

	1	47
AaCHS1	MSAIRHRPLATQ-----NESDDNFTDDESTPLTQDIYGGSQRTVQETKGWDV	
AgCHS1	MSAIRHRPLANGP-----NESDDNFSDDDESTPLTHDIYGGSQRTVQETKGWDV	
Dm_kkv	MSAMRHRPMAPPQGPGAGTAGEHVSDDDNNFTDDESSPLTHDIYGGSQRTIQETKGWDV	
	:*:*	:..*:*
	48	107
AaCHS1	FRDPPIKEDTGSMADQACLELTIKILKIFAYLLTFVIVLTGGVVAKGCVLFMSSQLKRDR	
AgCHS1	FRDPPIKEDTGSMADQACLDLTIKILKIFAYLITFVIVLLGGVVAKGCVLFMSSQLRRDR	
Dm_kkv	FRDPPIKIETGSTANQECELELTVKILKIFAYVITFIIIVLTGGVIAKGTMLFMTSQVRKDK	
	***** :*** *:* **:	
	108	167
AaCHS1	KITYCNRDLARDKQFVATLPEEERIAWMWALMIAFAVPEIGTFIRSTRICFFKSMKKPFK	
AgCHS1	KITYCNRDLARDKSFIVSLPEEERIAWMWALMIAFAVPEIGTFIRSTRICFFKSMKKPLK	
Dm_kkv	KMEYCNDLGRDKSFVVRLEPEERVAVIWIALLIAYALPEIGALIRSARICFFKTFKVPKT	
	*: ***:*.*	
	168	227
AaCHS1	SHFLLVFLMESFHTIGLVLLFFVVLPEVDSVKGAMLTNCLCVIPGLLGMFSRTNKEGKRA	
AgCHS1	SHFLLVFLMESFHTIGLVLLFFVVLPEVDSVKGAMLTNCLCVIPGMLGLFSRTNKEGKRA	
Dm_kkv	GHFLFVWLMESLSAVGMALLMFVVLQIDAIQGAMLTNCLCVVPGIFGLLSRTSKEGKRF	
	.***:*:*:*:*:*: :*.*.*.*.*.*	
	228	287
AaCHS1	VKSIVDLAAIAAQITGFVWPLLENRPVLWLI PVSALLTSCGWWENYVSPQSPFGFIRAM	
AgCHS1	VKSIVDLAAIAAQITGFIVWPLLENRPVLWLI PVSALLTSCGWWENYVSPQSPFSFVRSL	
Dm_kkv	VKVIIDLAAVAQVTGLVIWPLLENRRELWVIPVACVMISCGWWENYVSPQSPLGLVRAL	
	** *:***:*	
	288	347
AaCHS1	GRVKEDLKQTRYFTYMFLSLWKVMLFFCIVLVIMFFNGDEVANLFSLFGVGFPHKIVVE	
AgCHS1	GRVKEDLKQTRYFTYMFLSVWKILLFCFVSVILFVRGDEVANLFSLFGAGYGFPHKIVVE	
Dm_kkv	GRIKEEMKYTRYFCHIFLSIWKILLFFTVTLLIYWAQGEEPGNLFAMYGDAFGPHKIVY	
	::*:*:* *.*	
	348	407
AaCHS1	EVATAFSSALPDLVEASQAGDTVVIDASYNTVTVYVLI IQILGAYLCYVFGKFACKILIQG	
AgCHS1	EVALPFSSALPDLVEAAQAVDTIDIDAAYNTVTVYVLI IQILAAYLCYIFGKFACKILIQG	
Dm_kkv	ELPAGLGGVLPDTLESAN-IDTVDVDAAYNTVVYVLLLIQIFGAYLCYIFGKFACKILIQG	
	*:.. :...*** :*	
	408	467
AaCHS1	FSYAFPVNLTIPVAISLLIAACGIRNDDPCFFHGSIPDYLFFESPPVFRLSDFASRQMAW	
AgCHS1	FSYAFPVNLTVPVAISLLIAACGIRNDDPCFFHGSIPDYLFFESPPVFRLNDFASRQMAW	
Dm_kkv	FSYAFPVSLTVPLSVTFLIAACGIRIDDPFFHDTIPDYLFFTSNFRFNNFVTEQMAW	
	*****.*:*.*.*.*.*	
	468	527
AaCHS1	AWLLWLLSQTWITLHIWTPKCERLANTEKLFVTPMYNALLIDQSMALNRRRDDQADVKTE	
AgCHS1	AWLLWLLSQTWITLHIWTPKCERLANTEKLFVTPMYSALLIDQSMAMNRRRDDQADVKTE	
Dm_kkv	AWILWLLSQTWIALHIWTPKCERLATTEKLFVQPMYSSLLIDQSMALNRRRDDQADVKTE	
	::*:*:*:*:*:*:*:*:*:*.*	
	528	586
AaCHS1	DLAEIEKEKGDEYYETISVHTDGSALP-RPSVKSSDHITRIYACATLWHETKEEMIVFLK	
AgCHS1	DLAEIEKEKGDEYYETISVHTDGSALP-RPSVKSSDHITRIYACATLWHETKEEMMVFLK	
Dm_kkv	DLSEIEKEKGDEYYETISVHTDRSSAPNKPSIKSSDNITRIYSCATMWHETKDEMIEFLK	
	:.*:*:*:*:*:*:*:*	


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1183                                     1241
AaCHS1 -SVAEDSEEEDEQSDSETSTLQRNERDFLTNPYWIEDPDLKKGEVDFISSTEIQFWKDLI
AgCHS1 -SVAEDTEDDDEDEDSETSTLQORDERDFLTNPYWIEDPDLKKGEVDFISSTEIQFWKDLI
Dm_kkv TSVAEKSGDESDESDDTSAEPKQERDFLTNPYWIEDPDVRKGEVDFLSSTEIQFWKDLI
      ****.: :.:.:.*:.*: :.:*****:*****:*****
1242                                     1302
AaCHS1 DQYLYPIDQNKEEQARIAHDLKELRDSSVFGFIMINALFVLIVFLLQLNKDNIHVKWPLG
AgCHS1 DKYLYPIDQNKEEQARIAVDLKELRNKSVFAFFMFNALFVLIVFLLQLNKDKLHIIWPLG
Dm_kkv DQYLYPIDNDPVEQARIAKDLKELRDSSVFAFFMINALFVLIVFLLQLNKDNIHVKWPFQ
      *:*****.: ***** *****:.*.*:.*:*****:*****:.*:.*
1303                                     1362
AaCHS1 VKTNITYDEATQEVHISKEYLQLEPIGLVFVFFFALILIIQFTAMLFHRFGTLSHILAST
AgCHS1 VKTNITYDEVTAEVHISKEYLQLEPIGLVFVFFFALILIIQFVAMMFHRFGTLSHILAST
Dm_kkv VRTNITYDESTQEVHISKEYLQLEPIGLVFVFFFALILIIQFTAMLFHRFGTISHILAST
      *:***** * **********.*****:*****:*****
1363                                     1422
AaCHS1 ELNWGCNKKPEELSQDALIDKHAVEIVKNLQRLQIGDGDYDNDSGSGPDRIARRRTIQNL
AgCHS1 ELNWACNKKPEELSQDALIDKHAVEIVKNLQRLQIGDGDYDNDSGSGPDRIARRRTIQNL
Dm_kkv ELNF-CKKSEDLTQDQLIDKHAVEIVKNLQRLQIGDGDYDNDSGSGPDRIARRKTIQNL
      ***: *:*.*:.*:.* **********:*****
1423                                     1481
AaCHS1 EKARQPRRQIGTLDVAFKKRFLKLTAD-ENNAGTPILTRRMTMRRETIRALEVRKNSVMA
AgCHS1 EKARQPRRQIGTLDVAFKKRFLKLTAD-ENNTATPILTRRMTMRRETIRALEVRKNSVMA
Dm_kkv EKARQPRRQIGTLDVAFKKRFLKLTADAENNPATPILTRRLTMRAETIRALEVRKNSVMA
      ********** *.*.*****:*** **********
1482                                     1538
AaCHS1 ERRKSQMOTLGANNEYGIT-GVNNTNNNAPQ--RPLRTSNAGVSVKIDIFNVNGGPGGDIY
AgCHS1 ERRKSQMOTLGANNEYGIT-GVPNGNNAPP--RPTRTSNAGVSVKIDIFNVNGGPGGEIY
Dm_kkv ERRKSAMOTLGAKNEYGITGAPINNGALPNQRSGRVSNAGISIKDVFNVNGGGAEQIY
      *****:***** *. **.* *.*.*****:.*:***** .:.*
1539                                     1576
AaCHS1 GVTG--QVNQAYEPVIEDD-DRNSLRLQPRN-----QVTWSNS-NGRL-----
AgCHS1 GVTG--QVNQAYEPVIEDD-DRNSLRLQPRN-----QVTWGNNGNARL-----
Dm_kkv GSNGGGTINQGYEHVIDEDGDGNSLRLTTRNPHPHPHQVSWGQNTNGGGGNGTGRL
      * .* :*.** *:.* * ***** .* **:*.*. *

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Additional Figure 2: Alignment of predicted protein sequences of Dipteran CHS1 sequence. Alignment of predicted Chitin Synthase 1 (CHS-A) amino acid sequence of *Ae. aegypti* (AaCHS1), *An. gambiae* (AgCHS1) and *D. melanogaster kkv* using ClustalW software. ▼ indicates the position of the first intron (28,587 bp) in the *AaCHS1* coding sequence. The region highlighted in gray corresponds to AaCHS1 exon 6a (see Fig. 5). Symbols below the aligned amino acid sequences indicate identical (*), highly conserved (:), and conserved (.) residues.