

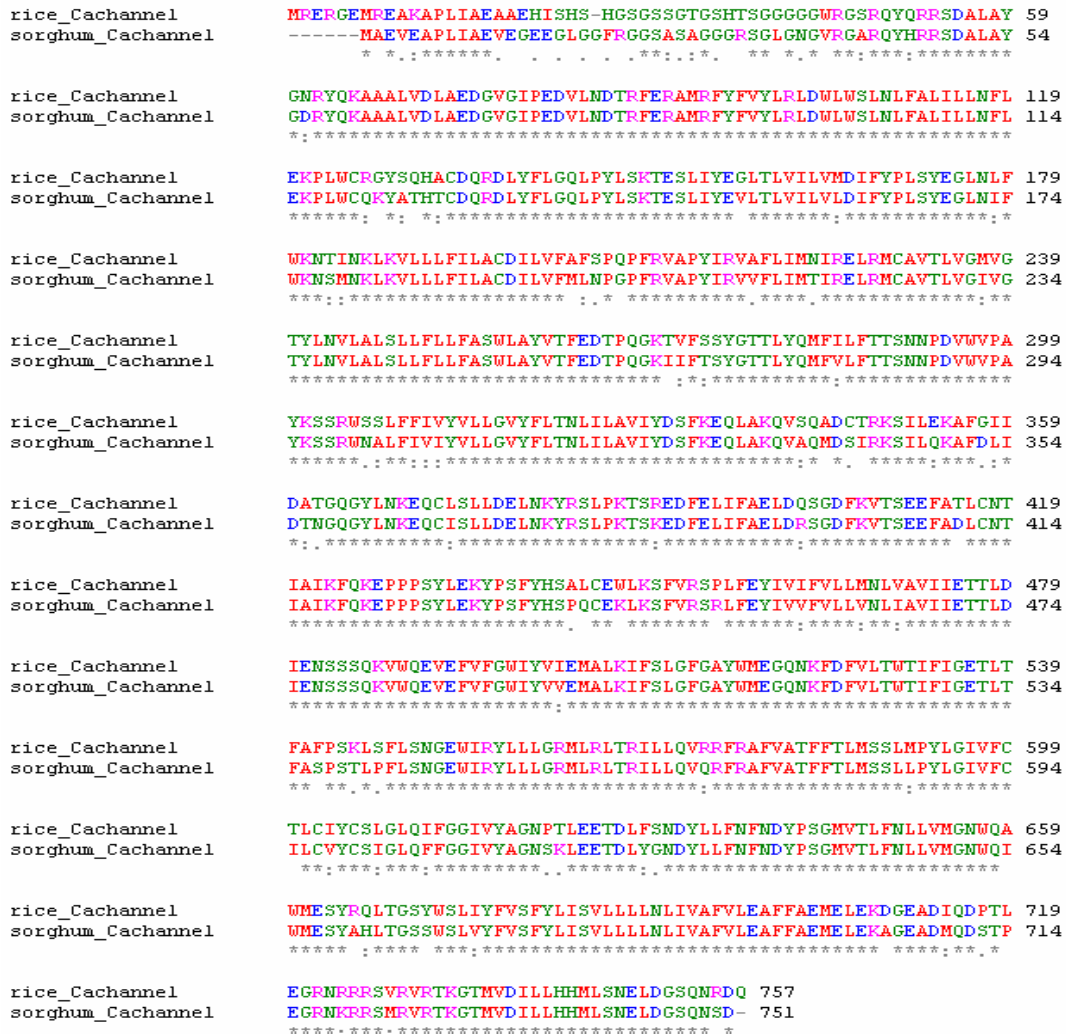
Supplementary Material

Goel, A., *et al.* 2011. Genome-wide comparative *in silico* analysis of calcium transporters of rice and sorghum. *Genomics Proteomics Bioinformatics* 9(4-5): 138-150.

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Figure S1

Figure S1 Multiple sequence alignment of calcium transporter proteins in rice and sorghum. ClustalW alignment of amino acid sequences of calcium channel (A), ATPase (B) and exchanger (C) from rice and sorghum was indicated. The conserved signature sequences of the calcium ATPase are boxed.



A

Os01g71240	LPLAVTSLA	FAMKMLQER	ALVRHLSACE	TMGSASCICT	DRTGLTTNH	VVVERKIASG	AAQTMNSARG
Os02g08018							
Os03g17310	LPAVITTCIA	LGRKMAQKN	ALVRKLPSE	TLGCTTVICS	DRTGLTTNQ	SAVKLVAIG	RWPD--LRS
Os03g42020	LPLAVTSLA	FAMKMMNDK	ALVRQLAACE	TMGSATVICS	DRTGLTTNR	STVVKACICG	NTIQVNPQT
Os03g52090	LPAVITTCIA	LGRKMARLN	AIYRSLPSE	TLGCTTVICS	DRTGLTTNM	ISVSRKCVFR	SVHRPITDE
Os03g10640	LPLAVTSLA	FAMKMMNDK	ALVRHLAACE	TMGSATTICS	DRTGLTTNH	STVVKACICG	KIKDVESASD
Os04g51610	LPLAVTLTA	FSMKMMNDK	ALVRHLSACE	TMGSATTICS	DRTGLTLNQ	STVVEAYFGG	KKMDPPDN--
Os05g41580	LPLAVTSLA	FAMKMLHDK	ALVRHLAACE	TMGSASCICT	DRTGLTTNH	IVDKVWIGD	VK--FVGDKI
Os05g02940							
Os08g40530				TMGSATTICS	DRTGLTLNK	STVQAYFGG	TMLDPCDD--
Os10g28240	LPLAVTLTA	FSMKRMVREN	ALVRHLSACE	TMGSVTAICT	DRTGLTLNQ	KVTEFWVG--	--ADRPR--
Os11g04460	LPLAVTSLA	FAMKMLNDK	ALVRHLSACE	TMGSAGTICT	DRTGLTTNY	VVDRKIWISE	NSKSVTSNTI
Os12g04220	LPLAVTSLA	FAMKMLNDK	ALVRHLSACE	TMGSAGTICT	DRTGLTTNH	VVDRKIWISE	NSKSVTSNTI
Os12g39660	LPLAVTSLA	FAMKMMNDK	ALVRHLAACE	TMGSATTICS	DRTGLTTNH	STVVKACICG	NIKEVNPKN
Sb01g038990	LPAVITTCIA	LGRKMAQKN	ALVRKLPSE	TLGCTTVICS	DRTGLTTNQ	SAVKLVAIG	RWPD--LRS
Sb01g021870	LPLAVTLTA	FSMKRMVKEH	ALVRTLSACE	TMGSVTAICT	DRTGLTLNQ	KVTEFWVG--	--DDRPK--
Sb01g043620	LPLAVTSLA	FAMKMMNDK	ALVRHLAACE	TMGSATVICS	DRTGLTTNH	STVVKACICG	KIKEVDGSD
Sb01g014620	LPLAVTSLA	FAMKMMNDK	ALVRQLAACE	TMGSATVICS	DRTGLTTNR	STVVKACICG	NIMEVTPPV
Sb02g028935	LPLAVTLTA	YSMKMMNDK	ALVRLSSCE	TMGSATTICS	DRTGLTMNK	STVVEAYLGG	KEMDPYDN--
Sb03g045370	LPLAVTSLA	FAMKMLQER	ALVRHLSACE	TMGSASCICT	DRTGLTTNH	VVVERKIASG	AAQTVSTARG
Sb04g005130	LPLAVTLTA	YSMKMMADK	ALVRHLSACE	TMGSATTICS	DRTGLTLNQ	STVQOSIVGE	VKLOPPAN--
Sb05g002380	LPLAVTSLA	FAMKQLMNDK	ALVRHLSACE	TMGSAGTICT	DRTGLTTNH	VVVERKIWISE	NSKSVTSNNS
Sb06g027770	LPLAVTLTA	FSMKMMNDK	ALVRHLSACE	TMGSATTICS	DRTGLTLNQ	STVVEAYFGG	KKMDPPDN--
Sb07g028160	LPLAVTSLA	FAMKMMNDK	ALVRHLAACE	TMGSATTICS	DRTGLTTNH	STVVKACICG	KIKDVSSAE
Sb07g026810	LPLAVTLTA	YSMKMMNDK	ALVRLSSCE	TMGSATTICS	DRTGLTLNK	STVVEAYFAG	TKLDPCDD--
Sb08g001260	LPLAVTSLA	FAMKMLNDK	ALVRHLSACE	TMGSAGTICT	DRTGLTTNH	VVDRKIWISE	NSKSVTSNNS
Sb09g024300	LPLAVTSLA	FAMKMLNDK	ALVRHLAACE	TMGSASCICT	DRTGLTTNH	IVDKVWIGD	NSKSVNDTN
Sb09g001850	LPAVITTCIA	LGRKMAAKN	ALVRKLPSE	TLGCTTVICS	DRTGLTTNK	SAVKLVAIG	DSSQE--VRS
Sb06g029175							

B

Os01g11414	CIITKAVGLLLGSAIAAAFADPLVDVHNFNASHISPSFTISFIALPHATNSSEAVSAIIFASRKKLRSSLTSEYVGGVMMNNTLCLGFLIATIKR--NLTWDFSEVLLILLVCMIGLFTS
Sb04g008850	TSEKATISLLLLGTAMAAAFADPLVDVHGFNASTISPSFTISFIAMPLATNSSEAVSAIIFASRKKQRSSLTSEYVGGVMMNNTLCLAVFLGIIVR--GLTWDFSEVLLIIFVCMIGLFTS
Os05g51610	GFSSAMTWLWMLTLLALLSEYVSTTEAESWELSWSPISITLLPIVGNAAEHAGAVIFAKNM---DITLGVLSGSAIQISMVFPVSWIIVAMTGMPLDNLNLETGSLRLAIVLTAFTL
Sb09g030750	GFSSAMTWLWMLTLLAVLSEYVSTTE---DITLGVLSGSAIQISMVFGW---
Os01g37690	GFASALFWLADTAVISVLSSEYVSTTEPESQWGLSWSPISITLLPIVGNAAEHAGAIIFAKNKL---DITLGVLSGSAIQISMFPVPLSWLWAMTGMPLDNLNLETGSLRMAVILVTAFTL
Os02g21009	GFASAMWVLLGMAVITAMLSSEYVSTTEPESMGLVPRFISITLLPIVGNAAEHAGAIIFAPNKI---DITLGVLSGSAIQISMLVFPVILWISWNNAIPLMDLNLNLETGSLAMAVITVTAFTL
Sb04g010130	GSASVIVWLGITVVIIVLNSVYVSTTEPESDALGIVPRFISITLLPIVGNAAEHAGAIIFAPNKI---DITLGVLSGSAIQILLVFPVILWISWNNIPLMDLNLNLETGSLVMTVITVTAFTL
Os02g04630	-----ASKAWNIWAFISVWLLPVVGNISAGHANAVMFAVKDKL---DITLGVLSGSAIQISMFGIIFPCVWMMGKPMQMDNLNLETGSLVMTVITVVAELL
Sb04g003135	ISKWEAIWLAITFAWISVFSDFVEATEGASAKWIKWAFISVWLLPIVGNAAEHASAIMFAMDKL---DITLGVLSGSAIQISMFPVFPVWMMGKPMQMDNLNLETGSLVMTVITVVAELL
Os03g27960	TQCEAICWLFILWISLISEYLDATQASSENINFPWAFISVILLPIVGNAAEHASAIMFAMDKL---DITLGVLSGSAIQISMFPVFPVWMMGKPMQMDNLNLETGSLVMTVITVVAELL
Sb01g033220	TQCEAICWLFILWISLISEYLDATQASSENINFPWAFISVILLPIVGNAAEHASAIMFAMDKL---DITLGVLSGSAIQISMFPVFPVWMMGKPMQMDNLNLETGSLVMTVITVVAELL
Os04g55940	GMWESTAWLMLWISLISEYLDATQASSENINFPWAFISVILLPIVGNAAEHASAIMFAMDKL---DITLGVLSGSAIQISMFPVFPVWMMGKPMQMDNLNLETGSLVMTVITVVAELL
Sb06g031080	GMWESTAWLMLWISLISEYLDATQASSENINFPWAFISVILLPIVGNAAEHASAIMFAMDKL---DITLGVLSGSAIQISMFPVFPVWMMGKPMQMDNLNLETGSLVMTVITVVAELL
Os02g43110	-EIAHGWIAPICSLIFISGLAYGVTKITDQISCVTGVSYVYIAPTALAAAGTSPDVLVASKIAAERQIT--ADSATNTTCR-----YIS-AHLLSN-----
Os11g43860	-EIAHGWIAPICSLIFISGLAYGVTKITDQISCVTGVSYVYIAPTALAAAGTSPDVLVASKIAAERQIT--ADSATNTTCRNVNIYVGIWVPLVDMYNYVYQKPLIDNAAGLSFSLVFPAL
Os03g45370	RRVPLAAGFLMSVLWAYTLARELVALLVSIYVGVRSVWLVGTVLWAGDSLGLVSNVAMAHGGAG--GAQTAVSFCYAGPEFNWVGLGLSUTLAAGCAQHPAPPVFPADAAWVAVGFLGAGL
Sb01g012910	RRVPLAAGFLMSVLWAYTLARELVALLVSIYVGVRSVWLVGTVLWAGDSLGLVSNVAMAHGGAG--GAQTAVSFCYAGPEFNWVGLGLSUTLAAGCAQHPAPPVFPADAAWVAVGFLGAGL
Os12g42910	RLPWLAGGFLMSVLWYVLAARELVALLVSIYVGVRSVWLVGTVLWAGDSLGLVADVALAARRDGGAGQAVAGCYAAPAFENWVGLGLSUTLAAGARPEAVVGGAVVAVGFLAAGL
Sb08g022240	RLPWLAGGFLMSVLWYVLAARELVALLVSIYVGVRSVWLVGTVLWAGDSLGLVADVALAARRDGGAGQAVAGCYAAPAFENWVGLGLSUTLAAGARPEAVVGGAVVAVGFLAAGL
Os03g08230	LLFPWVGGFVMSIITWFYIIANELVALLVAFGVILGINSILGTVLWAGNSMGLDLSNVALAMNGGDG---VQIAMSFCYAGPEFNWVGLGLSMLLGAWSTANSVLPODSSLIYTMSEFLVAGL
Sb03g008600	LLFPWVGGFVMSIITWFYIIANELVALLVAFGVILGINSILGTVLWAGNSMGLDLSNVALAMNGGDG---VQIAMSFCYAGPEFNWVGLGLSMLLGAWSTANSVLPODSSLIYTMSEFLVAGL
Os10g30070	LAAPLAAAGFVMSVAVAYAVATELLALVSAHVMGSDAALGTVLWAGNSLGLVLANVAVASRGGGGG--GAQTAVAGCYGGFVFDVWVGLGWSMLLSSWASHRFPVAMPAPAGPQLTGFAPAAAI
Os11g01580	
Sb01g021270	LLGAWLGGFVMSVAVAYAVIANEVLISLVSAGTILSNDAALGTVLWAGNSLGLVLANVAVASRGGGA---QVAVSFCYGGFVFNWVGLGLSMLLSCWSGHPFPVETPREPGLMRTLAFAVAGL
Sb03g013753	
Sb04g011451	
Os11g05070	-----MDIDAEKAVSITETEVNGLGRVMDLPTVEDRKQ-----QHTLCTMPSKLLQSNSEF
Os03g01330	-----TEEDAGVAVGEVHEGGPLADLVEVEVDAGGGG-----CELVEEDLDAEVEGVEQGEVGEVVEGVELEEEV

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