

Supplementary Material

Identification of a Novel Gene Encoding the Specialized Alanine Decarboxylase in Tea (*Camellia sinensis*) Plants

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AtSDC1 :	MVGSLESDQTLSMATHLEPKLDI	SDDFDPTAVVTEPLPPPV-TNGIGADRGGGGGGEREMVIGRN	IHTSTAVTEPEVNTDEFTGDKE	: 85
OsSDC1 :	MVGSVGNGLVDELGGAAVAVNCVGKGMRPEAVAMEVESPP-RPAEEEGGSPTRREIVLGRNVH	IASFAVKPVEDDAEDEETGEERE	: 84	
OsSDC2 :	-----MVLINSEEVSCNDHHQVQDVVA-----	-----AAGLQCSGDMLGDKQVTSQVILEGPEIEPEPPAEEMEAEEKK	: 62	
OsSDC3 :	-----MATPK-EHIQERSAHSIGR-N-----	-----AHGYEDSNFLLT--K1TENKMSCPNTIS-----MLAPTL	: 52	
CL4912 :	MEG-----TVSLSVNSVSKVELLSKCFDLITIP	-----EPLPPVVASNGVAGGETKRMKEKDIVLGRNVHITSSTTDEDV	-----DDSTSMDME : 80	

AtSDC1 :	EYMASTLARWRTWVERTKHNHIGYPNLDIDDYCAIGOLQHES	INNNGDPPFESNYGVHSRFEEV	VLDWFARIWEIERDDYWGYIT	: 171
OsSDC1 :	EAMASVIALARRNLVERTKHNHIGYPNLDIDDYCAIGOLQHES	INNNGDPPFESNYGVHSRFEEV	VLDWFARIWELEKNEYWGYYIT	: 170
OsSDC2 :	ECISRLIMAGLVQHIIQHRSAYHIGYPNFDYDFESLAPFLNE	SLNNAGDPFESLAKAVANNSVHSRCFEVAVLNWFAFWDVQRDQFWGYIT	: 148	
OsSDC3 :	GWVGRNNE-----ESRTRRNAGYPNFEDFEGVIE	FLNMPLINNAGDPFEMCVNGIHKFFKIEV	VLDWFARIWEIPKDQYWGYVT	: 132
CL4912 :	EPMACVILVRWRTWILKTKYHIGYPNLDIDDYCAIGOLQHES	INNNGDPPFESNYGVHSRFEEV	VLDWFARIWEIQKEYWGYYIT	: 166

AtSDC1 :	NCGTEGNLHGILVGREMFDDGILYLASRESHYSVFKAA	MYRNDCRVDTLMSGEIDCDIRKFL	BNKDRPAAILNVNIGTTKGAV	: 257	
OsSDC1 :	NCGTEGNLHGILVGREVFDDGILYLASRESHYSVFKAA	MYRNDCRVDTLMSGEIDCDIFQKLL	INRDRPAAILNVNIGTTKGAV	: 256	
OsSDC2 :	SGCTEGNLYGLLVLGRELFFPDGILYLASNDSHYSVFKAA	MYRVKICRIATATVSGEMNYA	DSKIQHNTSPAIINANIGTTKGAV	: 234	
OsSDC3 :	SGCTEGNMGHLLVGRELFFPDGILYLASCDSHYSI	FKAAKMYRVQCCIKIDTF	ESGEMIDYAFDFRKLL	CNTRSPAIVNVNIGTTKGAV	: 218
CL4912 :	NCGTEGNLHGILVGREVFDDGIFTYTSQESHYSISFKAA	MRMYRBCVKVGTLLINGE	IDCADEPKLL	BNKDRPAAINLNIGTTKGAV	: 252
bb	b		b		

AtSDC1 :	DDLDIVVIKTLLEECCGFSDRFYIHCDGALE	GIMMPFVKA	PKVTFN	KPIGSVS	SVSGHKFVGCP	PCGVC	CITRMEHI-KV	LSSNVEYI	: 342	
OsSDC1 :	DDLDIVVIKTLLEECCGFSDRFYIHCDGALE	GIMMPFVKA	PKVTFN	KPIGSVS	SVSGHKFVGCP	PCGVC	CITRMEHI	-NELSSNVEYI	: 340	
OsSDC2 :	DDIDQTIISLEKCGF-CNRYYIHCD	SAISGMMTPPMK	QPKVSFK	PKGSI	SVSGHKFVGCP	PCGVC	CITRMEHA-EV	LSTIDIEYI	: 318	
OsSDC3 :	DDLDIEVVMLENCGF-ANRFYIHCD	SAIVGIMMPFI	QCPKLT	PKIGSIC	CISGHKFIGCP	IPCGV	CITRMEHI	-NHMSUNIEYI	: 303	
CL4912 :	DDIDIVVIQI	LEECCGFSDRFYIHCDGALE	GIMMPFVKA	PKVTFN	KPIGSVS	SVSGHKFVGCP	IPCGV	CITRMEHI	-NALSRNVEYI	: 337
b	b		b		b					

AtSDC1 :	ASRDATITMGSRNHGAPLILWYDILNRHGYRC	EQKEVQ	CLRNAHY	YLKDRL	REAGISAMINEL	SSTVVFERPKD	DEEVRRWQLACQGD	: 428
OsSDC1 :	ASRDATITMGSRNHGAPLILWYDILNRHGYRC	EQKEVQ	CLRNAHY	YLKDRL	KEAGIGAMINEL	SSTVVFERPKD	DEEVRRWQLACEGN	: 426
OsSDC2 :	ASRDATITMGSRNHGAPLILWYDILSRKHYGK	KLICKIEVH	CMGNA	YEVILKQ	CGVGSQNTL	NIVVFERPKD	DERIVCRWQQLACEGN	: 404
OsSDC3 :	SSNDITITMGSRNHGAPLILWYDILSRKHYG	NLCKEV	CLRNKNA	YALR	REMGSV	NALISTVVFERPKD	DEEVRRWQLACQSK	: 389
CL4912 :	ASRDATITMGSRNHGAPLILWYDILNRHGYRC	EQKEVQ	CLRNAHY	YLKDRL	REAGISAMINEL	SSTVVFERPKD	DEEVRRWQLACEGN	: 423

AtSDC1 :	IAHVVVMPSVTI	KLDI	FLKDI	VKH	LIWYEDGS-QP	PCLA	SEVE	TNNCIPCA	PK-----	: 482
OsSDC1 :	IAHVVVMPSVTI	DKLDI	FLN	TER	ATWYQDGSCQP	PCLA	KEV	BEN	CISIEKK-----	: 482
OsSDC2 :	IAHVVVMPSVTI	DKLDI	FLN	TER	ATWYQDGSCQP	PCLA	KEV	BEN	CISIEKK-----	: 467
OsSDC3 :	IAHVVVMPSVTI	DKLDI	FLN	TER	ATWYQDGSCQP	PCLA	KEV	BEN	CISIEKK-----	: 446
CL4912 :	MAHVIVMPNVTI	PKLDI	FLN	TER	ATWYQDGSCQP	PCLA	KEV	BEN	CISIEKK-----	: 478

Supplementary Figure S1. Multiple alignment of the protein sequence of pCsAlaDC with the characterized SDCs from other species. Identical amino acids are highlighted in black, and similar amino acids are shaded in gray. The conserved substrate binding site, pyridoxal 5'-phosphate binding pocket, and catalytic residue is marked with a, b and c, respectively. The UniProt knowledgebase accession number are as follows: AtSDC1(sp|Q9MA74); OsSDC1(sp|Q6ESZ9); OsSDC2(sp|Q8RV06); OsSDC3(sp|Q7X8D4). *Arabidopsis thaliana*, At; *Oryza sativa*, Os.



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