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Brief communication

Molecular phylogenetic study and expression analysis of ATP-binding cassette transporter gene family in *Oryza sativa* in response to salt stress

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A B S T R A C T

ATP-binding cassette (ABC) transporter is a large gene superfamily that utilizes the energy released from ATP hydrolysis for transporting myriad of substrates across the biological membranes. Although many investigations have been done on the structural and functional analysis of the ABC transporters in *Oryza sativa*, much less is known about molecular phylogenetic and global expression pattern of the complete ABC family in rice. In this study, we have carried out a comprehensive phylogenetic analysis constructing neighbor-joining and maximum-likelihood trees based on various statistical methods of different ABC protein subfamily of five plant lineages including *Chlamydomonas reinhardtii* (green algae), *Physcomitrella patens* (moss), *Selaginella moellendorffii* (lycophyte), *Arabidopsis thaliana* (dicot) and *O. sativa* (monocot) to explore the origin and evolutionary patterns of these ABC genes. We have identified several conserved motifs in nucleotide binding domain (NBD) of ABC proteins among all plant lineages during evolution. Amongst the different ABC protein subfamilies, 'ABCE' has not yet been identified in lower plant genomes (algae, moss and lycophytes). The result indicated that gene duplication and diversification process acted upon these genes as a major operative force creating new groups and subgroups and functional divergence during evolution. We have demonstrated that rice ABCI subfamily consists of only half size transporters that represented highly dynamic members showing maximum sequence variations among the other rice ABC subfamilies. The evolutionary and the expression analysis contribute to a deep insight into the evolution and diversity of rice ABC proteins and their roles in response to salt stress that facilitate our further understanding on rice ABC transporters.

1. Introduction

ATP-binding cassette (ABC) transporters, belonging to one of the largest gene family, are abundant in the genomes of both prokaryotes and eukaryotes (Dassa and Bouige, 2001; Rea, 2007; Locher, 2009; Licht and Schneider, 2011). Animal ABC transporters, especially the mammalian ones that have been extensively characterized, transport a wide range of compounds including proteins and chemotherapeutic drugs (Dean et al., 2001; Rea, 2007; Locher, 2009; Licht and Schneider, 2011). Bacterial ABC transporters have been implicated in the uptake of simple nutrients such as phosphates and amino acids while in yeast an ABC transporter has been reported to export mating factors (Davidson and Chen, 2004; Kovalchuk and Driessen, 2010). Plants are particularly rich in ABC proteins: the model plant *Arabidopsis thaliana* itself being capable of encoding more than 120 such proteins (Sánchez-Fernández et al., 2001a) in comparison to the relatively fewer amount of 50–70 ABC proteins encoded by the human genome (Sánchez-Fernández et al., 2001b). Most of the ABC proteins behave as ATP-dependent cassette transporters coupled with ATP hydrolysis playing active role in the transport of wide range of substrates across biological membranes. In addition to membrane transporters, some of the ABC proteins also act as regulators of ion channels, receptors and proteins involved in mRNA translation and ribosome biogenesis (Rea, 2007). Some ABC transporters have also been implicated for multidrug resistance in microbial pathogens and tumor cells hindering the efficacy of the drug used for the treatment of infectious diseases and cancer (Piddock, 2006; Lubelski et al., 2007; Hollenstein et al., 2007). Mutated version of many human ABC genes are involved in the hereditary diseases that includes cystic fibrosis, adrenoleukodystrophy, disorders of cholesterol metabolism and other diseases

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Table 1
Predicted topology of each members of ABC superfamily tranporters in *Oryza sativa* obtained from SMART domain analyses.

Sr. no.	New systematic name[a]	RAPDB locus ID[a]	TIGR5 locus ID[a]	TIGR protein length (aa)	Predicted topology
1	*OsABCA1*	Os02g0211000	LOC_Os02g11960.1	964	1TMD–6TMD–NBD
2	*OsABCA2*	Os06g0589300	LOC_Os06g38950.1	949	1TMD–4TMD–NBD
3	*OsABCA3*	Os08g0398000	LOC_Os08g30740.1	968	1TMD–5TMD–NBD
4	*OsABCA4*	Os08g0398300	LOC_Os08g30770.1	957	1TMD–6TMD–NBD
5	*OsABCA5*	Os08g0398350	LOC_Os08g30780.1	988	1TMD–4TMD–NBD
6	*OsABCA6*	Os09g0360900	LOC_Os09g19680.1	875	1TMD–6TMD–NBD
7	*OsABCB1*	Os01g0290700	LOC_Os01g18670.1	1285	(TMD–NBD)$_2$
8	*OsABCB2*	Os01g0533900	LOC_Os01g34970.1	843	3TMD–NBD–4TMD
9	*OsABCB3*	Os01g0534700	LOC_Os01g35030.1	1179	(3/5TMD–NBD)$_2$
10	*OsABCB4*	Os01g0695700	LOC_Os01g50080.1	1154	(3/5TMD–NBD)$_2$
11	*OsABCB5*	Os01g0695800	LOC_Os01g50100.1	1181	(5/3TMD–NBD)$_2$
12	*OsABCB6*	Os01g0696600	LOC_Os01g50160.1	1274	(5/6TMD–NBD)$_2$
13	*OsABCB7*	Os01g0723800	LOC_Os01g52550.1	1234	(6/3TMD–NBD)$_2$
14	*OsABCB8*	Os01g0976100	LOC_Os01g74470.1	1397	(6TMD–NBD)$_2$
15	*OsABCB9*	Os02g0190300	LOC_Os02g09720.1	1245	(6/5TMD–NBD)$_2$
16	*OsABCB10*	Os02g0323000	LOC_Os02g21750.1	788	4TMD–NBD
17	*OsABCB11*	Os02g0693700	LOC_Os02g46680.1	1264	(6/5TMD–NBD)$_2$
18	*OsABCB12*	Os03g0181700	LOC_Os03g08380.1	1482	(5/4TMD–NBD)$_2$
19	*OsABCB13*	Os03g0280000	LOC_Os03g17180.1	1411	(6/7TMD–NBD)$_2$
20	*OsABCB14*	Os04g0459000	LOC_Os04g38570.1	1259	(6/4TMD–NBD)$_2$
21	*OsABCB15*	Os04g0481700	LOC_Os04g40570.1	1279	(4TMD–NBD)$_2$
22	*OsABCB16*	Os04g0642000	LOC_Os04g54930.1	649	6TMD–NBD
23	OsABCB17	Os05g0137200	LOC_Os05g04610.1	524	4TMD–NBD
24	*OsABCB18*	Os05g0548300	LOC_Os05g47490.1	1302	(3/5TMD–NBD)$_2$
25	*OsABCB19*	Os05g0548500	LOC_Os05g47500.1	1213	(4TMD–NBD)$_2$
26	*OsABCB20*	Os08g0153000	LOC_Os08g05690.1	1245	(6/5 TMD–NBD)$_2$
27	*OsABCB21*	Os08g0153200	LOC_Os08g05710.1	1242	(3/2TMD–NBD)$_2$
28	*OsABCB22*	Os08g0564300	LOC_Os08g45030.1	1344	(6TMD–NBD)$_2$
29	*OsABCB23*	Os06g0128300	LOC_Os06g03770.1	733	5TMD–NBD
30	*OsABCB24*	Os01g0911300	LOC_Os01g68330.1	497	2TMD–NBD
31	*OsABCB25*	Os03g0755100	LOC_Os03g54790.1	641	5TMD–NBD
32	*OsABCB26*	Os07g0464600	LOC_Os07g28090.1	690	5TMD–NBD
33	*OsABCB27*	Os04g0413000	LOC_Os04g33700.1	549	2TMD–NBD
34	*OsABCC1*	Os04g0620000	LOC_Os04g52900.1	1650	5NTE–(4/5TMD–NBD)$_2$
35	*OsABCC2*	Os01g0902100	LOC_Os01g67580.1	1386	2NTE–(3/5TMD–NBD)$_2$
36	*OsABCC3*	Os01g0173900	LOC_Os01g07870.1	1505	5NTE–(4/5TMD–NBD)$_2$
37	*OsABCC4*	Os02g0288733	LOC_Os02g18700.1	1198	(2TMD–NBD)$_2$
38	*OsABCC5*	Os02g0288400	LOC_Os02g18670.1	1186	(2/5TMD–NBD)$_2$
39	*OsABCC6*	Os04g0588600	LOC_Os04g49890.1	1074	(3/6TMD–NBD)$_2$
40	*OsABCC7*	Os04g0588700	LOC_Os04g49900.1	1318	(5/4 TMD–NBD)$_2$
41	*OsABCC8*	Os01g0356000	LOC_Os01g25386.1	1527	5NTE–(3/7TMD–NBD)$_2$
42	*OsABCC9*	Os04g0209200	LOC_Os04g13210.1	1207	(3/6TMD–NBD)$_2$
43	*OsABCC10*	Os04g0209300	LOC_Os04g13220.1	1512	2NTE–(3/5TMD–NBD)$_2$
44	*OsABCC11*	Os06g0561800	LOC_Os06g36650.1	1195	(TMD–NBD)$_2$
45	*OsABCC12*	Os06g0184700	LOC_Os06g08560.1	1415	4NTE–(5TMD–NBD)$_2$
46	*OsABCC13*	Os03g0142800	LOC_Os03g04920.1	1505	4NTE–(TMD–NBD)$_2$
47	*OsABCC14*	Os05g0196100	LOC_Os05g10730.1	1474	5NTE–(5TMD–NBD)$_2$
48	*OsABCC15*	Os06g0158900	LOC_Os06g06440.1	1474	5 NTE–(4/5TMD–NBD)$_2$
49	*OsABCC16*	Os11g0155600	LOC_Os11g05700.1	674	3TMD–NBD
50	*OsABCC17*	Os12g0562700	LOC_Os12g37580.1	1200	(2TMD–NBD)$_2$
51	*OsABCD1*	Os01g0218700	LOC_Os01g11946.1	771	4TMD–NBD
52	*OsABCD2*	Os01g0966100	LOC_Os01g73530.1	1317	NBD$_2$
53	*OsABCD3*	Os05g0107600	LOC_Os05g01700.1	1130	NBD$_2$
54	*OsABCE1*	Os02g0282900	LOC_Os02g18180.1	608	NBD$_2$
55	*OsABCE2*	Os11g0546000	LOC_Os11g34350.1	604	NBD$_2$
56	*OsABCF1*	Os02g0826500	LOC_Os02g58020.1	722	NBD$_2$
57	*OsABCF2*	Os03g0441500	LOC_Os03g32630.1	710	NBD$_2$
58	*OsABCF3*	Os04g0658400	LOC_Os04g56330.1	606	NBD$_2$
59	*OsABCF4*	Os08g0564100	LOC_Os08g45010.1	592	NBD$_2$
60	*OsABCF5*	Os09g0572400	LOC_Os09g39910.1	575	NBD$_2$
61	*OsABCF6*	Os11g0603200	LOC_Os11g39020.1	690	NBD$_2$
62	*OsABCG1*	Os01g0121600	LOC_Os01g03144.1	668	NBD–3TMD
63	*OsABCG2*	Os01g0615500	LOC_Os01g42900.1	613	NBD–5TMD
64	*OsABCG3*	Os01g0836600	LOC_Os01g61940.1	749	NBD–6TMD
65	*OsABCG4*	Os03g0157400	LOC_Os03g06139.1	771	NBD–7TMD
66	*OsABCG5*	Os03g0281900	LOC_Os03g17350.1	787	NBD–7TMD
67	*OsABCG6*	Os03g0282100	LOC_Os03g17370.1	765	NBD–6TMD
68	*OsABCG7*	Os03g0859500	LOC_Os03g64200.1	711	NBD–6TMD
69	*OsABCG8*	Os04g0194500	LOC_Os04g11820.1	1065	TMD–NBD–4TMD
70	*OsABCG9*	Os04g0528300	LOC_Os04g44610.1	711	NBD–6TMD
71	*OsABCG10*	Os05g0120000	LOC_Os05g02870.1	680	NBD–6TMD
72	*OsABCG11*	Os05g0120200	LOC_Os05g02890.1	699	NBD–6TMD
73	*OsABCG12*	Os05g0222200	LOC_Os05g13520.1	700	NBD–TMD
74	*OsABCG13*	Os05g0384600	LOC_Os05g31910.1	614	NBD–5TMD
75	*OsABCG14*	Os06g0503100	LOC_Os06g30730.1	624	NBD–6TMD