SUPPLEMENTARY INFORMATION FOR SELA ET AL., "Neddylation and CAND1 independently stimulate SCF ubiquitin ligase activity in *Candida albicans*"

Supplementary methods

Plasmids and strains construction

CaRUB1 (orf19.330.1) deletion plasmids KB1477-1, -2 were generated by cloning the CaRUB1 -800 to -1 and +300 to +740 sequences (relative to the translation start site) into KB985, KB986 (1), carrying the hisG-CaURA3-hisG fragment in two orientations. The CaJAB1 (orf19.3371) deletion plasmids 1474-1, -2 were similarly constructed, using sequences -610 to -10 and +621 to +1470 of CaJAB1. The CaTIP120 (orf19.6729) open reading frame was reassessed (see Fig. S1 below) and found to start 139 nt beyond the described start site, i.e. at Chr.3 position 1735569 of assembly 21 of the C. albicans genome; the following coordinates are relative to the new start site. The CaTIP120 deletion plasmids were constructed in two steps: first, the CaTIP120 genomic region (-867 to +3725) was cloned as a SacI-SalI fragment into pBSII-SK+ (Stratagene). The resulting plasmid KB1640 was then digested with Bcll, which cuts at positions -67 and +3007 of the 3585 nt-long CaTIP120 ORF. The hisG-CaURA3-hisG blaster fragment (3) was introduced in BclI-digested KB1640, to generate KB1657-1, -2 (both orientations). The long version of CaTIP120 open reading frame (position -139 to +3725) was constructed by cloning the BamH1-Sal1 PCR fragment into p415GAL1 (8) to generate KB1586. CaTip120 fused to 6xMyc at the C-terminus was created by replacing SOL1 in plasmid KB1798 (described below) with CaTIP120 (position -1000 to +3581). The CaTIP120 overexpression plasmid KB1958 was created by transferring the CaTIP120(-1 to +3581)-6xMyc construct as a Smal-Sall fragment into p415GAL1. KB1960 was generated by cloning CaTIP120(-1 to +3725) as a BamHI-Sall PCR fragment into KB1947, a vector based on p415-GAL1 (8) containing a Myc epitope tag sequence in the polylinker (our collection). KB1962 was generated by transferring a Xba1-Kpn1 Myc-CaTIP120(-1 to +3726) fragment into KB1317 (1) digested with SpeI-KpnI. KB2029 was constructed by cloning Not1-Kpn1 CaTIP120-6xMyc fragment (position -1000 to +3726) into pBES116 (2). A Candida albicans construct for Cterminal 3xHA epitope-tagging was generated by fusing the CaURA3 BamHI-PmeI fragment of pFA-URA3-MAL2p (5) to BglII-PmeI-digested pFA6a-3HA-TRP1 (7), to generate pFA6a-3HA-CaURA3 (KB1570). KB1734 contains the CaCDC53 region, cloned

as a -910 - +2500 SacI-XhoI PCR fragment into p413MET25 (8). KB1735, KB1847 were generated by site-directed mutagenesis of KB1734 to introduce mutations [Lys699, 701, 702 to Arg] to generate Cacdc53^{*RRR*}, and [Arg462 to Cys] to generate Cacdc53-1, respectively. The PstI-XhoI fragments of KB1734, KB1735, 1847, extending from positions +135 to +2500 of CaCDC53, were cloned into pBES116 (2) to generate KB1782, KB1783 and KB1848, respectively. Plasmid KB1869 was generated by cloning CaCDC53 (positions -889 to +2500) as a SpeI-XhoI fragment into pBES116 (2) digested with SpeI-Sall. Plasmids KB1192 (CaMAL2p-CaGCN4-6xMyc) and KB1578 (CaMAL2p-SOL1-6xMyc) were described before (1, 4). Plasmids KB1697 (CaMAL2p-CaCLN3-6xMyc) and KB1698 (CaMAL2p-CCN1-6xMyc) were constructed by substituting the TEC1 open reading frame of KB1610 (1) with either a CaCLN3 PstI-HindIII or a CCN1 PstI-ApaI PCR product. For KB1799 (CaGRR1-6xMyc), first the SOL1-6xMyc PstI-KpnI fragment of KB1578 (1) was cloned into pBES116 (2) to generate KB1798, and then a CaGRR1 NotI-ApaI PCR product (-1500 to +2340) was substituted for SOL1 in KB1798. KB1869 is a CaCDC53 (-889 to +2500) SpeI-XhoI PCR fragment cloned into pBES116 digested with SpeI and SalI. KB1897 (CaCUP1p-Myc-CaCDC53) consists in a CaCDC53 BglII-XhoI fragment (+1 to +2500) cloned into KB1321 (1) digested BglII-SalI. To generate KB2152 (MAL2p-CaCLN3-3xHA), an EcoRV-HindIII PCR fragment of the CaCLN3 open reading frame was cloned into KB2083, carrying the 3xHA sequence under the MAL2 promoter of pBES118 (2).

The S. cerevisiae strains were all derived from the EUROSCARF BY4741 (a $ura3\Delta 0$ met15 $\Delta 0$ leu2 $\Delta 0$ his3 $\Delta 1$) and BY4742 (α ura3 $\Delta 0$ lys2 $\Delta 0$ leu2 $\Delta 0$ his3 $\Delta 1$) background strains, except for the cdc53-1 mutant (MTY740, obtained from M. Tyers), which is in the W303 background. Strains KY1293 (BY4742 CDC53p-CaCDC53 HIS3) and KY1294 (BY4742 CDC53p-CaCDC53^{RRR} HIS3), carrying the CaCDC53 open reading frame integrated instead of the CDC53 open reading frame, were built by oligonucleotide-directed site-specific recombination of a CaCDC53 HIS3 fragment into the CDC53 locus, using plasmids KB1734 and KB1735, respectively, as templates. KY1352 (BY4742 CDC53p-FLAG-CaCDC53 HIS3) was constructed similarly, but using a FLAG-tag-encoding amplification integration (primer 5'oligonucleotide for and sequence CAAAGAATAACAACAAAATCGCAAGCAAGCAAGCATGGACTACAAGGACGAC

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GACGACAAGTCATCTACTCTTCCACCA). KY1310 ($ura3\Delta 0 \ lys2\Delta 0 \ leu2\Delta 0 \ his3\Delta 1 \ rub1\Delta::KANr \ CDC53p-CaCDC53 \ HIS3$) is the product of a cross between KY1293 and BY4741 $rub1\Delta::KANr$ (EUROSCARF). KY1309 ($ura3\Delta 0 \ met15\Delta 0 \ leu2\Delta 0 \ his3\Delta 1 \ jab1\Delta::KANr \ CDC53p-CaCDC53 \ HIS3$) is the product of a cross between KY1293 and BY4741 $jab1\Delta::KANr$ (EUROSCARF). KY1306 ($ura3\Delta 0 \ lys2\Delta 0 \ leu2\Delta 0 \ his3\Delta 1 \ dcn1\Delta::KANr \ CDC53p-CaCDC53 \ HIS3$) is the product of a cross between KY1293 and BY4741 $dcn1\Delta::KANr$ (EUROSCARF). KY1306 ($ura3\Delta 0 \ lys2\Delta 0 \ leu2\Delta 0 \ his3\Delta 1 \ dcn1\Delta::KANr \ CDC53p-CaCDC53 \ HIS3$) is the product of a cross between KY1293 and BY4741 $dcn1\Delta::KANr$ (EUROSCARF).

C. albicans deletions of Ca*RUB1*, Ca*JAB1* and Ca*TIP120* were achieved by sequential deletion of both alleles using plasmid sets KB1477, KB1474, KB1657 respectively. C-terminal epitope tagging of Ca*CDC53* was achieved by site-specific targeting of a 3xHA-Ca*URA3* PCR product amplified from KB1570, using additional 65nt homology at each end to the Ca*CDC53* 3' end. The Ca*cdc53* knock-in alleles were generated by deleting one copy of Ca*CDC53* in strain SN78, using the described method (9). The second allele was generated by integration of plasmids KB1782, KB1783 and KB1848 - digested with EcoRV that cuts within the Ca*CDC53* coding sequence - at the remaining Ca*CDC53* allele, generating KC326, KC327, KC362. These strains have one copy of the plasmid-borne allele under the chromosomal Ca*CDC53* promoter, followed by Ca*URA3* and vector sequences, and by one promoterless N-terminal truncation allele, Ca*cdc53* ΔN . KC363 was generated by 5-fluoroorotic acid selection of KC362 for ura³⁻ clones that have "popped out" the cointegrate by homologous recombination, and screening of the resulting clones for those that have retained the mutant allele.

Supplementary figures

Fig. S1. Assignment of the translation start site of CaTip120 (orf19.6729). A. Western blot of 6xMyc-tagged orf19.6729 expressed from the *GAL1* promoter in *S. cerevisiae*. 1: *C. albicans* no-tag control; 2. orf19.6729-6xMyc expressed in *C. albicans* under its native promoter; 3, 4: orf19.6729-6xMyc expressed in *S. cerevisiae* under the Sc*GAL1* promoter. 5 *S. cerevisiae* no-tag control. B. Alignment by MAFFT (6) of the N-terminal region of several fungal Tip120 homologs, as well as of human CAND1. Arrow indicates the site of presumed actual start of CaTip120 translation.

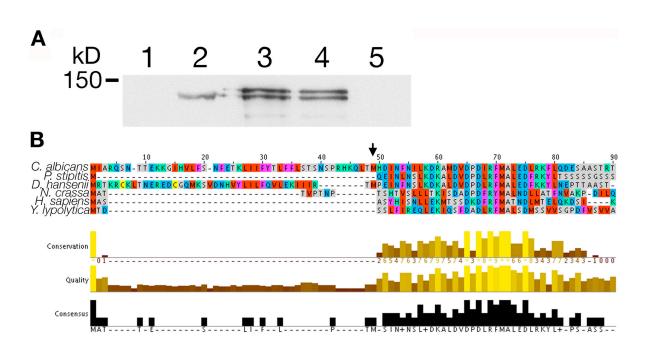


Fig. S2. CaCdc53 is specifically sensitive to CaTip120. 5-fold dilutions of overnight cultures of the indicated strains, transformed with either vector plasmid or with plasmid KB1586 (*GAL1p-CaTIP120*), were spotted on an SC-LEU, 2% galactose plate, and the plate was incubated for 3 days at 30°C.

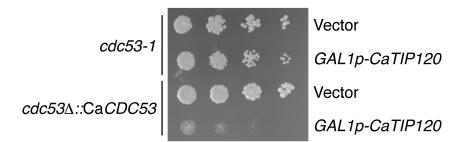


Fig. S3. Morphology of cell lawns (left column) and microscopic cell morphology (right column) of indicated strains. For cell lawns, 500 cells were spotted on YPD agar and the plates were incubated for 2 days at 30°C. For microscopic morphology, cells were grown to mid-log phase (O.D. 600 of 1-2) and photographed with a 10X objective. The strains, uniformly in KC274 background and all URA+, are KC471, KC326, KC327, KC395, KC424 and KC427, respectively.

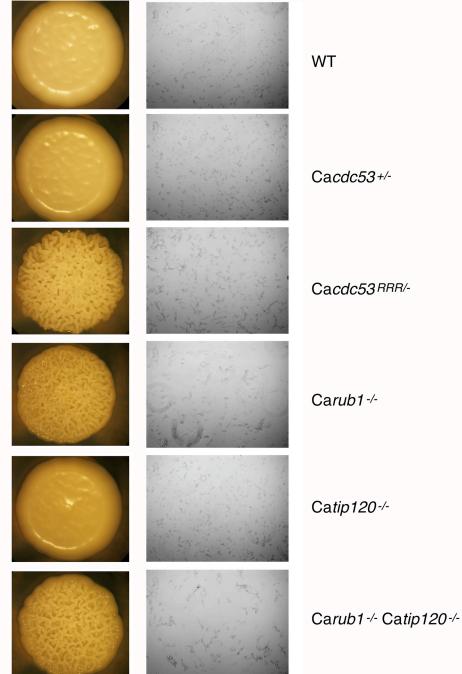


Fig. S4. Complementation of the *S. cerevisiae* $cdc53\Delta$ allele with Myc-CaCdc53 (plasmid KB1824) or CaCdc53-3xHA (plasmid KB1828) under the *MET25* promoter, vs. vector plasmid. A $cdc53\Delta$ deletion strain, kept alive with a *CDC53 URA3* 2µ plasmid (strain KY484) was transformed with the indicated plasmids, then grown overnight in SC – TRP, and spread on a SC –TRP plate containing 1 mg/ml 5-fluoroorotic acid. The plate was incubated for 2 days at 30°C.

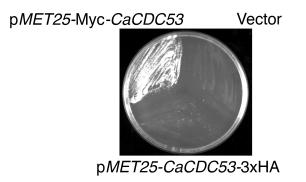
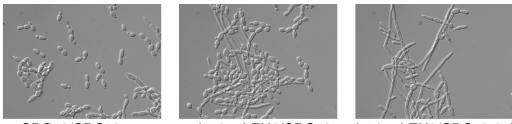


Fig. S5. Phenotype of the *C. albicans* strain expressing only CaCdc53-3xHA. Cultures of strains with the indicated genotypes (KC271, KC325, KC329, respectively), were diluted in the morning, grown to logarithmic phase and photographed.



CDC53/CDC53

cdc53A::LEU2/CDC53 cdc53A::LEU2/CDC53-3xHA::URA3

Supplementary references

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