

# **Convergent evolution of a modified, acetate-dependent TCA cycle in bacteria**

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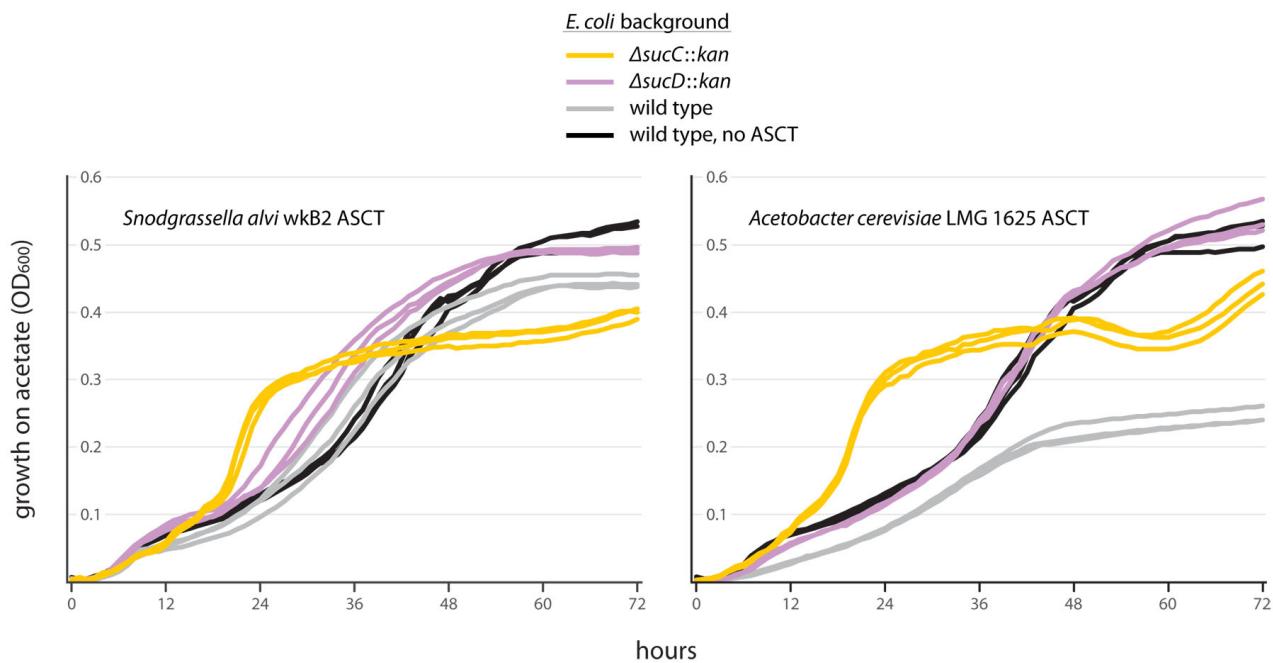
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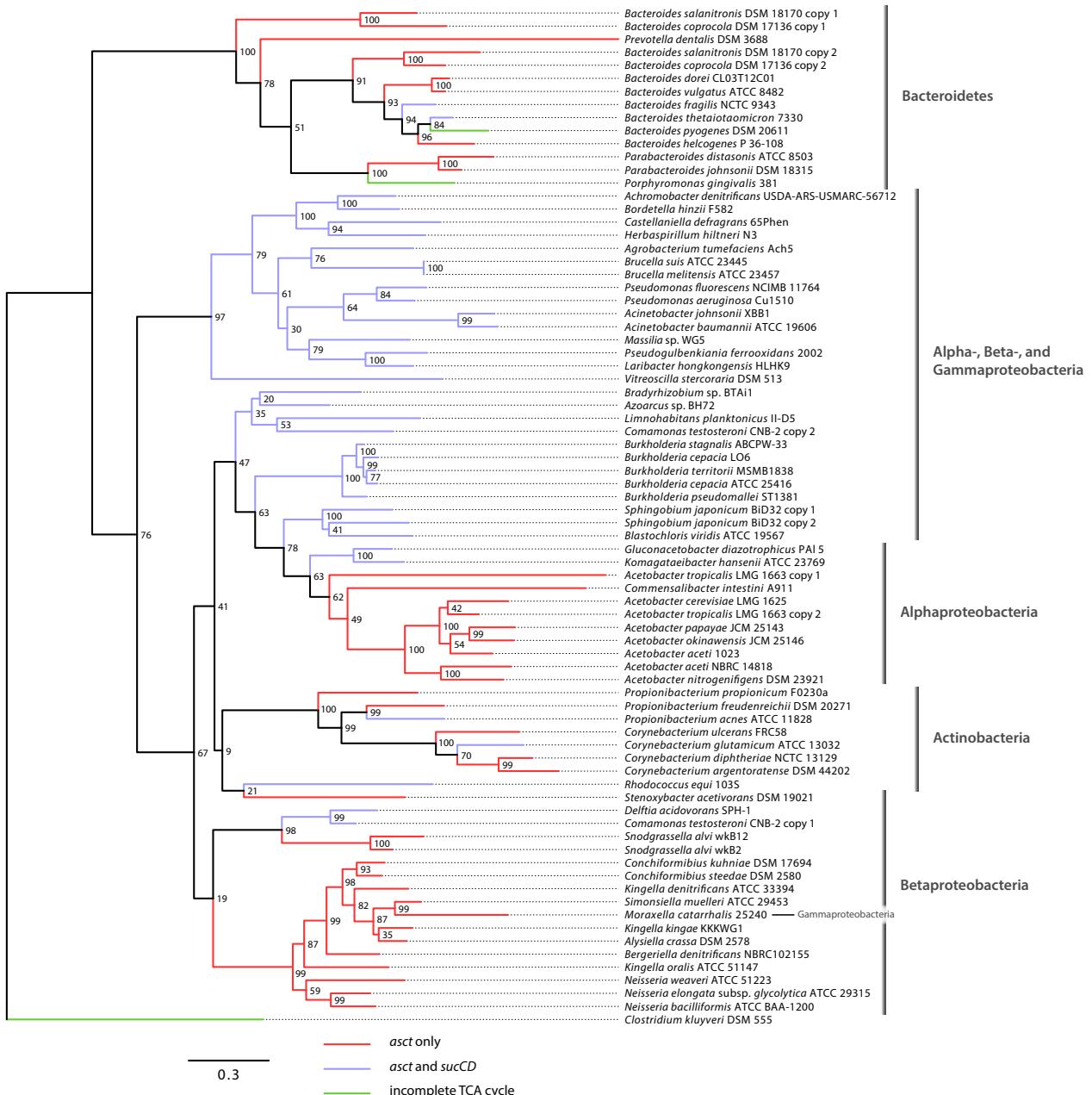
Supplementary Figures 1–3

Supplementary Tables 1 & 2

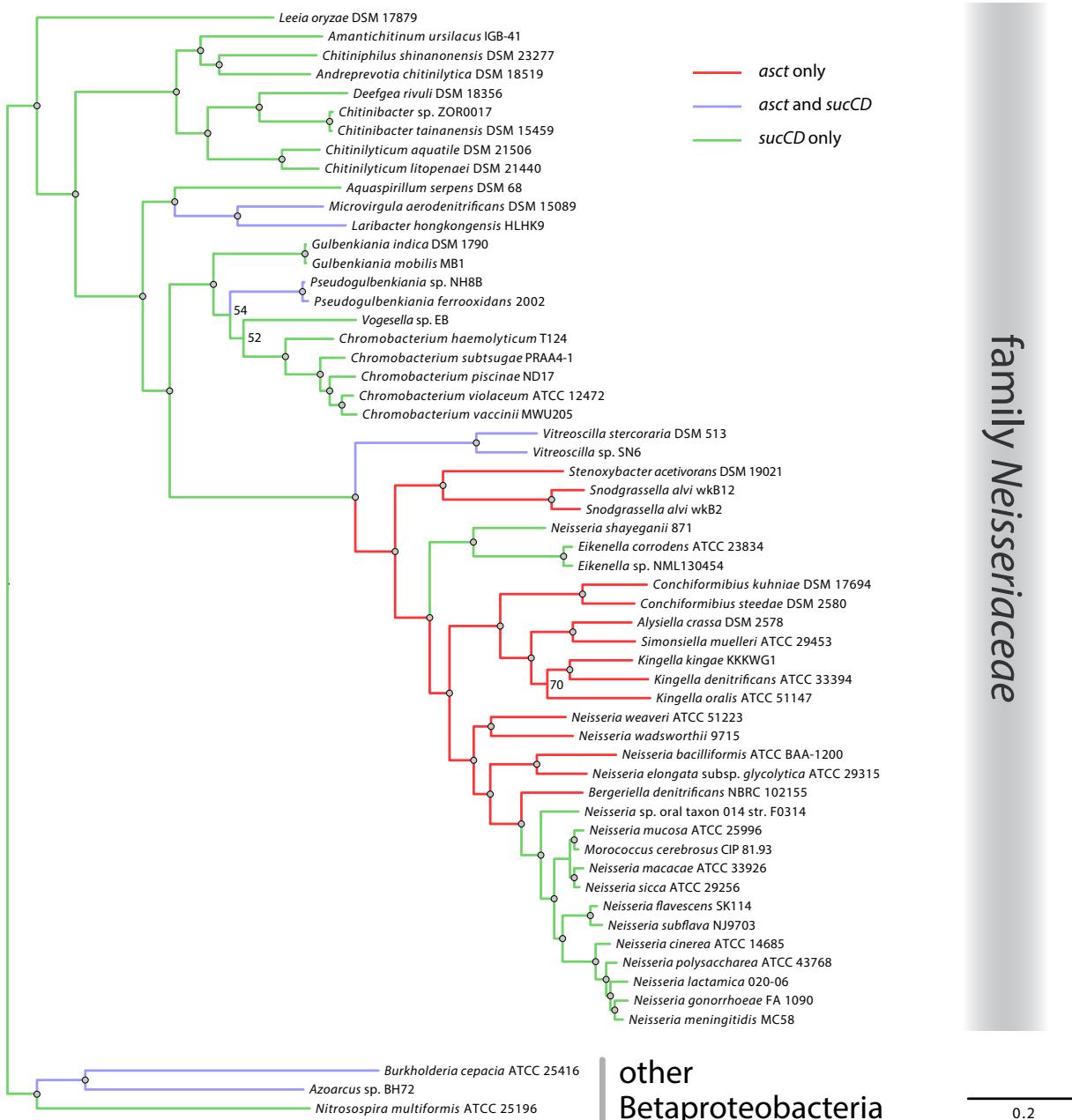
**Supplementary Figure 1.** Growth effects of ASCT-complementation in different *E. coli* mutant backgrounds. Strains with both ASCT and SCS had slowest growth, suggesting competitive inhibition. Strains with  $\Delta$ sucC backgrounds had fastest growth, but at the cost of achieving lower final densities. Strains were grown in M9 minimal media supplemented with 0.3% w/v sodium acetate and 75 mg/ml carbenicillin for plasmid maintenance. OD<sub>600</sub> readings were taken hourly. Lines represent replicates (n = 3 for each strain).



**Supplementary Figure 2.** Rectangular tree representation of *asct* phylogeny in Fig. 1c. Values at nodes indicate bootstrap support from maximum-likelihood analysis (1,000 replicates). Bar, substitutions per site.



**Supplementary Figure 3.** Prevalence of *asct* in the *Neisseriaceae*. The maximum likelihood algorithm was used to construct a whole genome phylogeny, based on 363 orthologous genes (108,434 amino acid residues). Branches are colored based on presence of *asct* and *sucCD* in tip taxa, and extrapolated using parsimony to interior branches. Circles indicate nodes with 100% bootstrap support (1,000 replicates). Bar, substitutions per site.



**Supplementary Table 1.** Genes, plasmids, and strains used in this study.

	Description	Reference
<b>Gene</b>		
SALWKB2_RS03080	<i>asct</i> from <i>Snodgrassella alvi</i> wkb2	NZ_CP007446
AD928_RS13430	<i>asct</i> from <i>Acetobacter cerevisiae</i> LMG 1625	NZ_LHZA01000000
DIP_RS20725	<i>asct</i> from <i>Corynebacterium diphtheriae</i> NCTC 13129	NC_002935
DR90_RS06235	<i>asct</i> from <i>Moraxella catarrhalis</i> ATCC 25240	NZ_CP008804
F911_00479	<i>asct</i> from <i>Acinetobacter baumannii</i> ATCC 19606	NZ_APBG01000000
BF9343_RS00125	<i>asct</i> from <i>Bacteroides fragilis</i> NCTC 9343	NC_003228
<b>Plasmid</b>		
pBad-EBFP2 (control)	pBad backbone, EBFP2 (blue fluorescent protein) insert	[15]
pWK1	pBad backbone, SALWKB2_RS03080 insert	This study
pWK24	pBad backbone, DIP_RS20725 insert	This study
pWK25	pBad backbone, AD928_RS13430 insert	This study
pWK29	pBad backbone, DR90_RS06235 insert	This study
pWK34	pBad backbone, F911_00479 insert	This study
pWK39	pBad backbone, BF9343_RS00125 insert	This study
pWK31 (control)	pBad backbone, F911_00479 insert (reversed)	This study
<b>Strain</b>		
<i>E. coli</i> CGSC 7636	F-, $\Delta(araD-araB)567$ , $\Delta lacZ4787(\text{:rrnB-3})$ , $\lambda^-$ , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$ , <i>hsdR514</i>	[16]
<i>E. coli</i> CGSC 8788	F-, $\Delta(araD-araB)567$ , $\Delta lacZ4787(\text{:rrnB-3})$ , $\Delta sucC777::kan$ , $\lambda^-$ , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$ , <i>hsdR514</i>	[16]
<i>E. coli</i> CGSC 11810	F-, $\Delta(araD-araB)567$ , $\Delta lacZ4787(\text{:rrnB-3})$ , $\Delta sucD778::kan$ , $\lambda^-$ , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$ , <i>hsdR514</i>	[16]

