

Nc	-MDTQPTSHSLFEVYLRRLRPANTVST-SGDRFLDVDVP-----EPSESAPKHITLN	49
Mo	METPSATKDNLFKVFLRLRPPPAGVA-PSEFLTVEPQS-----SDSTSSTPTHVTLT	52
An	--MASNSPSSLFQVYLRRLRPPISQDDQPERCLTVEKSNTSHSNNDVSSSVSVPTHITLQ	58
Sp	-----MIQIFLRVKK--AQPSSDAS-----NKGFLTVLNDYEILLE	35
Yl	-----MSLPVYLRRLRKDDEQPSSRPS-----SATDKPYLEIASDDPSTIITN	42
	: : * * * : : . : :	
Nc	PPAD-----RRRAIEKFAFTQVFEEDATQLDVFHCTGVAGLVEGLVAPY-GDGTDALL	101
Mo	PPSN-----ARKHATEKYCFTQVLEEDASQLDVFQGTGVIPLIEGVLGPNNGDGTDALL	106
An	PPSD-----ARKRGVERFGFTQVFEDEWASQLNVFEDTGLQSLIRGVLE----QRDGLV	108
Sp	SPEDSHAYRVSKSKTLEKASFTKVFPPSCTQLDVFSTI-CAPLIADSLVN----MNDTLL	90
Yl	PPEK-----SRTRTKEKFASFSEVFDG-STQEVEVYKKV-MLPMVKNVVTG----SGDGLL	90
	* . : : * : * * * : . * * : : : * * :	
Nc	ATLGVTGSGKTHTMLGTR--SQRGLTQMSLDLIYRSLGHRVLDPST--YPNLEQSIASASD	157
Mo	ATLGVTGAGKTHTLGSK--TQRGMTQLSLEVLFRSIGQNIASPGA--YPPLETSVAAYD	162
An	ATLGVTGSGKSHTILGSK--TQRGITQMSLDVIFKSLASTIKPPDNSIPPYLLASVSASD	166
Sp	FTLGVSAGKTYTLFGPS--DRPGVAFLALDALFYAIKGREASPQTV---FLRS----Q	141
Yl	FAMGTTGSGKTHTLGNPRLGRPGMVHYALKSVFDAIGDRLCLFDEAE---AVAESAGP	147
	: * . : * * * * : * : . * . : : : .	
Nc	PSEANILPATAYLESVYSTDPTISFLRSGNGRSTPLQNESS-----TPR--	202
Mo	ASEATILSASAFLESVFADPHGPSRS---NSRAPTPMIGESAAPP-----LTPRRL	210
An	ASESQMFTAQTFLEAVYGESD-----RGRNSRAQTPMSNTRAHTPMADPMPALIFPRRHA	221
Sp	LEKCKIVEASKFLRGEA-----PLD-----IKVP-NT	167
Yl	NRESHVLEAIPFIDNGILTQS-----QHQLN-----QFIENAVVAE-NA	185
	: . : . * : : :	
Nc	RFRPSALPQNPDISHLTIPFDASAEYAIVISMYEVYNDRIFDLLSSPVKSA-----	253
Mo	LNRPSSYPTIPDVGAI SVPCDPSAEYAVLVSMYEVYNNAIHDLLTPPIRSA-----	261
An	PIRTSTLPRSPDVGHLTLELNPHSEYIVLVSMYEVYNDRIFDLLSPAIVPGQGSAMSRQG	281
Sp	EYYAS-----HFPKIEEKNYQYAIYLSFAEIYNDRIFDLLEKASFFGHRH-----	212
Yl	DLYSS-----VGQRSSHGVYISMVEIYNDRVFDLLDKRRPVV-----	222
	* . : : * * : * * * : . * * *	
Nc	-ATKEYRRRPLLFKPTELSPDRKVVAGLRKVVCGSLDQALMVLEAGLQERRVAGTESNTQ	312
Mo	-ATKEYRRRALLFKATELSPDRKVVAGLKKILCTNLQQALMVLEAGLQERSVAGTNSNRT	320
An	TSSQKDRRKPLYFKSTEGSPDRKVVAGLRKIACSTYEEALAVLEIGLTERKVTGTGANSV	341
Sp	-----ALSLK-KSSTSDKKSIAGIQKVFVSNTTEAYKLIQKVLQLRKSTSTKSNSV	262
Yl	-----V-KCDTKGKFGIPSQTKLFCATIQEAFQVLEQAHALRSTHSTESNSV	268
	. : . : . * : . * : : * . * * :	
Nc	SSRSHGFFVVEVKKRFSLGGQHTGWYGGAGWTGNSLTIVDLA-GSERARDAKTGVQTLAE	371
Mo	SSRSHGFFCVEVKKRRKS--RRQGHSTEAPWAGSTFTIVDLA-GSERAREAKTTGVTLAE	377
An	SSRSHGFFCLEVKRRMRN-----KRTGEETWIGNTLTIADLAAGSERARTAKTAGSTLVE	396
Sp	SSRSHLIMSIELFKVCTK-----SNKFESCQIDLVDLA-GSERTRSAETSGLLLRE	312
Yl	SSRSHALFTVTVKRLG-----RTMLTTSLTIGDLA-GSERNKSTRAEGERLSE	315
	***** : : : : : : : * * * * * : : . : * * *	

Nc	AGKINESLMYLGQCLQM QVAGGK -EKNLGLIRRCKLTEL LFTNSFPTGNN ---QQQHRN	427
Mo	AGKINESLMYFGQCLQLQATAGNSAKPTNLSFRHCKLTEL ILFSNNFASNGFSKSYSARRA	437
An	AGKINESLMYLGQCLQM QSGIQDGNKTAMV PYRQCKLTEL LFSNSF PSHQT---SSMHRN	453
Sp	GASINRSL LLTLGQCLEALRRKHE -GKQHIIPFRQSKLTEL LFSHSGHLSGLA -----	362
Yl	ACSINQSLMMLGQCLQRQ REVKG -YK DRSILRSSKLAQ LLLPVAF-SRDA-----	364
	. . ** . ** : : ***** : * * . ** : : * : :	
Nc	PQKGIMIVTADPHGDFNATSQILRYSALAKEVTVPRQPPSFP-----	469
Mo	PQKGV LIVNADPHGEFSSTS QILRYSALACEVMAPRIPSITQ TILAAA AKTIHPNNHREA	497
An	PQKAIMIVTADPLGDYNATSQILRYSALAREVTVPRATSAESILSSTL-----	501
Sp	--GINMLVNIDPFGSFDENAQVMRYSANAREILPPPLNENS-----	401
Yl	--MTALLITANQNADFSSTIQIMRYSALARDTIKPPVTPAYLK-----	405
	: : : . : * : : * * * : * :	
Nc	-----PPNSFS---NSLPPIG----SPN-----HQYLS	490
Mo	NNTMLLSSSPISSSPAVHHRPFFPPGSVAGSSNSV PQYN --DNSPNIQRTFSPASNSSSD	555
An	-----GSRKGGG-----RH-----TPQLD	516
Sp	-----GSQSPSHSL LQKSKNTSS -----TKA	422
Yl	-----RAGSGPSTPAQRAVSNSIS-S-----TGS	429
Nc	FQQTLESAALEISRLQEDLTYLRHALDSERSLR--EQAEAHLLSMEDKMVELEQAIREDC	548
Mo	DRATMEAAALEIARLSEELEYMRQSCETERARR--VEAEDQLLSVEDRLIDLEQEIREDC	613
An	LAEDLEKALAEIERLTAENERLSLRLTEEEVLR--AETETALIVSEERCLLIEQEVREEC	574
Sp	LTSHLEQL-----QQENQQLR-----MLLADADSEMMNLEYEIRQQM	459
Yl	TMSHMSSASH-----TSHDDTKDNLIRTI AALQEQLYQAQQ REDALEIQIREEV	478
	: . : . * * : . . : * : * :	
Nc	AEEFEKRLELEVNRWKTIVDGEREREGEEFWRGKGVFERMVEADGDVDMMDVDSPKKPE	608
Mo	AAEFEQRLAVELARWKASMELEKERGEEHWDRKIEVYERAANVQVLATDG-DENDGDN--	670
An	WAEMDERMEQERKRWQA AWEQTGHND DHIDKKIELLSQRFQIHEDPQP-----	623
Sp	TREMEERVSEVERTFLTKLLEESAQ IEYTDQKLEKMG GWMMK LQDENSE KTETIA----	515
Yl	NQEMETHMEQMRQWYLDQ LQATDAAQNFTDKKISILGRRV NSDN-----	523
	* : : : : : * * :	
Nc	NTRLVETRTAEGQEARRQLEILADENERLQRENESLKQALAACIDPAKSTSKNKSPSRRS	668
Mo	-----KENVLIENLEEENTRLRREVQVLKRELLG-----RSPTKRK	706
An	-----SSDERVQELEFENDRLRSKITALERELN-CRSPSKKSSSKNA-----	664
Sp	-----QLEQIIIEELHEELRSLEEE-----SIKESATQQNENQHKRSSRK	555
Yl	-----VSDELVKLRKE-----NQLL---KQ	540
	: * * . :	
Nc	PSRSRRKKAQLNYAE---DDDGFFQELKRDQGD MAMDGF GEGNGVG---GSHGTGSPTK	721
Mo	PLAERDDLATEDMAAPHQTGDSLHS---KMEQLRVSEVGRASSTSNSSRATVQSTAGGS	762
An	ALETSRNA---NILG---RESDIEVALRKMDQLKLADS-----MF-----KSPAVNTP	706
Sp	LLYE---DKQAIQEAHT-INTKRKLW-PQSTLIQAPNSDDE-----ENVPSPSP	599
Yl	RLNV---DKENVEIAHG-PDSFRS-----D-----	561
	: .	

Nc	KKRIRRLGAKKWQGLDDDPF-----	743
Mo	PRKVRKLVAKRWDLAANDDGF-----	784
An	GKKQRKMATRKWDLAPEDDL-----	726
Sp	KKK--VVSPIKPLSPSRPPLTSLYSGTTDIDINEL	633
Yl	-----	561

Figure S2. Alignment of selected *kin-9* homologues from species in the phylum Ascomycota. The amino acid sequences of the *Neurospora crassa* (Nc, subphylum Pezizomycotina, class Sordariomycetes) *kin-9* kinesin-like protein (NCU05180) splice variant 1, *Magnaporthe oryzae* (Mo, subphylum Pezizomycotina, class Sordariomycetes) MGG_05060 kinesin family protein, *Aspergillus nidulans* (An, subphylum Pezizomycotina, class Eurotiomycetes) AN3124 kinesin family protein, *Schizosaccharomyces pombe* (Sp, subphylum Schizosaccharomycetina, class Schizosaccharomycetes) SPBC15D4.01c, and *Yarrowia lipolytica* (Yl, subphylum Saccharomycetina, class Saccharomycetes) YALIOE10879p proteins were aligned. The closest homologue to the *N. crassa kin-9* in the other organisms was selected for the comparison. The position of the myosin/kinesin motor domain is shown by yellow highlighting. The location of the D to N change present in the four high-expressing *aod-1 N. crassa* strains is highlighted in green at residue 740. The D residue highlighted in green is not conserved in the *S. pombe* or *Y. lipolytica* proteins. “*” indicates positions that have a fully conserved residue; “:” indicates conservation between residues of strongly similar properties - scoring > 0.5 in the Gonnet PAM 250 matrix. “.” indicates conservation between residues of weakly similar properties scoring ≤ 0.5 in the Gonnet PAM 250 matrix. Alignment was done using clustal omega (Goujon et al. 2010; Sievers et al. 2011; McWilliam et al. 2013). Identification of protein domains was achieved using the Inter-Pro protein sequence analysis and classification software at the European Bioinformatics Institute (GB) (<https://www.ebi.ac.uk/interpro/>).

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