Supporting information

The p25 subunit of the dynactin complex plays a dual role in cargo binding and dynactin regulation

Rongde Qiu, Jun Zhang and Xin Xiang*

Department of Biochemistry and Molecular Biology, the Uniformed Services University of the Health Sciences- F. Edward Hébert School of Medicine, Bethesda, Maryland 20814, USA.

*Corresponding author:

Xin Xiang (Ph. D.) Department of Biochemistry and Molecular Biology Uniformed Services University of the Health Sciences 4301 Jones Bridge Road Bethesda, Maryland 20814 Tel: (301) 295-0000 Fax: (301) 295-3512 Email: <u>xin.xiang@usuhs.edu</u>

This supporting information file contains 4 Supplemental figures.

Figure S1. Sequence alignment of p27 proteins. The first four amino acids of all the betastrands are highlighted with gray color. Residues in the hydrophobic ridge pointing to the surface of L β H are boxed with red color (1). Note that the hydrophobic residue Isoleucine (I) at position 6 (boxed with blue color) in human or mouse p27 is replaced by Lysine (K) in *A. nidulans* p27 (1). The alignment was done using CLUSTALW. Residues that are identical (*), strongly similar (:) or weakly similar (.) are indicated below the sequences.

	1	
A.nidulans	MDIKPPLSSYSSSQHLRPPPHHRPSASPASAQTQAQSAGAPRIPAKTTADPSAVIAEQTY	60
Human	MAEKTQKSVKIAPGA <mark>vv</mark> CVESE	22
Mouse	MAEKTQKSVKIAPGA <mark>v</mark> vCvese	22
	* : *.**:. ::	
	<u>2</u> <u>3</u>	
7	FOODVOTCTORONUTUDDUDTON MEGDIDIONOCOTOCEVOUTOPUDDANDADADADCECCOCO	120
A. III GUIAIIS		120
Mouse	TRGDVTIGFRIVINFRARITAEAGFIVIGEGNDIEEQADIINAIFDNIIFDIEDF	77
nouse	• * • • * * * * * * * * * * * * * * * *	
	4 5 6	
	ž ž ž	
A.nidulans	GSGEEKSIVISNNV <mark>I</mark> IGLQAVVHPGARVHSFA <mark>V</mark> VDNQAVIGRGVDVGGHAKVCARCEIFQ	180
Human	EPKPMIIGTNNVFEVGCYSQA-MKMGDNNVIESKAYVGRNVILTSGCIIGACCNLNT	133
Mouse	EPKPMIIGTNNVFEVGCHSQA-MKMGDNNVIESKAYVGRNVILTSGCIIGACCSLNT	133
	* *.::** :: : . :. :: . *::.:* :**.* : : * *.:	
	7	
A.nidulans	GARVKEWSVVWGGGKGTGLKTRMKAOKKVVSPFAMGEKGFEGVLEGKAIEDARLVAVKRE	240
Human	FEVIPENTVIYGADCLRRVQTERPQPQTLQLDFLMKILPNYHHLKKT	180
Mouse	FEAIPENTVIYGADCLRRVQTERPQPQTLQLDFLMKILPNYHHLKKT	180
	: * :*::* ::*. :.: * * :* . :*:	
A.nidulans	RDALSRLIVGKKRG 254	
Human	MKGSSTPVKN 190	
Mouse	MKGSSTPVKN 190	
	* :.	

Figure S2. PCR verification of site-specific integration of the Δ p27 construct into the p27 locus in *A. nidulans* genome. (A) A diagram showing the Δ p27 linear construct with the *AfpyrG* (*pyrG* from *A. fumigatus*) marker flanked by the 5' and 3' flanking sequences of the p27 gene. Homologous recombination events occurred between this construct and the wild-type genome (wild type) are indicated by crosses. The resulting Δ p27 locus is shown at the bottom. The positions of the primers, 27N3 and 27C, used for PCR analyses are indicated by arrows, and the sizes of the predicted PCR products are indicated. (B) A DNA gel image showing the PCR products amplified with the same pair of primers 27N3 and 27C. The wild type product is missing in the Δ p27 mutant, and instead, a larger-sized product appears as predicted. Sequencing analysis of the product from the Δ p27 mutant further confirms that the gene encoding p27 is indeed deleted and replaced with the selective marker *AfpyrG*.



Figure S3. PCR verification of site-specific integration of the p25^{Δ L1}-GFP construct into the p25 locus in *A. nidulans* genome. (A) A diagram showing three different p25 alleles in the p25 locus: wild type, p25-GFP and p25^{Δ L1}-GFP. The positions of the primers, Q1 and GFP-5R, used for PCR analyses are indicated by arrows, and the sizes of the predicted PCR products are indicated. Note that sequence of the primer GFP-5R is not present in wild-type genome. (B) A DNA gel image showing the expected PCR products amplified with the same pair of primers, Q1 and GFP-5R. Names of the samples are indicated on the right. The p25-GFP allele has been published previously (2). Sequencing analysis of the product from the p25^{Δ L1}-GFP mutant further confirms that the p25^{Δ L1}-GFP mutant allele has indeed replaced the wild-type allele in the p25 locus.



Figure S4. Microtubule (MT) organization and dynactin localization in wild type and the $\Delta p25$ mutant. (A) MTs labeled by CFP-TubA in wild type and the $\Delta p25$ mutant. The images indicate that the MT organization is normal in the $\Delta p25$ mutant. (B) Localization of dynactin labeled by p150-GFP in wild type and the $\Delta p25$ mutant. MT is pseudo-colored red and dynactin is green in merged images. Yellow arrows indicate positions of hyphal tips. Bar, 5 μ m.



References

- 1. Yeh, T. Y., Kowalska, A. K., Scipioni, B. R., Cheong, F. K., Zheng, M., Derewenda, U., Derewenda, Z. S., and Schroer, T. A. (2013) Dynactin helps target Polo-like kinase 1 to kinetochores via its left-handed beta-helical p27 subunit. *The EMBO journal* **32**, 1023-1035
- 2. Zhang, J., Yao, X., Fischer, L., Abenza, J. F., Penalva, M. A., and Xiang, X. (2011) The p25 subunit of the dynactin complex is required for dynein-early endosome interaction. *The Journal of cell biology* **193**, 1245-1255