

Supporting material

Supplementary figure legends

Supplementary Figure 1. Functional complementation of Pcp1 by the human mitochondrial rhomboid protease PARL. Wild type (WT) or *Δpcp1* (Δ) spores expressing either the human (*PARL*) or the yeast (*PCP1*) mitochondrial rhomboid protease were used. Growth of indicated strains was tested by drop dilutions on rich media containing indicated carbon sources.

Supporting tables

Supplementary Table 1. Plasmids used in this study.

Name	Description	Vector	Reference
pYES2-OPA1 (URA3)	OPA1 cDNA expression constructs for splice variants 4, 7 or 8	pYES2 (Invitrogen)	this study
pYES2-OPA1 (<i>ura3::TRP1</i>)	OPA1 cDNA expression constructs for splice variants 4, 7 or 8	pYES2 (Invitrogen)	this study
pCAG-OPA1-SP7-IRES-mDsRed	OPA1 splice variant 7 cDNA for overexpression in mammalian cells	pCAG-IRES	this study
pES425-PARL	PARL cDNA expression construct	pES425#1 (Doron Rapaport)	this study
pYES2-Pcp1	Pcp1 expression construct	pYES2 (Invitrogen)	this study
pVT100U-mtGFP	Fluorescence microscopy	pVT100U	(Westermann and Neupert, 2000)
pRS314 ^{ADH1} -Yta10 (1-61)-hAFG3L2 (36-798)-Myc	expression construct for human AFG3L2	pRS314 (Sikorski and Hieter, 1989)	this study
Yeplac111 ^{ADH1} -Yta10 (1-63)-hparaplegin (59-795)-HA,	expression construct for human paraplegin	Yeplac111 (Gietz and Sugino, 1988)	(Atorino <i>et al.</i> , 2003)
Yeplac112 ^{ADH1} -Yta10 (1-61)-hAFG3L2 (36-798)-Myc	expression construct for human AFG3L2	Yeplac112 (Gietz and Sugino, 1988)	(Koppen <i>et al.</i> , 2007)
Yeplac112 ^{ADH1} -Yta10 (1-61)-hAFG3L2 ^{E575Q} (36-798)-Myc	expression construct for proteolytically inactive hAFG3L2	Yeplac112 (Gietz and Sugino, 1988)	(Koppen <i>et al.</i> , 2007)
Yeplac181 ^{YTA10} -Yta10 (1-61)-paraplegin (44-781)	expression construct for murine paraplegin	Yeplac181 (Gietz and Sugino, 1988)	(Nolden <i>et al.</i> , 2005)
Yeplac181 ^{YTA10} -Yta10 (1-61)-paraplegin ^{E575Q} (44-781)	expression construct for proteolytically inactive paraplegin	Yeplac181 (Gietz and Sugino, 1988)	(Koppen <i>et al.</i> , 2007)
Yeplac195 ^{YTA10} -Yta10 (1-61)-Afg3l1 (25-789)-Myc	expression construct for murine Afg3l1	Yeplac195(Gietz and Sugino, 1988)	(Koppen <i>et al.</i> , 2007)
Yeplac195 ^{YTA10} -Yta10 (1-61)-Afg3l1 ^{E567Q} (25-789)-Myc	expression construct for proteolytically inactive Afg3l1	Yeplac195 (Gietz and Sugino, 1988)	(Koppen <i>et al.</i> , 2007)
Yeplac112 ^{YTA10} -Yta10 (1-61)-Afg3l2 (36-802)-HA	expression construct for murine Afg3l2	Yeplac112 (Gietz and Sugino, 1988)	(Nolden <i>et al.</i> , 2005)
Yeplac112 ^{YTA10} -Yta10 (1-61)-Afg3l2 ^{E574Q} (36-802)-HA	expression construct for proteolytically inactive Afg3l2	Yeplac112(Gietz and Sugino, 1988)	(Koppen <i>et al.</i> , 2007)

Supplementary Table 2. Strains. The following strains were transformed with plasmids encoding OPA1 splice variants as indicated in the text and figures.

Description	Name	Background	Plasmids	Reference
WT		W303α W303a		(Rothstein and Sherman, 1980)
<i>PCP1/Apcp1</i>		BY4743		Euroscarf acc. No. Y24731
<i>Apcp1 + PCP1</i>	jw1-4c	spore of <i>PCP1/Apcp1</i>	pYES2-Pcp1	this study
<i>PCP1</i>	jw2-1a	spore of <i>PCP1/Apcp1</i>		this study
<i>Apcp1 + PARN</i>	jw2-6c	spore of <i>PCP1/Apcp1</i>	pES425-PARN	this study
<i>Apcp1</i>	jw2-1c	spore of <i>PCP1/Apcp1</i>		this study
<i>Ayta10Ayta12</i>	YKO100	W303α		(Atorino <i>et al.</i> , 2003)
<i>Ayta10Ayta12 + PARN</i>		YKO100	pES425-PARN	this study
<i>Ayta10Ayta12 + hAFG3L2 + hparaplegin(LEU2)</i>	YKO117	W303α	Ycplac111 ^{ADH1} -Yta10 (1-63)-hparaplegin (59-795)-HA, pRS316 ^{ADH1} -Yta10 (1-61)-hAFG3L2 (36-798)-Myc	(Atorino <i>et al.</i> , 2003)
<i>Ayta10Ayta12 + hAFG3L2 + hparaplegin(TRP1)</i>	jw8-1	YKO117	Ycplac111 ^{ADH1} -Yta10 (1-63)-hparaplegin (59-795)-HA, pRS314 ^{ADH1} -Yta10 (1-61)-hAFG3L2 (36-798)-Myc	this study
<i>Ayta10Ayta12</i>	YKO200	W303α		(Koppen <i>et al.</i> , 2007)
<i>Ayta10Ayta12 + hAFG3L2</i>	YKO203	YKO200	Yeplac112 ^{ADH1} -Yta10 (1-61)-hAFG3L2 (36-798)-Myc	(Koppen <i>et al.</i> , 2007)
<i>Ayta10Ayta12 + hAFG3L2^{EQ}</i>	YKO204	YKO200	Yeplac112 ^{ADH1} -Yta10 (1-61)-hAFG3L2 ^{E575Q} (36-798)-Myc	(Koppen <i>et al.</i> , 2007)
<i>Ayta10Ayta12 + paraplegin</i>	YKO209	YKO200	Yeplac181 ^{YTA10} -Yta10 (1-61)-paraplegin (44-781)	(Koppen <i>et al.</i> , 2007)
<i>Ayta10Ayta12 + Afg311</i>	YKO211	YKO200	Yeplac195 ^{YTA10} -Yta10 (1-61)-Afg311 (25-789)-Myc	(Koppen <i>et al.</i> , 2007)
<i>Ayta10Ayta12 + Afg311^{EQ}</i>	YKO212	YKO200	Yeplac195 ^{YTA10} -Yta10 (1-61)-Afg311 ^{E567Q} (25-789)-Myc	(Koppen <i>et al.</i> , 2007)
<i>Ayta10Ayta12 + Afg312</i>	YKO213	YKO200	Yeplac112 ^{YTA10} -Yta10 (1-61)-Afg312 (36-802)-HA	(Koppen <i>et al.</i> , 2007)
<i>Ayta10Ayta12 + Afg312^{EQ}</i>	YKO214	YKO200	Yeplac112 ^{YTA10} -Yta10 (1-61)-Afg312 ^{E574Q} (36-802)-HA	(Koppen <i>et al.</i> , 2007)
<i>Ayta10Ayta12 + paraplegin + Afg311^{EQ}</i>	YKO217	YKO200	Yeplac181 ^{YTA10} -Yta10 (1-61)-paraplegin (44-781), Yeplac195 ^{YTA10} -Yta10 (1-61)-Afg311 ^{E567Q} (25-789)-Myc	(Koppen <i>et al.</i> , 2007)
<i>Ayta10Ayta12 + paraplegin^{EQ} + Afg311^{EQ}</i>	YKO218	YKO200	Yeplac181 ^{YTA10} -Yta10 (1-61)-paraplegin ^{E575Q} (44-781), Yeplac195 ^{YTA10} -Yta10 (1-61)-Afg311 ^{E567Q} (25-789)-Myc	(Koppen <i>et al.</i> , 2007)
<i>Ayta10Ayta12 + paraplegin + Afg312^{EQ}</i>	YKO221	YKO200	Yeplac181 ^{YTA10} -Yta10 (1-61)-paraplegin (44-781), Yeplac112 ^{YTA10} -Yta10 (1-61)-Afg312 ^{E574Q} (36-802)-HA	(Koppen <i>et al.</i> , 2007)
<i>Ayta10Ayta12 + paraplegin^{EQ} + Afg312^{EQ}</i>	YKO222	YKO200	Yeplac181 ^{YTA10} -Yta10 (1-61)-paraplegin ^{E575Q} (44-781), Yeplac112 ^{YTA10} -Yta10 (1-61)-Afg312 ^{E574Q} (36-802)-HA	(Koppen <i>et al.</i> , 2007)

References

- Atorino, L., Silvestri, L., Koppen, M., Cassina, L., Ballabio, A., Marconi, R., Langer, T., and Casari, G. (2003). Loss of m-AAA protease in mitochondria causes complex I deficiency and increased sensitivity to oxidative stress in hereditary spastic paraplegia. *J Cell Biol* 163, 777-787.
- Gietz, R.D., and Sugino, A. (1988). New yeast-Escherichia coli shuttle vectors constructed with in vitro mutagenized yeast genes lacking six-base pair restriction sites. *Gene* 74, 527-534.
- Koppen, M., Metodiev, M.D., Casari, G., Rugarli, E.I., and Langer, T. (2007). Variable and tissue-specific subunit composition of mitochondrial m-AAA protease complexes linked to hereditary spastic paraplegia. *Mol. Cell. Biol. in press*.
- Nolden, M., Ehses, S., Koppen, M., Bernacchia, A., Rugarli, E.I., and Langer, T. (2005). The m-AAA protease defective in hereditary spastic paraplegia controls ribosome assembly in mitochondria. *Cell* 123, 277-289.
- Rothstein, R.J., and Sherman, F. (1980). Genes affecting the expression of cytochrome c in yeast: genetic mapping and genetic interactions. *Genetics* 94, 871-889.
- Sikorski, R.S., and Hieter, P. (1989). A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in *Saccharomyces cerevisiae*. *Genetics* 122, 19-27.
- Westermann, B., and Neupert, W. (2000). Mitochondria-targeted green fluorescent proteins: convenient tools for the study of organelle biogenesis in *Saccharomyces cerevisiae*. *Yeast* 16, 1421-1427.