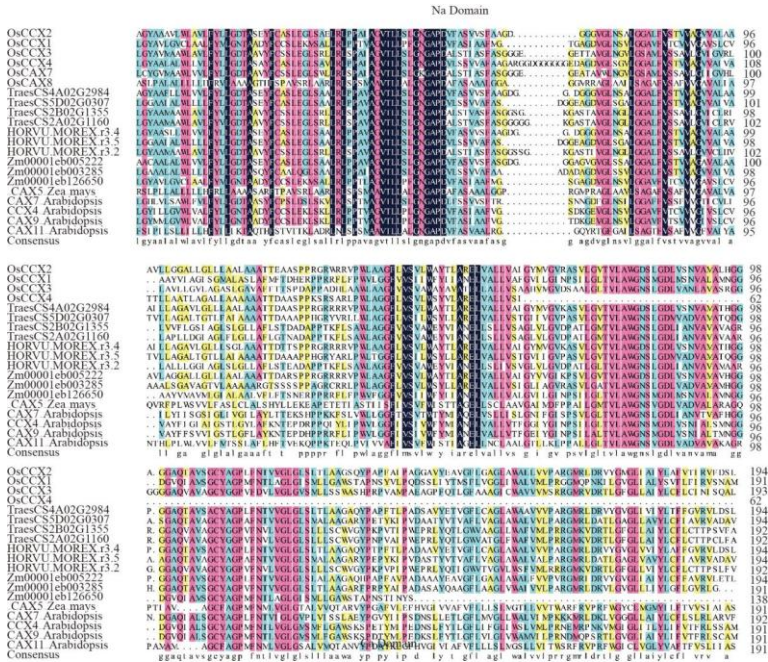
基因编号	注释信息
Gene ID	Annotation
<i>LOC_Os03g45370</i>	钠钙离子交换蛋白
<i>LOC_Os03g45390</i>	glucan endo-1,3-beta-glucosidase precursor, putative, expressed
<i>LOC_Os03g45400</i>	质体蛋白
<i>LOC_Os03g45410</i>	TATA 结合蛋白
<i>LOC_Os03g45420</i>	U-box 家族 E3 泛素连接酶

附图



基于不同物种 CCX/CAX 家族蛋白氨基酸序列构建的系统发生树。加粗标记的为 *OsCCX2*。
Phylogenetic tree constructed based on the amino acid sequences of CCX/CAX family proteins from different species. *OsCCX2* is indicated in bold.

图 1 CCX2 系统发生关系图
Figure. 1 Phylogenetic analysis of CCX2



选取水稻、玉米、小麦、大麦和拟南芥等物种中的 *CCX/CAX* 家族同源蛋白进行多序列比对。不同颜色表示不同类型的氨基酸残基，序列中相同或相近氨基酸集中分布的区域反映出较高的保守性
Homologous proteins of the *CCX/CAX* family from rice, maize, wheat, barley, and *Arabidopsis thaliana* were selected for multiple sequence alignment. Different colors represent different types of amino acid residues, and regions with clustered identical or similar residues indicate relatively high sequence conservation.

图 2 CCX2 及其同源蛋白的多序列比对分析
Figure. 2 Multiple sequence alignment analysis of *CCX2* and its homologous proteins