

Supplemental Data

Sss1p is required to complete protein translocon activation

Barrie M. Wilkinson, Judith K. Brownsword, Carl J. Mousley¹, and Colin J. Stirling

From the Faculty of Life Sciences, Michael Smith Building, University of Manchester, Oxford Road, Manchester, M13 9PT, U.K. and the ¹Department of Cell and Developmental Biology, Lineberger Comprehensive Cancer Center, University of North Carolina School of Medicine, Chapel Hill, NC 27599-7090, USA.

Running head: The role of Sss1p in ER protein translocation

Address correspondence to: Professor Colin J. Stirling, Faculty of Life Sciences, Michael Smith Building, The University of Manchester, Oxford Road, Manchester, M13 9PT, UK.
Phone: 44-161-275-5104, Fax: 44-161-275-5082 E-mail: colin.stirling@manchester.ac.uk

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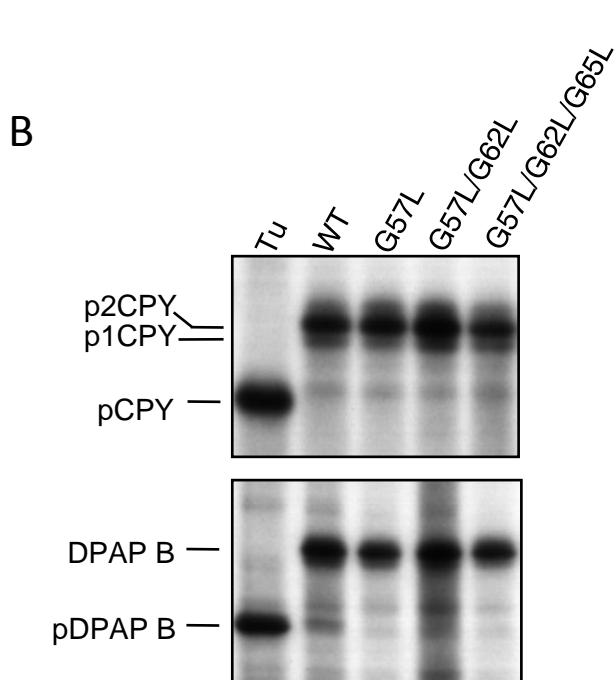
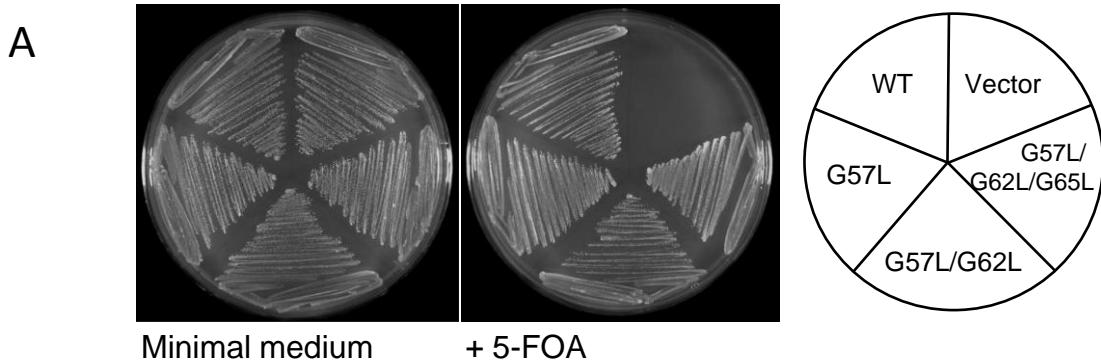


Figure S1. Functional analysis of Sss1p glycine mutants. *A*, Vector (pRS313) and plasmids encoding *SSSI*, the G57L, G57L/G62L and G57L/G62L/G65L *sss1* mutations were transformed into the *SSSI* plasmid shuffle strain BWY530. All transformants grew normally after 3 days on minimal medium minus uracil and histidine for selection of the *SSSI*, *URA3* plasmid (FKp53) and the pRS313 (HIS3) transformed plasmids. After 3 days incubation on 5-FOA containing minimal medium, the vector only strain was unable to grow due to the lethality of the *Δsss1* mutation upon FKp53 counter-selection, whilst the transformants containing the wild-type (*SSSI*) and glycine mutation plasmids grew by providing Sss1p function. *B*, After passage on 5-FOA medium, the strains now containing the *SSSI* or glycine mutations on the pRS313 vector as the sole source of Sss1p function were analysed for defects in protein translocation. Whole cell extracts prepared from cells grown at 30°C and 35 S-labelled for 5 min were immunoprecipitated with ppCPY or DPAP B specific antisera and the products were resolved by 10 and 7.5% SDS-PAGE respectively. Upon ER translocation, ppCPY is signal-cleaved and modified by N-linked glycan addition in the ER (p1 CPY) and the Golgi (p2CPY). The type II membrane protein, DPAP B which acquires N-linked glycans upon correct ER membrane integration, and decreases in gel mobility. Tunicamycin (Tu) treatment yields the signal-cleaved, but unglycosylated pro-CPY and the unglycosylated pre form of DPAP B (pDPAP B).

Table S1. Oligonucleotide primers

Name	Sequence (5'-3')
<i>SSS1-G1</i>	CCAAGATTGTCAGGCTGTTGGTATTCTATTAAATTGCAGTCGGTATCATTGG
<i>SSS1-G1a</i>	CCAATGATAACCGACTGCAATTAAATAGAACATACCAACAGCCTGACAATCTTGG
<i>SSS1-G2</i>	GGTATTCTATTAAATTGCAGTCGGTATCATTCTGTACGCCATCAAGTTGATTTC
<i>SSS1-G2a</i>	GAATCAACTTGATGCGTACAGAACATGATAACGACTGCAATTAAATAGAACACC
<i>SSS1-G3</i>	GGCTGTTGGTATTCTATTAAATTGCAGTACTTATCATTCTGTACGCCATCAAG
<i>SSS1-G3a</i>	CTTGATGGCGTACAGAACATGATAAGTACTGCAATTAAATAGAACACAGCC
<i>SSS1-ΔC</i>	AAGGAATACACCAAGAAGATTGTCAAGTAAGTTGGTATTGGTTAATTGC
<i>SSS1-ΔCa</i>	GCAATTAAACCAATACCAACTTACTTGACAATCTGGTGTATTCTT
<i>UBC6-2</i>	TTGGTTATTGTTGTTCAGAAA
<i>UBC6-3</i>	GGGGGATCCTGAAGAACTATCATTAGGTT
<i>SSS1-1</i>	TTCAAGGTGCGTGGAA GAG
<i>SSS1-4</i>	GGGGGATCCGCTGTTGGTATTGGTTAAT
<i>USSS1C</i>	GGGATCCATGGTTTATATTGGTATCGCTATTTTTGTTTTGGTGGCCTTTAT GAAGTTGATTCATATTCCAATCAG
<i>USSS1Ca</i>	GCAGTAATATTATATGGGAAG
<i>SSS1-NdeIF</i>	GTATAACATTGAAAAATCATATGGCTAGAGCTAGTG
<i>SSS1-NdeIR</i>	CACTAGCTCTAGCCATATGATTTTCAATGTTATAC
<i>ΔssS1-1</i>	TTTACCAAAGATAAAATCACGTATAACATTGAAAAATAACGTACGCTGCAG GTCGAC
<i>ΔssS1-1a</i>	GTGCCGTTGTTTTATTTTCTCGTCTTTATCTCTTATCGATGAATTGAGCTCG
<i>SEC61-121</i>	GCTAAAAGGTGGCCGCTATTATTCTGATC
<i>SEC61-121a</i>	GATCAGAATAATAGCGGCCACCTTTGAGC
<i>SEC61-150</i>	CTCGGATTGCCATGCCCTGTTGTTAATC
<i>SEC61-150a</i>	GATTAACAACAAGGCGATGGCAATCCGCG
<i>SEC61-373</i>	GTTCTGGTTCAGCCCGAGTATTTC
<i>SEC61-373a</i>	GGAAAATACTGCGGCTGAACCAAGAAC
<i>SEC61tm9C</i>	CATTCCAATGCTGCATGCTGCGGTGCTACCATC
<i>SEC61tm9Ca</i>	GATGGTAGCACCGCAGCAGCAGCATGCAGCAGTTGGAATG