

	1	20	40	60	80	100
heurippa-1	AQSCIKELQSCMDERQATEADTMKELVEETKAITRDYVEIQIKILRDEMEQMEEYESRLNKTVSASNGETPLKNMQLIKQLMTENAILEKYTAEKLARARA					
heurippa-2	AQSCIKELQSCMDERQATEADTMELVEETKAITRDYVEIQIKILRDEMEQMEEYESRLNKTVSASNGETPLKNMQLIKQLMTENAILEKYTAEKLARARA					
melpomene-1	AQSCIKELQSCMDERQATEADTMKELVEETKAITRDYVEIQIKILRDEMEQMEEYESRLNKTVSASNGETPLKNMQLIKQLMTENAILEKYTAEKLARARA					
melpomene-2	AQSCIKELQSCMDERQATEADTMKELVEETKAITRDYVEIQIKILRDEMEQMEEYESRLNKTVSASNGETPLKNMQLIKQLMTENAILEKYTAEKLARARA					
cydno-1	AQSCIKELQSCMDERQATEADTMKELVEETKAITRDYVEIQIKILRDEMEQMEEYESRLNKTVSASNGETPLKNMQLIKQLMTENAILEKYTAEKLARARA					
cydno-2	AQSCIKELQSCMDERQATEADTMKELVEETKAITRDYVEIQIKILRDEMEQMEEYESRLNKTVSASNGETPLKNMQLIKQLMTENAILEKYTAEKLARARA					
		120	140	160	180	200
heurippa-1	EGEVQHLRACIDERDEKTDDEDIPMKEDLVLDLCESESDDDDDSCNESLEPIPKREDMNRSGMIHQSAIIDENSFSSDHSNLSVLNKTYGTLKDENINNSNGND					
heurippa-2	EGEVQHLRACIDERDEKTDDEDIPMKEDLVLDLCESESDDDDDSCNESLEPIPKREDMNRSGMIHQSAIIDENSFSSDHSNLSVLNKTYGTLKDENINNSNGND					
melpomene-1	EGEVQHLRACIDERDEKTDDEDIPMKEDLVLDLCESESDDDDDSCNESLEPIPKREDMNRSGMIHQSAIIDENSFSSDHSNLSVLNKTYGTLKDENINNSNGND					
melpomene-2	EGEVQHLRACIDERDEKTDDEDIPMKEDLVLDLCESESDDDDDSCNESLEPIPKREDMNRSGMIHQSAIIDENSFSSDHSNLSVLNKTYGTLKDENINNSNGND					
cydno-1	EGEVQHLRACIDERDEKTDDEDIPMKEDLVLDLCESESDDDDDSCNESLEPIPKREDMNRSGMIHQSAIIDENSFSSDHSNLSVLNKTYGTLKDENINNSNGND					
cydno-2	EGEVQHLRACIDERDEKTDDEDIPMKEDLVLDLCESESDDDDDSCNESLEPIPKREDMNRSGMIHQSAIIDENSFSSDHSNLSVLNKTYGTLKDENINNSNGND					
		220	240	260	280	300
heurippa-1	CTLETNDNVVAGEVVTTELNIDVHNNIEFKNHIKLSRETCLVENNDSFVNDKKEKVLVSTLSRASNEDIVVDIDDKTKTNKNRNSFKDSSLETVDNNKPNTFV					
heurippa-2	CTLETNDNVVAGEVVTTELNIDVHNNIEFKNHIKLSRETCLVENNDSFVNDKKEKVLVSTLSRASNEDIVVDIDDKTKTNKNRNSFKDSSLETVDNNKPNTFV					
melpomene-1	CTLETNDNVVAGEVVTTELNIDVHNNIEFKNHIKLSRETCLVENNDSFVNDKKEKVLVSTLSRASNEDIVVDIDDKTKTNKNRNSFKDSSLETVDNNKPNTFV					
melpomene-2	CTLETNDNVVAGEVVTTELNIDVHNNIEFKNHIKLSRETCLVENNDSFVNDKKEKVLVSTLSRASNEDIVVDIDDKTKTNKNRNSFKDSSLETVDNNKPNTFV					
cydno-1	CTLETNDNVVAGEVVTTELNIDVHNNIEFKNHIKLSRETCLVENNDSFVNDKKEKVLVSTLSRASNEDIVVDIDDKTKTNKNRNSFKDSSLETVDNNKPNTFV					
cydno-2	CTLETNDNVVAGEVVTTELNIDVHNNIEFKNHIKLSRETCLVENNDSFVNDKKEKVLVSTLSRASNEDIVVDIDDKTKTNKNRNSFKDSSLETVDNNKPNTFV					
		320	340	360	380	400
heurippa-1	NNIINSIKESNLSIQSNNSLASFEKLEEATKIDTGTNSNVTSSFNIKILKEKRNFFNYDDVLKSLEKPATVVVKSDDKKIYFDNSNNNDTSNNNDNEKIKIDDDY					
heurippa-2	NNIINSIKESNLSIQSNNSLASFEKLEEATKIDTGTNSNVTSSFNIKILKEKRNFFNYDDVLKSLEKPATVVVKSDDKKIYFDNSNNNDTSNNNDNEKIKIDDDY					
melpomene-1	NNIINSIKESNLSIQSNNSLASFEKLEEATKIDTGTNSNVTSSFNIKILKEKRNFFNYDDVLKSLEKPATVVVKSDDKKIYFDNSNNNDTSNNNDNEKIKIDDDY					
melpomene-2	NNIINSIKESNLSIQSNNSLASFEKLEEATKIDTGTNSNVTSSFNIKILKEKRNFFNYDDVLKSLEKPATVVVKSDDKKIYFDNSNNNDTSNNNDNEKIKIDDDY					
cydno-1	NNIINSIKESNLSIQSNNSLASFEKLEEATKIDTGTNSNVTSSFNIKILKEKRNFFNYDDVLKSLEKPATVVVKSDDKKIYFDNSNNNDTSNNNDNEKIKIDDDY					
cydno-2	NNIINSIKESNLSIQSNNSLASFEKLEEATKIDTGTNSNVTSSFNIKILKEKRNFFNYDDVLKSLEKPATVVVKSDDKKIYFDNSNNNDTSNNNDNEKIKIDDDY					
		420	440	460	480	500
heurippa-1	RSPSIKEDVTNDYEPSMIKKLLGQSITNQNDNLNALQKIRTCDDKKNDSIDLFEALDSPQACNKNKVNDIENIRKSVQNVAIQEDAIVCGNIEHNQEIVS					
heurippa-2	RSPSIKEDVTNDYEPSMIKKLLGQSITNQNDNLNALQKIRTCDDKKNDSIDLFEALDSPQACNKNKVNDIENIRKSVQNVAIQEDAIVCGNIEHNQEIVS					
melpomene-1	RSPSIKEDVTNDYEPSMIKKLLGQSITNQNDNLNALQKIRTCDDKKNDSIDLFEALDSPQACNKNKVNDIENIRKSVQNVAIQEDAIVCGNIEHNQEIVS					
melpomene-2	RSPSIKEDVTNDYEPSMIKKLLGQSITNQNDNLNALQKIRTCDDKKNDSIDLFEALDSPQACNKNKVNDIENIRKSVQNVAIQEDAIVCGNIEHNQEIVS					
cydno-1	RSPSIKEDVTNDYEPSMIKKLLGQSITNQNDNLNALQKIRTCDDKKNDSIDLFEALDSPQACNKNKVNDIENIRKSVQNVAIQEDAIVCGNIEHNQEIVS					
cydno-2	RSPSIKEDVTNDYEPSMIKKLLGQSITNQNDNLNALQKIRTCDDKKNDSIDLFEALDSPQACNKNKVNDIENIRKSVQNVAIQEDAIVCGNIEHNQEIVS					

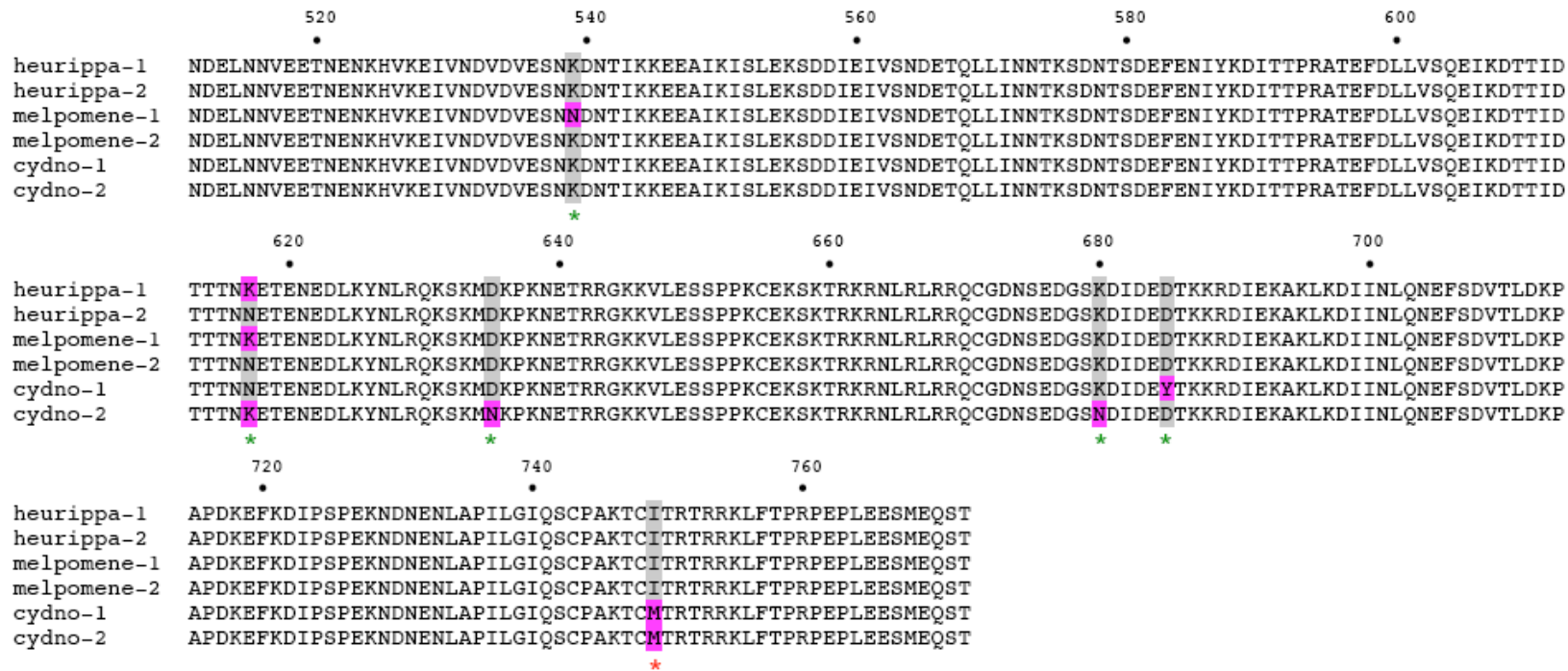


Figure S2. Protein sequence alignment of 3' kinesin. The *kinesin* protein product from exon 9 to exon 14 is shown. Two representative sequences per species are shown. Residues with amino acid changes are highlighted. Polymorphic residues are indicated by a green asterisk (*), those residues where *H. heurippa* is different from *H. c. cordula* and *H. m. melpomene* are indicated by a blue asterisk (*) and the red asterisk (*) indicates one residue where *H. c. cordula* is different from *H. heurippa* and *H. m. melpomene*. We observed five amino acid differences between *H. melpomene* vs. *H. heurippa*. This might reflect adaptive change subsequent to formation of *H. heurippa*, although there was no significant evidence for selection on the locus. Perhaps more likely however, these changes may represent fixation of nearly-neutral variation due to a population bottleneck during the origin of *H. heurippa*. Only one amino acid difference was found between *H. melpomene* and *H. cydno* in a residue also relating *H. melpomene* with *H. heurippa*. Although this amino acid replacement might be responsible for a structural protein change causing the red band, several intronic sites show a similar pattern and may have regulatory functions.