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Mutation in a homolog of yeast Vps53p accounts for the heat and osmotic hypersensitive phenotypes in *Arabidopsis hit1-1* mutant

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Unfortunately, Fig. 2 was published with errors. The correct figure is given here:

The online version of the original article can be found at <http://dx.doi.org/10.1007/s00425-005-0216-6>

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HIT1 (1) -----MNKSSALEYINQFPTEASLTG
Vps53p (1) -----MLEGTVDIPEDITNLLFSKESLNID
C. e. (1) -----MEEPITSEKLQDNVMEISDICTIEY--CKPMSLDAQINLEFPTEGSLTQID
D. m. (1) MSESAYAVEPEERVMANKHFHSEKVKQVIDKILKTDPPMDAPDENTDYNILFLFNEGSLAGID
H. s. (1) ---MMEEEELFVEEELAVQLQPEVQLATEQFPTSQDPLDRADENAEYINTLFFTEGSLANID

HIT1 (25) PLEKTKQGEIRKNDASILAVRQSSGTAKKEDLAATRAEELSHKIQIKSAEQSEAMVOE
Vps53p (29) ELISITRSYKKQLQEDILKEE---NELKHFHNSAEIEASRKIFQDFKTCQVVASIELTSEN
C. e. (53) SLLASVEGELGELDNEIAYVETNANVSEGEALKAQADAMIELEKISGISREHTKSSDEIVRE
D. m. (66) ETIQKQCELSLDNIRSVYRQGNQGGQGLALCEAGAVSSLSFHHIDVKTAEKTEEMVRE
H. s. (63) EYNNKRLKIRLRDLNIRTVYRQGNVGGQGRQALEAGAKLQQLFGKIKIKDKAEKSEQMIRE

HIT1 (90) ICRDKRLDFAKNNTITITLALHRTVMQSVVEQLQVMASTRQYKEAAQLEANNLQCHHEAY
Vps53p (90) ITEGSYLLDIAKSNLDFSLDFNKKITDSYIQCNELSGQSEKKVSPYKINGSLAENTISY
C. e. (118) ITRDKRLDFAKNLDASITTLHHEHITGVESLGAWDKRDYSSARQLPAILNVLLEADAY
D. m. (131) ITRDKRLDFAKNLDASITTLNHHMAGGVSESLKLEKRSYGEELNPLQATEVNGHQQE
H. s. (128) ITRDKRLDFAKRLITSTITLNNHHMAGGVSELEANTRRQYGEANLQGVNVLEHQQY

HIT1 (154) RDVPAITFEREKNNIKQLKSHVDSFSSLGCKEIEFTN---LILKLSCLVLDALFSPVRE
Vps53p (155) KSLDENYLLSSSRKGDITLSIKIQNINAFSGNITSHD-TALTMELREGACELDCDTSTRA
C. e. (182) KESIQANSGQDKIKASLTIQAKDLNAFGTQLSDR-----ITDMCRVAALGNVKE
D. m. (195) SLLIEPKNSQSNDKLVTLAQQTEDFEAFSKPISQNHRLGLNOLADCKVSVLDPKVKK
H. s. (192) MGLPQEQSERKAAQTELGQQLADFEAFPSQCKRQ---GGPSNVLRLCLVANILDPKIKQ

HIT1 (216) EYNNFCSRPISYEQIFEG-AELANKDKTHFVAVKRRIRTNELI---WKLSPASADPYKCL
Vps53p (219) QMDWCKDLFEMKEIFRVDDEASSENSEPHVFKILNPNFSK-EADYAKDEMIVRLTT
C. e. (239) NFVKWFIQQLSEXYTHADNEGAWDKDIPKWFYRKLTDFERAGLSNIPADHMGRLTS
D. m. (260) ELKKWFIAGQEEYTHFHNGAWDKDIPKWFYRKLTDFERAGLSNIPADHMGRLTS
H. s. (255) ELKKFIRQQLSEYLVFQNGQAWDKDIPKWFYRKLTDFERAGLSNIPADHMGRLTS

HIT1 (278) GCKCKRKKQESLVNMEK---PVVALLLAQSVTEFEKELKGGVPTKDIEDDIEEIGTW
Vps53p (283) TPIHITDKDLQTLAKREFKKNPSIDLEHTAQSTLDEPKYIDVRA-----
C. e. (304) EECTIDRDLIRMTIRKQ---LQWLLGLAQHFWPALLTKRQ---
D. m. (324) EECRDEKREGLAQIMARTNE---LDVHLLLFHKKQAQALSKRRTGVTLAGQPTDKAR---
H. s. (319) EECITRAELAKIMRTAKL---LVVLLLFHQRITNDEGLAKRSGCTLTDGTLKLESPPPS

HIT1 (341) EDNSQNIKIRKKYKFAASQETEENGFGQEKTKGNKLDVSGAGFNFRMGISSCEPHITPYIE
Vps53p (330) -----KKIK-----EPKISSCEPHITPYIE
C. e. (349) -----EKDGISFEKA-----IWSVDTTHDVTIN
D. m. (382) -----VLAEPITTDGAVG-----LTVFHDQIGGCRPHIDPYIR
H. s. (382) TNPFLEDEPTPEMEELATEKGDLDQPK-----KPKAPDNPHGILSKCEPHITPYIE

HIT1 (406) LEKNTLMDLEIVQESWD---VEDGSQNVLSSTQLSNIKKSARKNTSKN---QTL
Vps53p (351) HQNQMEKKFLMSBPRYP---SNEESLYLFSADLRRTVSVITQTLIEDNANDSL
C. e. (373) HQKTLNEFDTCARKSGEKEEPSRESSHAVPPISADPFLLLKVITESSKSSSEPD---ALL
D. m. (416) SIDNLSLMDKTVMSRE---PYKFAEAKTTVYSSDLFFYKCKHVQCQSNSE---QPM
H. s. (435) SQKNLGELIDRYVDFBAQGP-PKPNTDEGAVLSCADLEIYYKKCHVQCQSTG---EPN

HIT1 (462) FNLKVFQRYVAKAIFKFFKLP-----KGGTGIVVAATGMDG-----
Vps53p (410) TSLNFFSRMLQTSQKILLPLLLPDNIEVQKLEMAKYIVLINTADVCAT-----
C. e. (436) RDMIGVRYCGRGAFISCLVFLP---SLGSQSGAANFSLIRREIAYP-----
D. m. (473) YDLALVFKVREDAKWLKLESTPKLVPATISSSIGKSSLLTRDQNLSTAAGQVFNHFLKEGD
H. s. (495) IALTTFQKVMREDAKWLKLESTPKLVPATISSSIGKSSLLTRDQNLSTAAGQVFNHFLKEGD

HIT1 (500) QIVSEKERIKYICYIINAEYCHKTSGELEANSSEIDPHYADGVDSHVQDEFSANIKMIVTL
Vps53p (462) TIDQLEDKLEFSNGREKLANSTFKKNTYDOLLAKGTSFLNHWIPLDNFVREFINDNWSA
C. e. (483) -R-LTPDQGFVCCILATADCAETSIQLQELSQRPQ---VDISQETAFYSITNGSLQL
D. m. (538) TQRFARDLVIRICCLTTTEYCLETVQQLKLEKYSAYSKDMSHEKDVHRIISNCQLL
H. s. (541) VAKFLEELCLICNLSTAECYCLATQQLLEELKEKVDVSLERTNLGEMDTFSTVSSSQQLL

HIT1 (565) VLGLETKFDTEAVMIRVP-----WSTLESVGDQSGVNGNTVSGSLPVLGKILTP--
Vps53p (527) AIDYRSRYMVLKSLKLP-----ALTDASIKQQQIQPSTLAFILSQFNROVYKWNFDKVID
C. e. (541) VQDLESTCDANLQSLSKVCSIFVRIEKTWADVCGDESPFGSRAHQAQVFLTRDLSDRR
D. m. (603) VQDLEGCASLQMAKVQ-----WQHNVNGDQSAFSSICGNFQTVPTIRDTLSSR
H. s. (606) VQDLEAACDPALTAMKIQ-----WQNVHVGDSFYVTSILHKKQNVPTIRDTLSTR

HIT1 (618) VYFQFELDKLASSLGFHYANFRCKQLSETG-----EQQLLDTOQVKSILLETSLARQTS-
Vps53p (585) IITTFVYSNTIRLLQVPPPSLAGSKRKFTETRVVNIIEQLLDLELEIHFHTPESVNSDS
C. e. (606) KYFAELKILATLQHLAQHFGSLFRCHTISTHG-----EQQLLDTHLKLFLSSPDSSTINS
D. m. (658) KYFTFCHEFVAFIPKFINVLFRCKLTSDGNNVLGCEQLLDTHLKLALLELPSGSSVNR
H. s. (661) KYFTFCVCKFASIPKFINHLFCPKFSMVGAQVQVWT-----

HIT1 (676) -----TAASYSFVSREESRAELKVTLS--P-IDSVATYRALFP-EGTPMEFQRLKRGK
Vps53p (649) LRENTSYKRVKHADNNDQLKFKRLMAPDSADDYVYTSKLTNNPDSAVSFVLAIRGP
C. e. (665) K---PPTVYTSVNAALTKAEMTLKVACSETVDEYVQYIKLLP-ASDAAEKQVLEKCHK
D. m. (723) K---APTSTYTVVVKDMTRAEMLRKVMTPKAPPATITQVLKLLP-DITIAEKKILDKKVK
H. s. (700) -----

HIT1 (732) KALQSSLDQINKHGFPTQSSAAAMPQMPPTPPAPPLAITN--PATAAGFIANSEDLVLRKA
Vps53p (714) WDLAKKLLWSAYNLEDDTDEGSRPDSNRDLFIKWDKVLGQFENLARMQDPNWSKVFVRQJL
C. e. (725) KAFISANTNARLKIGSGSDPTQQ-----SNSLSIRIGGALPTVGSAS
D. m. (783) KVLQQLLDLKHITASAAVSGIIEPTTGEETQGAETVYVATSGTTDOAETSAPVTETTTATSS
H. s. (700) -----

HIT1 (795) LGRGAASTGFKKFIATTEAAKDRKDGLRLFNAS-----
Vps53p (779) KISPPVMKRIIVSTPQAAQKEEQKQKSLVKDFVSHSRFENRGT
C. e. (770) VSEFNAVVSMAADGSDQAVTSSLDKLRFLRVLRKQL-----
D. m. (848) PKRFIFPSVGSFTGSADKNADGSSQTGRRLRLVLLKKRFP-----
H. s. (700) -----

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Fig. 2 Amino acid sequence comparison of HIT1 protein with their putative orthologs in *C. cerevisiae* (Vps53p, accession number P47061), *C. elegans* (C.e., accession number CAA81595), *D. melanogaster* (D.m., accession number AAF51022) and *H. sapiens* (H.s., accession number AAS20944). Sequence alignment was performed with Vector NTI software (Invitrogen, Carlsbad, CA, USA). Amino acids which share identity (*black-shaded*) and similarity (*gray-shaded*) are indicated