

Group of Subsystems: Enterobactin metabolism

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Subsystem: Enterobactin biosynthesis

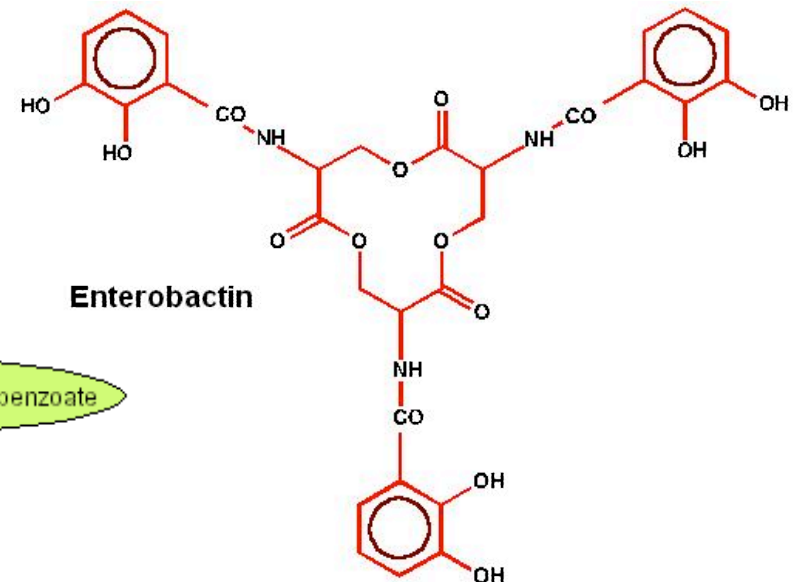
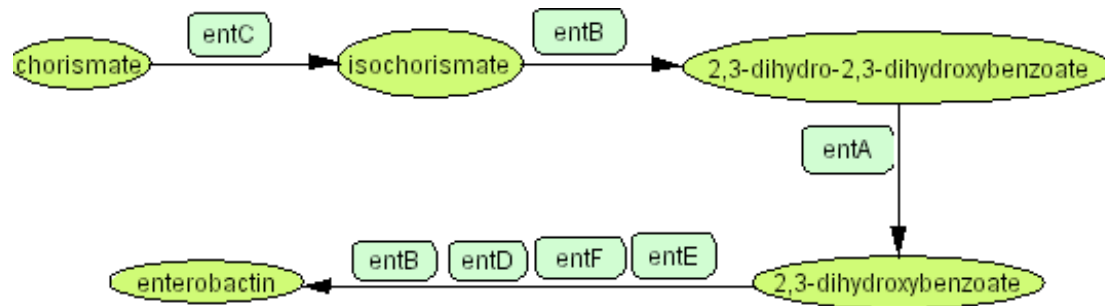
Siderophore enterobactin is a triscatechol derivative of a cyclic triserine lactone that enables bacteria to recover iron from their environment. Believed earlier to be unique to Gram-negative bacteria, enterobactin has been isolated recently from two Gram-positive *Streptomyces* species. It is a cyclic compound of three 2,3-dihydroxybenzoylserine units joined in a cyclic structure by lactone linkages (see molecular diagram on slide two). Enterobactin is synthesized under low iron concentration conditions and excreted into the environment where it binds Fe(III) with high affinity and specificity. The ferrisiderophore complexes are taken up into the cell by specific ATP-binding cassette transporter complex (see subsystem “ABC transporter ferric enterobactin (TC 3.A.1.14.)” for details). The biosynthesis of enterobactin starts with conversion of chorismic acid sequentially to isochorismate; 2,3-dihydro-2,3-dihydroxybenzoate; and then into 2,3-dihydroxybenzoic acid (DHB) catalyzed by EntC, EntB, and EntA. The amide linkage of DHB and L-serine is catalyzed by EntD, EntE, EntF, and EntB. Intermolecular cyclization of three molecules of DHB-Ser finally yields enterobactin. The functional role “Menaquinone-specific isochorismate synthase (EC 5.4.4.2)” has been included in this subsystem for clarity. MenF, similar to, although distinct from EntC, is an isochorismate synthase encoded by the *menF* gene.

Slide 3 shows a snapshot of the subsystem spreadsheet and graphic representation of conserved chromosomal clusters of *ent* genes. It also illustrates application of SEED tools for detection of un- and mis- called ORFs by comparing gene clusters across genomes.

References:

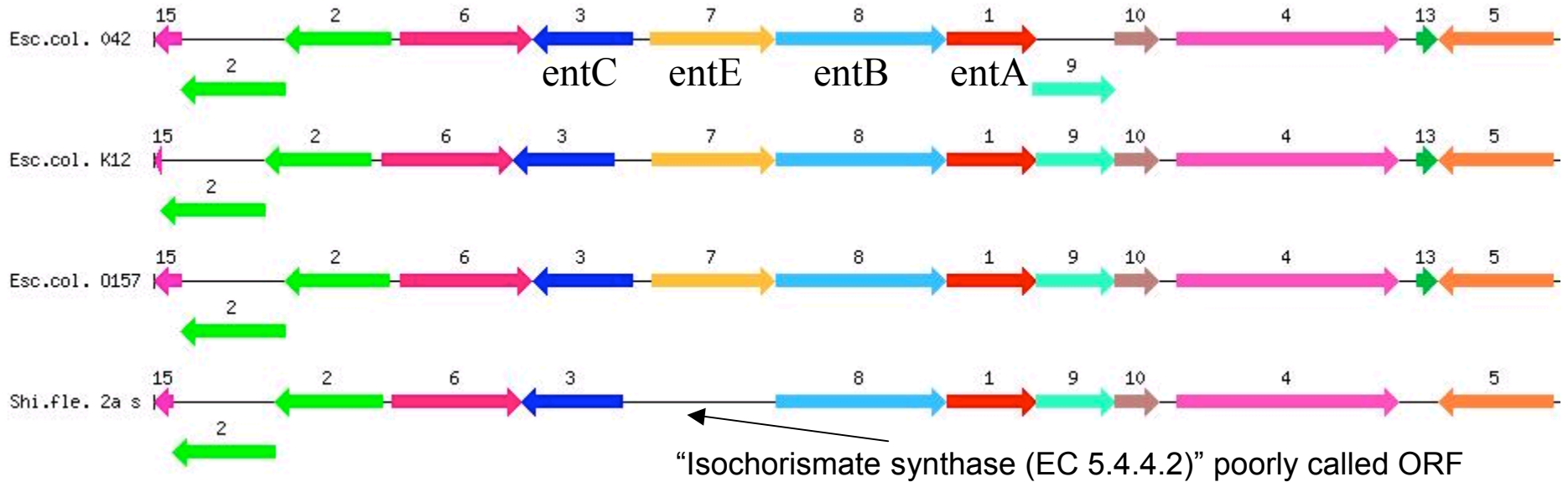
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4. Neidhardt FC, Curtiss III R, Ingraham JL, Lin ECC, Low Jr KB, Magasanik B, Reznikoff WS, Riley M, Schaechter M, Umberger HE "Escherichia coli and Salmonella, Cellular and Molecular Biology, Second Edition." American Society for Microbiology, Washington, D.C., 1996.

Pathway, Functional Roles, and
Molecular Diagram



Abbrev	Functional Role
entC	Isochorismate synthase (EC 5.4.4.2)
entE	2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58)
entB	Isochorismatase (EC 3.3.2.1)
entA	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase (EC 1.3.1.28)
entD	4'-phosphopantetheinyl transferase entD (EC 2.7.8.-)
entF	Enterobactin synthetase component F (EC 2.7.7.-)
menF	Menaquinone-specific isochorismate synthase (EC 5.4.4.2)

Chromosomal and spreadsheet views of clustering



Organism	entC	entE	entB	entA	entD	entF	menF
<i>Escherichia coli</i> 042 [B]	350	351	352	353	337	342	3088
<i>Escherichia coli</i> K12 [B]	593	594	595	596	582	586	2239
<i>Escherichia coli</i> O157:H7 EDL933 [B]	628	629	630	631	617	621	3151
<i>Shigella flexneri</i> 2a str. 301 [B]		489	490	491	478	481	2191

Subsystem: ABC transporter ferric enterobactin (TC 3.A.1.14.2)

This Subsystem is a companion subsystem created to help classify and categorize subunits of the specific ferric enterobactin ATP-binding cassette transporter. The TC number has been ascribed in accordance with the Transport Classification Database. A condensed spread sheet illustrating clustering on the chromosome of the genes encoding ferric enterobactin transporter subunits is shown on the next slide.

Abbrev	Functional Role
fepC	Ferric enterobactin transport ATP-binding protein fepC (TC 3.A.1.14.2)
fepG	Ferric enterobactin transport system permease protein fepG (TC 3.A.1.14.2)
fepD	Ferric enterobactin transport system permease protein fepD (TC 3.A.1.14.2)
fepB	Ferrienterobactin-binding periplasmic protein fepB (TC 3.A.1.14.2)

Organism	fepC	fepG	fepD	fepB
Trichodesmium erythraeum IMS101 [B]	2166	2164	2163	5936
Chromobacterium violaceum ATCC 12472 [B]	2234	2235	2236	2239
Escherichia coli 042 [B]	345	346	347	349
Escherichia coli CFT073 [B]	650	651	652	654
Escherichia coli E2348 [B]	3030	3029	3028	3026
Escherichia coli K12 [B]	588	589	590	592
Escherichia coli O157:H7 [B]	701	702	703	705
Photobacterium luminescens subsp. laumondii TTO1 [B]	1561	1563	1564	1565
Photobacterium luminescens subsp. laumondii TTO1 [B]	4411	4410	4409	4408
Salmonella enterica serovar Choleraesuis SC-B67 [B]	621	622	623	625
Salmonella enterica subsp. enterica serovar Gallinarum [B]	858	857	856	854
Salmonella enterica subsp. enterica serovar Typhi str. CT18 [B]	556	557	558	560
Salmonella typhimurium LT2 [B]	570	571	572	574
Shigella dysenteriae M131649 [B]	5061	5060	5059	5057
Shigella flexneri 2a str. 2457T [B]	475	476	477	479
Shigella flexneri 2a str. 301 [B]	484	485	486	488
Shigella sonnei 53G [B]	597	596	595	593
Yersinia enterocolitica 8081 [B]	3556	3555	3554	3552
Yersinia pseudotuberculosis [B]	2419	2420	312	71
Pseudomonas aeruginosa PAO1 [B]	4157	4160	4159	4158
Pseudomonas aeruginosa UCBPP-PA14 [B]	1759	1762	1761	1760
Salmonella bongori 12149 [V]	560	561	562	564