

Genome-wide Analysis of *potassium channel* Genes in Rice: Expression of the *OsAKT* and *OsKAT* Genes under Salt Stress

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Table S1. List of designed primers for Real-time PCR

Gene	Accession number	Primer (5'-3')	Gene ID in NCBI	Product size (bp)
<i>OsAKT1</i>	<i>Os01g0648000</i>	Forward: TACAGCCGACAATGTGGTGAAT Reverse: GTCAAGAACAAGCCATGTGGTA	LOC4326245	148
<i>OsAKT2</i>	<i>Os05g0428700</i>	Forward: CTACCTCATCGGCAACATGAC Reverse: CGAAATTGGAGGCAGCACGAA	LOC4338867	92
<i>OsKAT3</i>	<i>Os01g0756700</i>	Forward: CCATGTACTGGTCCATCACGA Reverse: TTGGTCATGTTGCCGATGAGG	LOC4325143	142
<i>OsKAT2</i>	<i>Os01g0210700</i>	Forward: GGACCAGGAATTTTAGGGACAC Reverse: CCTTGGGGGAGACTATCCAATGT	LOC4325560	159
<i>OsKAT1</i>	<i>Os02g0245800</i>	Forward: CCGAGTCAGTTCACTATTTGCC Reverse: TGCGAAGAGGGTCACAGAAATA	LOC4328864	97

Table S2. List of conserved motifs predicted in potassium channel proteins of rice

Motif No.	E-value	Amino acid sequence of motif	Width (aa)
Motif 1	3.6e-273	YWSITTLTTVGYGDLHAENTGEMLFSAFMLFNLGLTAYJIGNMTNLVVH	50
Motif 2	1.6e-162	RLWRLRRVSKLFARLEKDIRFNWTRCIKLSVTLFAVHCAACI	45
Motif 3	8.8e-139	ZSVYLFKGVSDFILQLVTEMKAEYFPPKEDIILQNEAPTDVYIVVSGAV	50
Motif 4	8.2e-123	GTSRTRKFRDTIQAASEFGARNQLPEAIKEQMLAHICLRFRTTEELLQQEM	50
Motif 5	1.2e-102	VDAFFAIDIALTFFVAYRDKKTYLLVDDPKKIATRYLSSWF	41
Motif 6	4.7e-091	FGEIGVLCNIPQPFVTRTRELQCLLRJSKTALLEIIQENREDGRIILSNL	50
Motif 7	5.8e-071	PSLGATANQSPKLRKFIISPYDPRYRIWETFLIVLVVYSAWICPFELAF	49

Motif 8	8.6e-065	DRYPIELTWIGAQIPNFEDRSLWFRYVT	29
Motif 9	1.7e-032	AADLDNDGRVKGADFVVYKLKELGKISZEDISMFLDZFDKLDADHSGKJS	50
Motif 10	2.2e-031	WKVEGLGWVDAFYLVVASVTTLGYGDRSFSSPAGRLFAVAWJLVSTJAVA	50
Motif 11	2.9e-029	GADPNESDYDGR TALHIAASKGYEDCVRFL LQQGADVNAKDKFGNTPL WE	50
Motif 12	4.3e-029	LDEL PKAIRSSIAQYLFLPVV	21
Motif 13	2.6e-025	LDVASTIPLQIIYQLVTGKRQGL	23
Motif 14	2.1e-016	GFRPTKILTVEGA EIDDIEVIRDGDHLF	28
Motif 15	6.4e-014	YGGDPNARDRDGR TPLHIAAAEGLYL VAKLLVENGADIDAKDRWGNTP	48

Table S3. The predicted duplicated gene pairs in the potassium channel protein family in rice

Gene 1	Gene 2	Ka	Ks	Ka/Ks	p-value	Divergence time (MYA)
<i>Os01g0756700</i>	<i>Os01g0210700</i>	0.26	1.1	0.236363636	1.04E-06	84.61538462
<i>Os01g0210700</i>	<i>Os02g0245800</i>	0.29	1.53	0.189542484	2.52E-08	117.6923077
<i>Os03g0752300</i>	<i>Os07g0108800</i>	0.28	2.66	0.105263158	1.30E-06	204.6153846
<i>Os06g0254200</i>	<i>Os04g0117500</i>	0.31	1.42	0.218309859	3.28E-05	109.2307692
<i>Os06g0254200</i>	<i>Os01g0718700</i>	0.35	1.83	0.191256831	1.46E-08	140.7692308

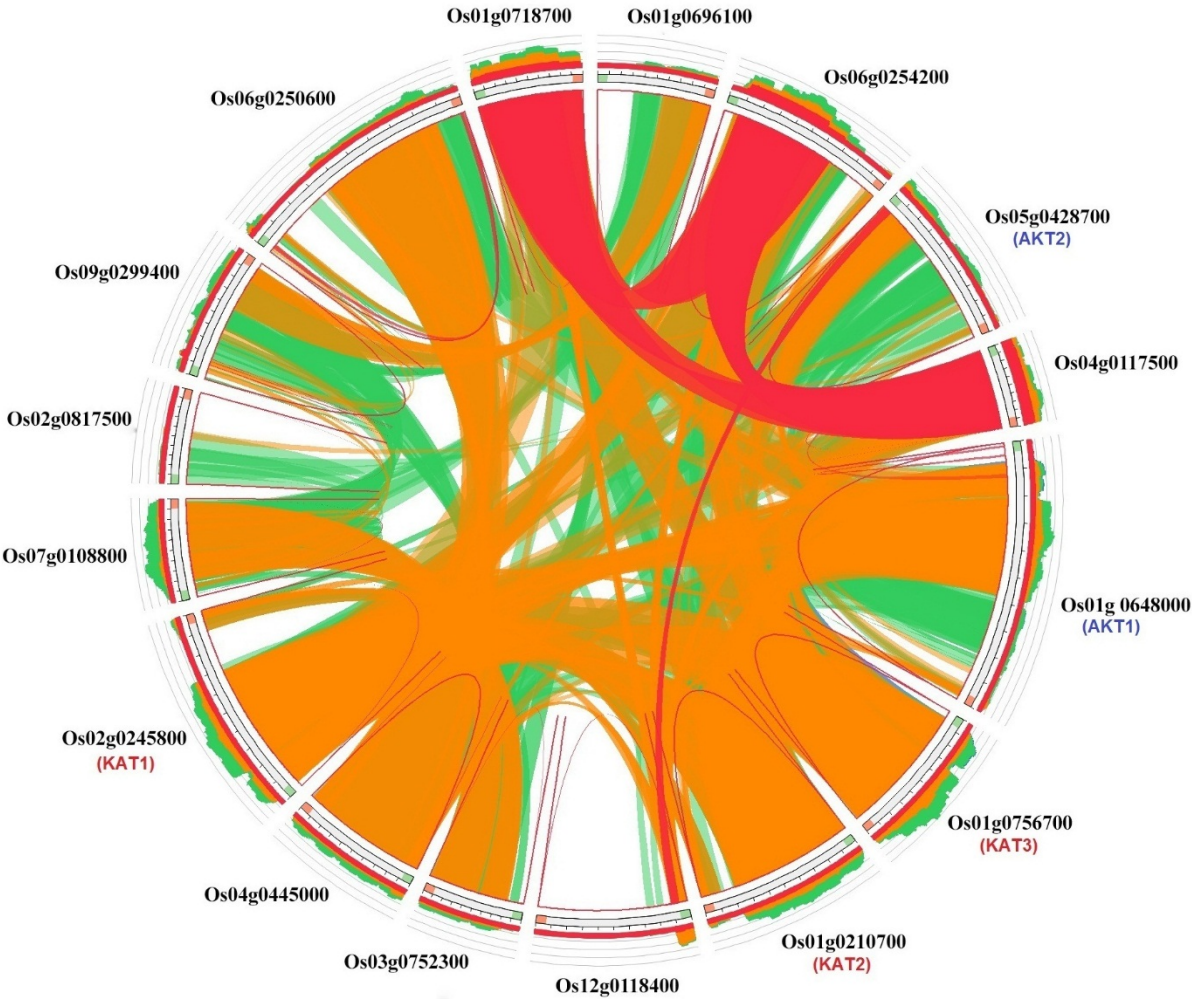


Figure S1. Synteny analysis of K^+ channel genes in rice

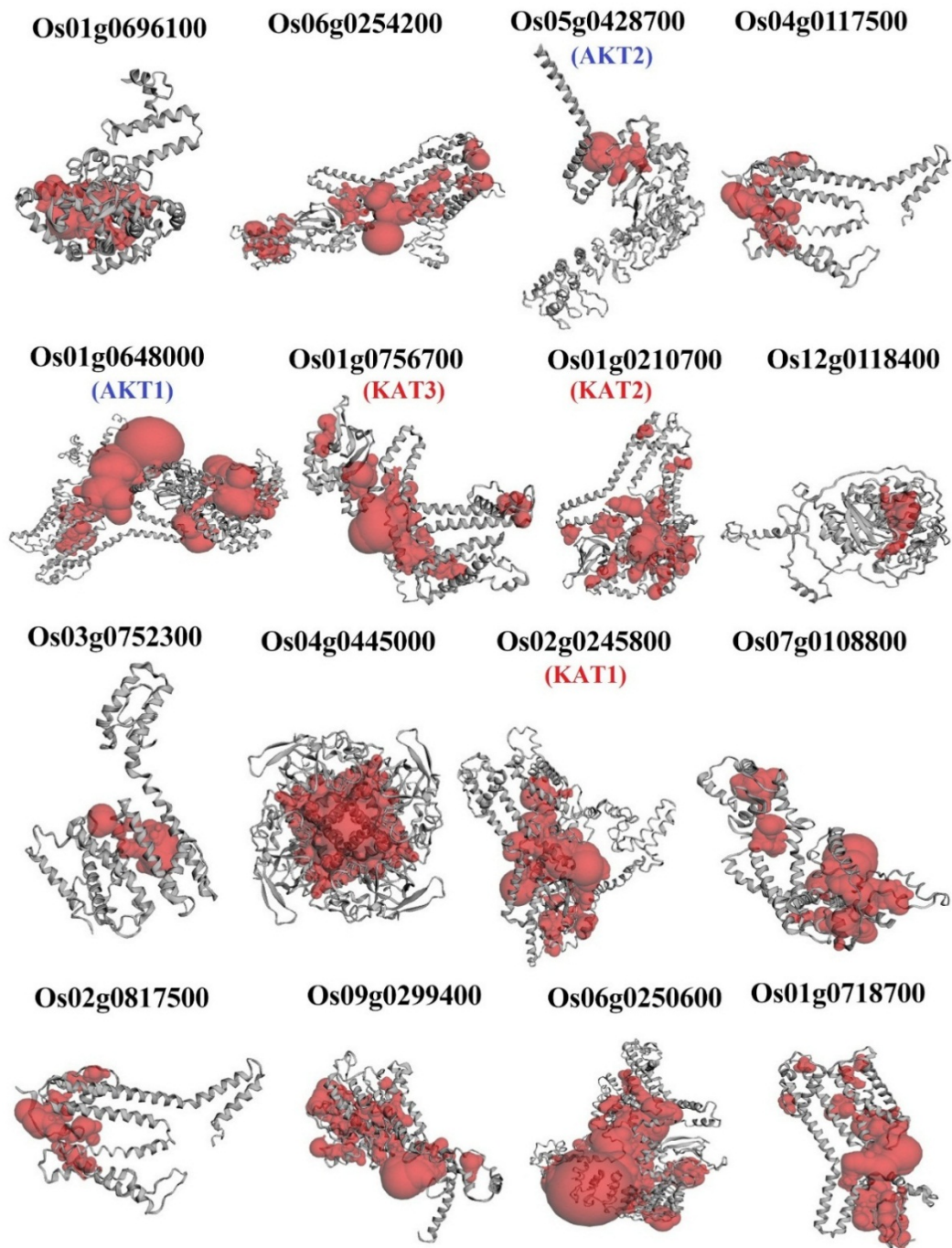


Figure S2. The protein channel regions predicted in K^+ channel proteins in rice