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Supplemental Materials for "Distinct Ceramide Synthases Regulate Polarized Growth in the Filamentous Fungus *Aspergillus nidulans*^{D^m}"

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Distinct Ceramide Synthases Regulate Polarized Growth in the Filamentous Fungus *Aspergillus nidulans*

Mol. Biol. Cell Li et al. 17: 1218

Supplemental Material

The following supporting material pertains to the above article:

Supplemental Figure 1

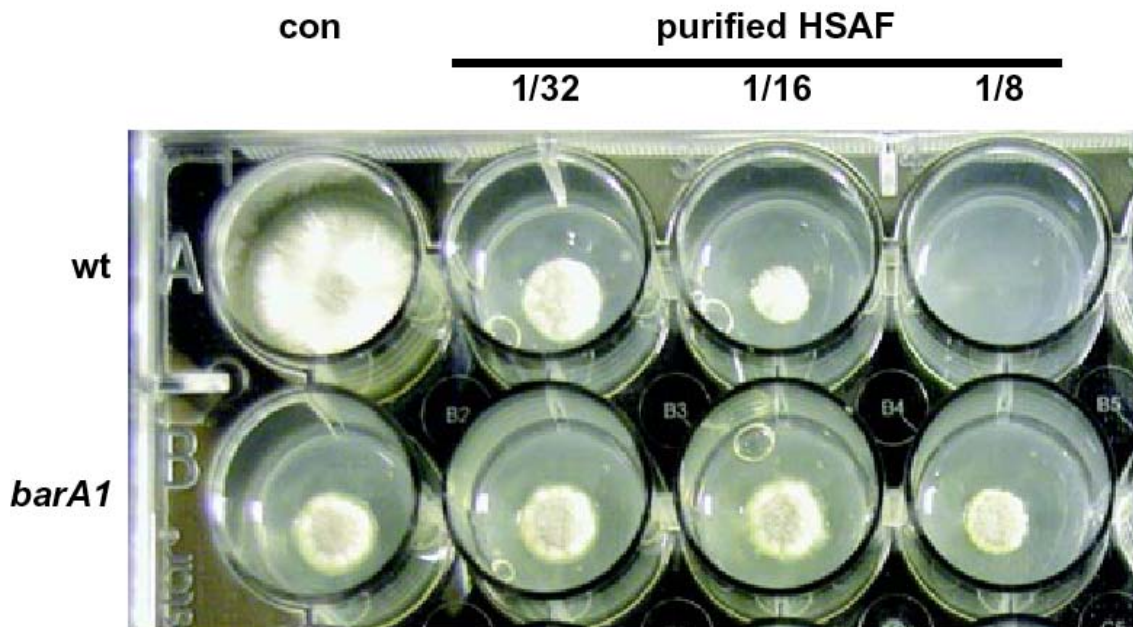


Figure 1 - *barA* mutants are resistant to the effects of HPLC-purified HSAF. Top row; purified HSAF inhibits the growth of wildtype hyphae in a dose-dependent manner. Bottom row, *barA1* mutants display equal growth at all tested doses of purified HSAF. Indicated doses represent dilutions of HPLC-purified HSAF.

Figure 2 (next page) - Alignment of Lag1 homologues. A multiple alignment was generated using ClustalW (MacVector v7.0). Identities are outlined in dark shaded boxes and similarities in light shaded boxes. Protein sequences used for the alignment include: An BarA (*A. nidulans* BarA, accession number: EAA60493); An LagA (*A. nidulans* Lag1 homologue, accession number: EAA64170); Sc Lag1 (*S. cerevisiae* Lag1p, accession number: UO8133); Sc Lac1 (*S. cerevisiae* Lac1p, accession number: NP_012917); and Hs Lag1 (*Homo sapiens* Lag1p homologue, accession number: BC032565). * indicates locations of nonsense mutations in *barA* mutants. The circled * indicates the *barA1* mutation.

Forward Alignment

10 20 30 40 50 60
An BarA
An LagA
Hs Lag1
Sc Lag1
Sc Lact

70 80 90 100 110 120 130
An BarA
An LagA
Hs Lag1
Sc Lag1
Sc Lact

140 150 160 170 180 190
An BarA
An LagA
Hs Lag1
Sc Lag1
Sc Lact

200 210 220 * 230 240 250 260
An BarA
An LagA
Hs Lag1
Sc Lag1
Sc Lact

270 280 * 290 300 310 320
An BarA
An LagA
Hs Lag1
Sc Lag1
Sc Lact

330 340 350 360 370 380 390
An BarA
An LagA
Hs Lag1
Sc Lag1
Sc Lact

400 410 420 * 430 440 450
An BarA
An LagA
Hs Lag1
Sc Lag1
Sc Lact

460 470 480 490 500 510 520
An BarA
An LagA
Hs Lag1
Sc Lag1
Sc Lact

Formatted alignment

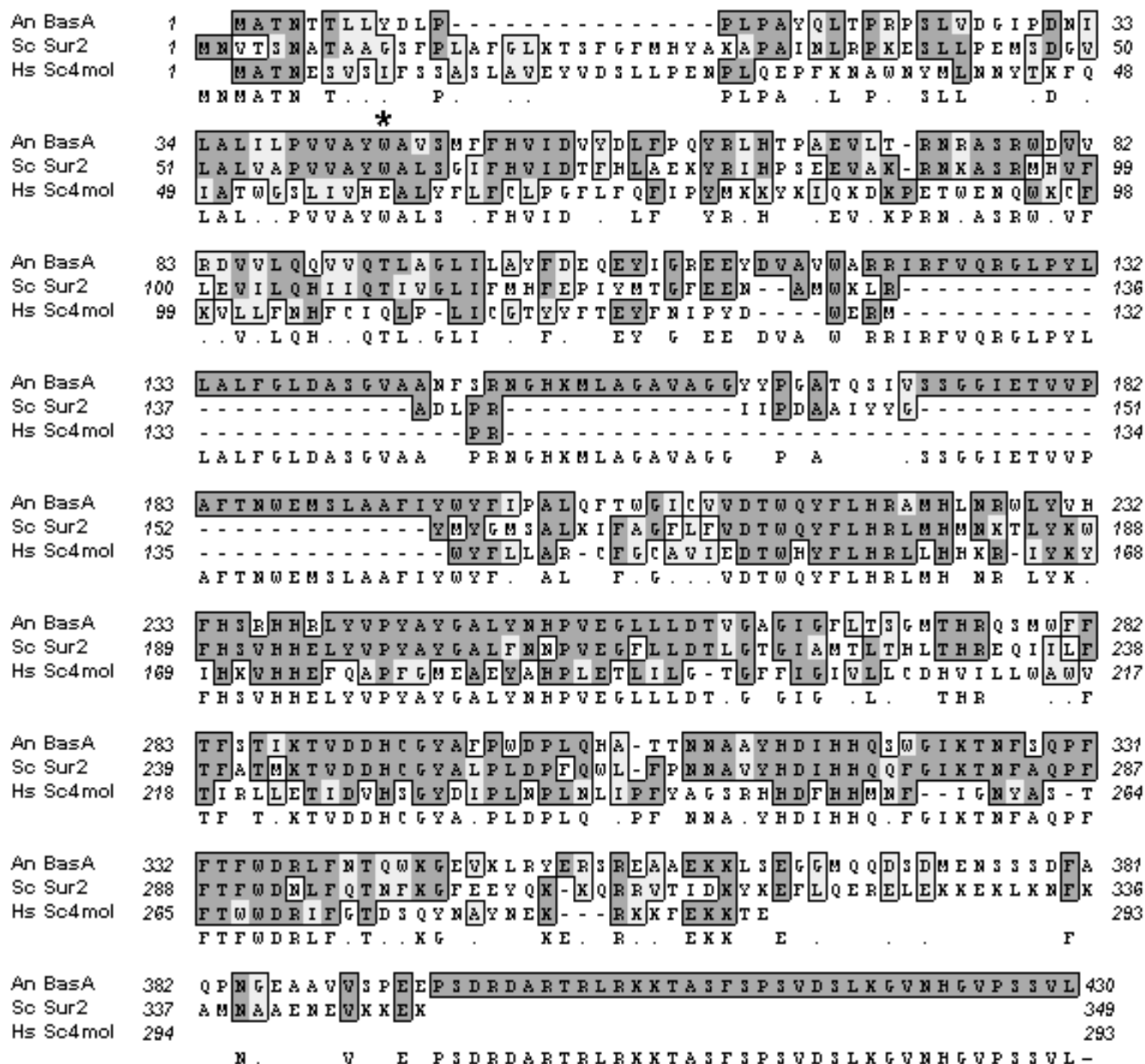


Figure 3 - Alignments of BasA homologues. A multiple alignment was generated using ClustalW (MacVector v7.0). Identities are outlined in dark shaded boxes and similarities in light shaded boxes. Protein sequences used for the alignment include: An BasA (*A. nidulans* BasA, accession number: XM_404777); Sc Sur2 (*S. cerevisiae* Sur2p, accession number: UO7171); Hs SC4MOL (*H. sapiens* methyl oxidase-like protein, accession number: NM_006745). * indicates location of the mutation in *basA1* mutant 8-145.

Supplemental Figure 4

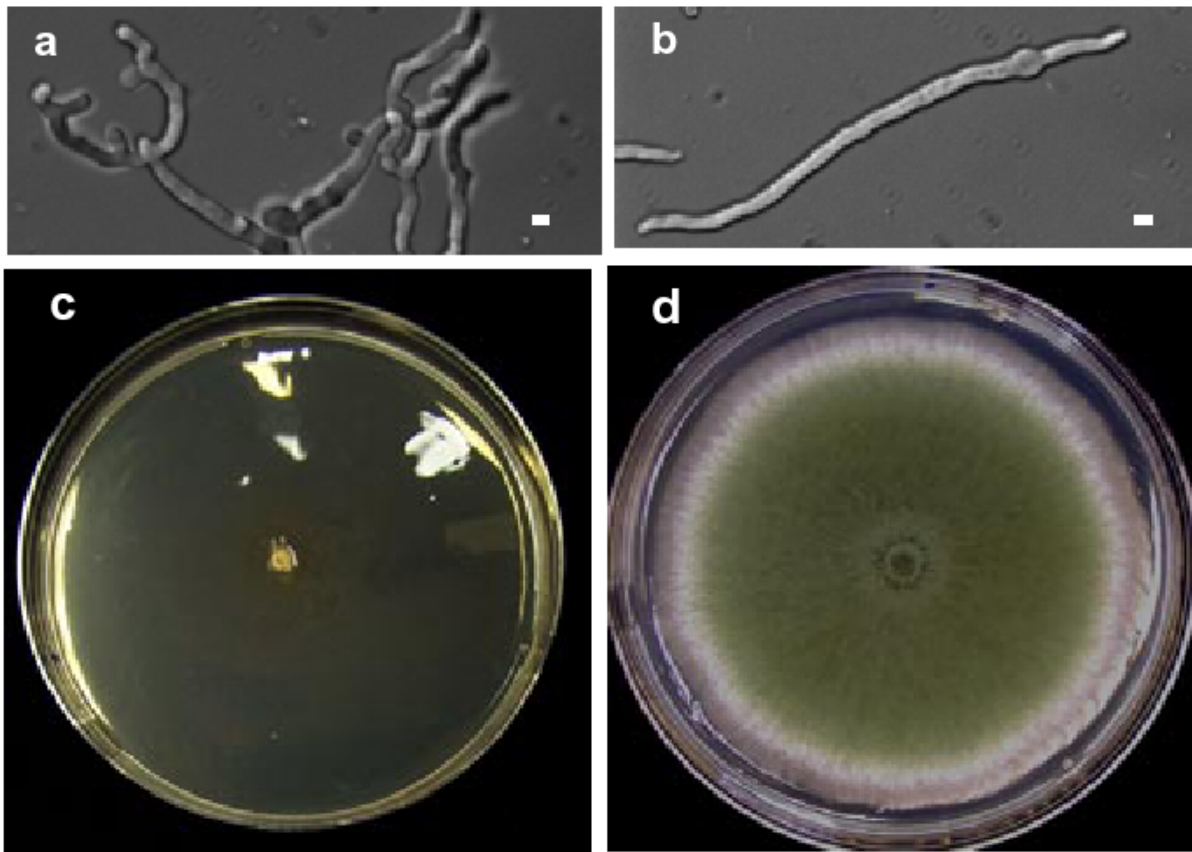


Figure 4 - Growth defects of *lagA* mutants. (A,B) Conidia from *lagA* deletion mutant ASL11 (A) and wildtype strain A28 (B) were germinated in YGV media for 12 h. (C,D) The *lagA* deletion mutant ASL11 (C) and wild type A28 (D) were incubated on MAG plates at 28°C for 10 days. Bar, 3 μ m.