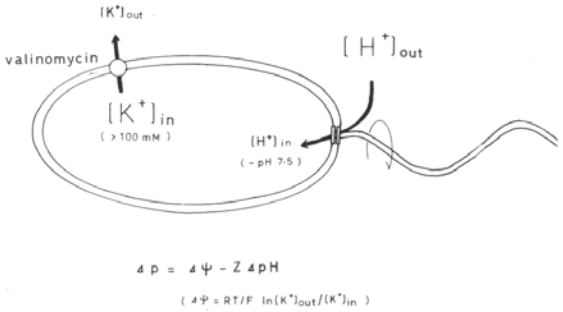
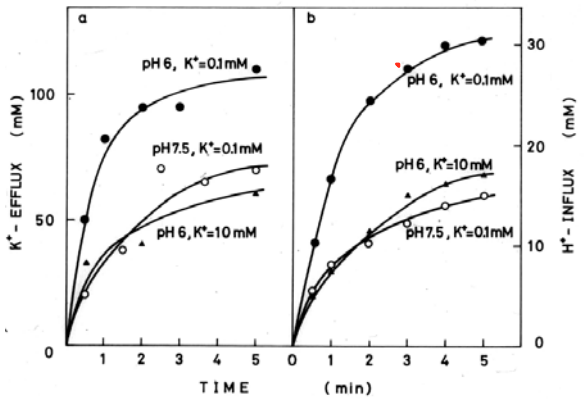
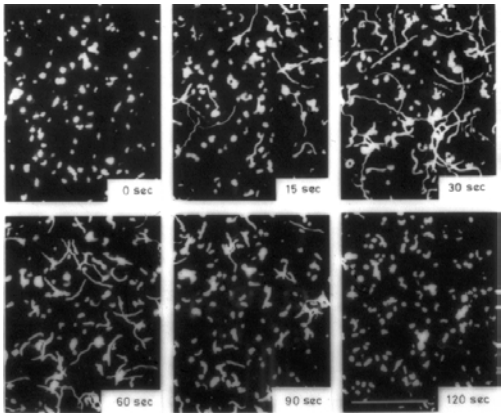
プロトン駆動力と運動



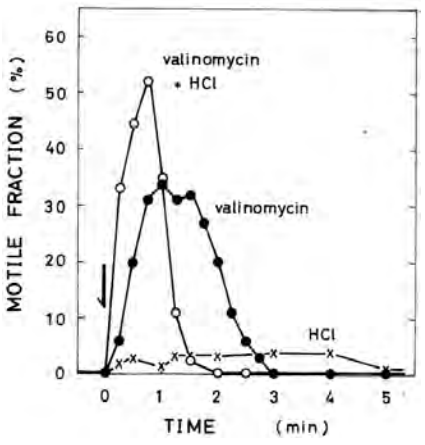
外液条件によるK⁺とH⁺の流入出



人工プロトン駆動力による枯草菌の運動を観察

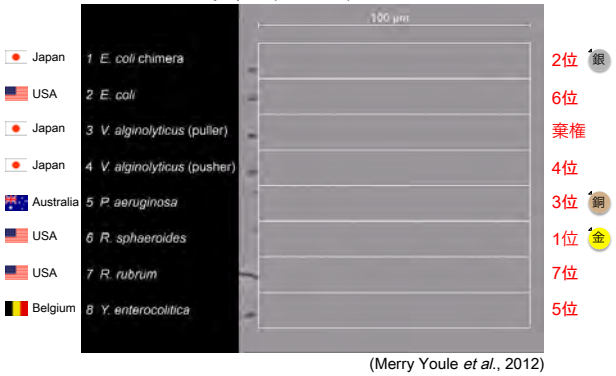


拡散電位によるべん毛運動



バクテリア100μm走

The Microbial Olympics (in Oxford)



(Merry Youle *et al.*, 2012)

ケイ光融合蛋白質の局在

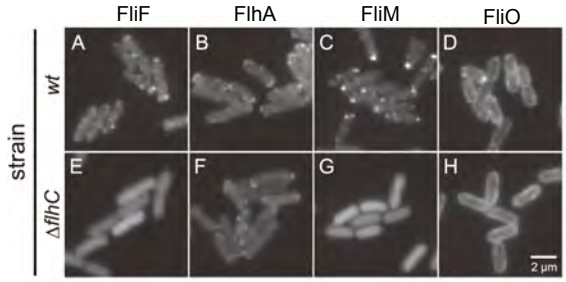
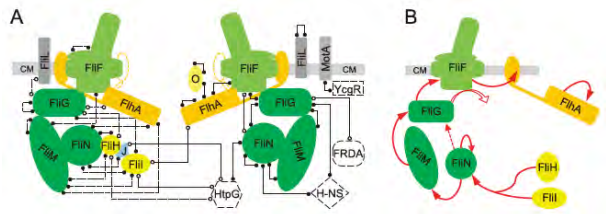


Table 2. Localization of selected fusion proteins in wild-type and knockout strains.[a]

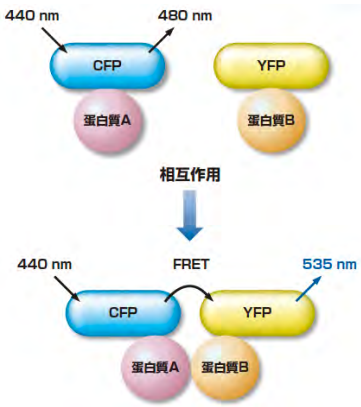
	Fusion						
Strain	FlhA–YFP	FliF–YFP	YFP–FliG	YFP–FliM	YFP–FliN	YFP–FliH	FliI–YFP
Wild type	+++	+++	+++	+++	+++	+++	+++
ΔflhC	+++	+	− (C)	− (C)	− (C)	− (C)	− (C)
ΔflhA	+++	++	++	++	++	++	++
ΔfliF	+++	+++	− (C)	− (A)	− (A)	− (C)	− (C)
ΔfliM	+++	++	++	+++	− (C)	− (C)	− (C)
ΔfliM ΔfliN	+++	++	++	++	− (C)	− (C)	− (C)
ΔfliM ΔfliG	+++	++	++	− (A)	− (C)	− (C)	− (C)
ΔfliH	+++	++	++	++	++	− (A)	− (C)
ΔfliI	+++	++	++	++	++	− (C)	+++

a. Localization patterns were classified as follows:
+++, motor-like localization, with several discrete foci (up to 10) distributed more or less evenly along the cell periphery (see Fig. 1);
++, suboptimal motor-like localization with fewer and less intense foci;
+, poor localization, with only few and very weak foci;
− (C), uniform cytoplasmic localization; and
− (A), cytoplasmic localization along with larger aggregates.
Representative images for each localization pattern are shown in Fig. S6.

べん毛蛋白質相互作用のモデル図

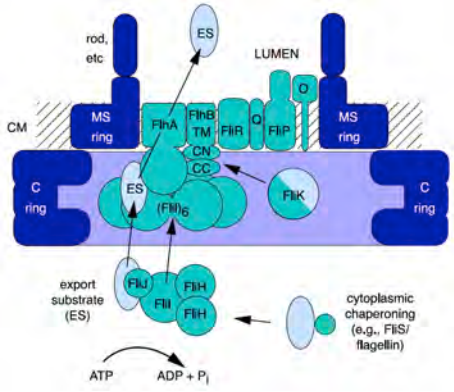


FRET

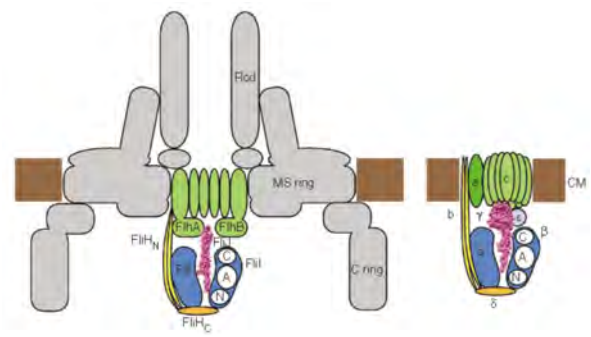


べん毛特異的分泌装置

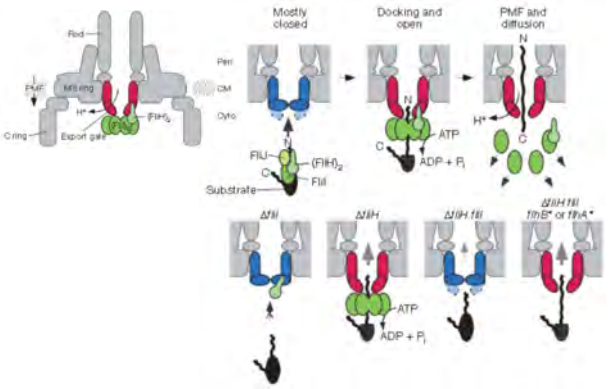
べん毛分泌装置のモデル図

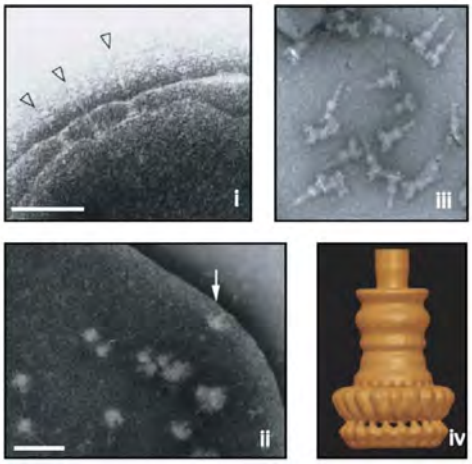


べん毛分泌装置とF型ATPaseの類似性

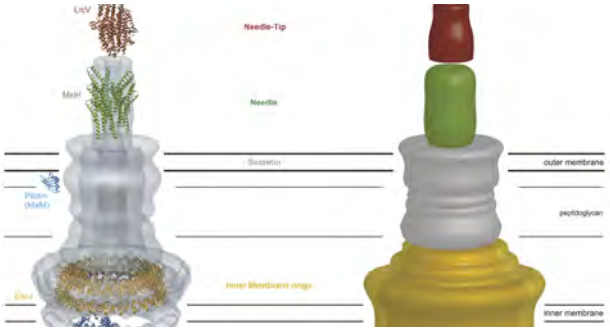


べん毛分泌系のエネルギー共役





Type III ピリの構造



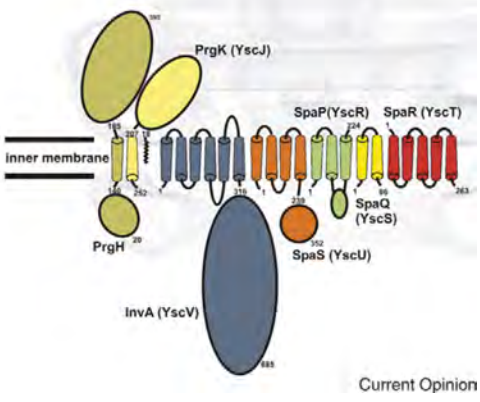
べん毛輸送蛋白質と相同な毒素分泌系因子との比較

Table 1
Type III flagellar protein export components and a comparison of their homologs in virulence factor secretion systems

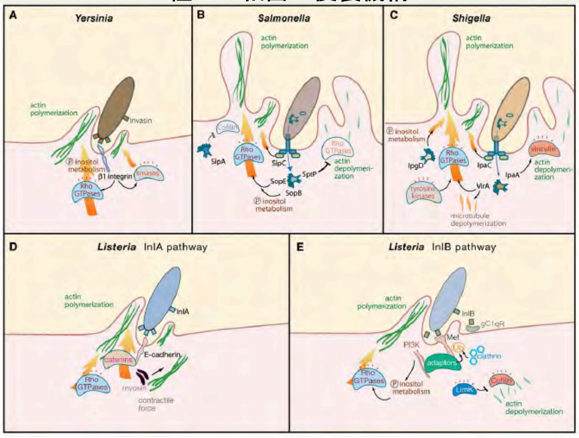
Flagellar protein[a]	Function/properties	Molecular mass (kDa)	Virulence protein[a]	Molecular mass (kDa)	E value[b]
FliH	Regulator of FliI activity	25.8	n.d.[c]		
		25.8	YscL (*Yersinia enterocolitica*)	24.9	0.1
FliH (*Treponema denticola*)		35.2	YscL (*Yersinia enterocolitica*)	24.9	10^{-11}
FliI	Export ATPase	49.3	InvC	47.6	5×10^{-72}
FliJ	General chaperone	17.3	n.d.[c]		
FliK	Hook-length control	41.8	InvJ	36.4	n.a.[d]
FlhA	Membrane component; interacts with soluble components	74.8	InvA	76.1	4×10^{-14}
FlhB	Membrane component; interacts with soluble components; specificity switching	42.4	SpaS	40.1	2×10^{-14}
FliO	Membrane component; function unknown	13.1	n.d.[c]		
FliP	Membrane component; cleaved signal sequence	26.8	YscR	24.1	5×10^{-9}
FliQ	Membrane component; function unknown	9.6	SpaQ	9.4	0.006
FliR	Membrane component; function unknown	28.9	SpaR	28.5	6×10^{-7}
FliN	C ring component, involved in motor function as well as export	14.6	SpaO	13.8	0.002
FliF	MS ring protein; necessary for export; interacts with FlhA	61.1	HrpC (*Pseudomonas syringae*); presumed lipoprotein	29.1	0.009
FlgE	Hook protein	42.1	PrgI	8.9	n.a.[d]
FlgJ	Murein idase and putative rod capping protein	34.4	n.d.[c]		

[a] Unless otherwise stated, the proteins are from *Salmonella*, but they exist in essentially all flagellated species and type III virulence species.
[b] A parameter generated by BLASTP [75] indicating the probability that the observed degree of sequence similarity would occur by chance.
[c] n.d., no homolog detected in *Salmonella*.
[d] n.a., not applicable; homology based on mutant phenotype or biochemical evidence, no significant sequence similarity.

Type III 分泌膜蛋白質のトポロジー



種々の細菌の侵襲機構


A
Yersinia
actin polymerization
invasin
Ⓟ inositol metabolism
β1 integrin
kinases
Rho GTPases
B
Salmonella
actin polymerization
Cofilin
SipA
Rho GTPases
SipC
Rho GTPases
actin depolymerization
SptP
SopE
SopB
Ⓟ inositol metabolism
C
Shigella
actin polymerization
Ⓟ inositol metabolism
IpgD
Rho GTPases
IpaC
vinculin
IpaA
actin depolymerization
tyrosine kinases
VirA
microtubule depolymerization
D
Listeria InlA pathway
actin polymerization
InlA
E-cadherin
catenins
Rho GTPases
myosin
contractile force
E
Listeria InlB pathway
actin polymerization
InlB
gC1qR
Met
PI3K
Ub
clathrin
adaptors
Rho GTPases
Ⓟ inositol metabolism
LimK
Cofilin
actin depolymerization