[Supporting Information]

Biochemical characterization of bacterial FeoBs: A perspective on nucleotide specificity

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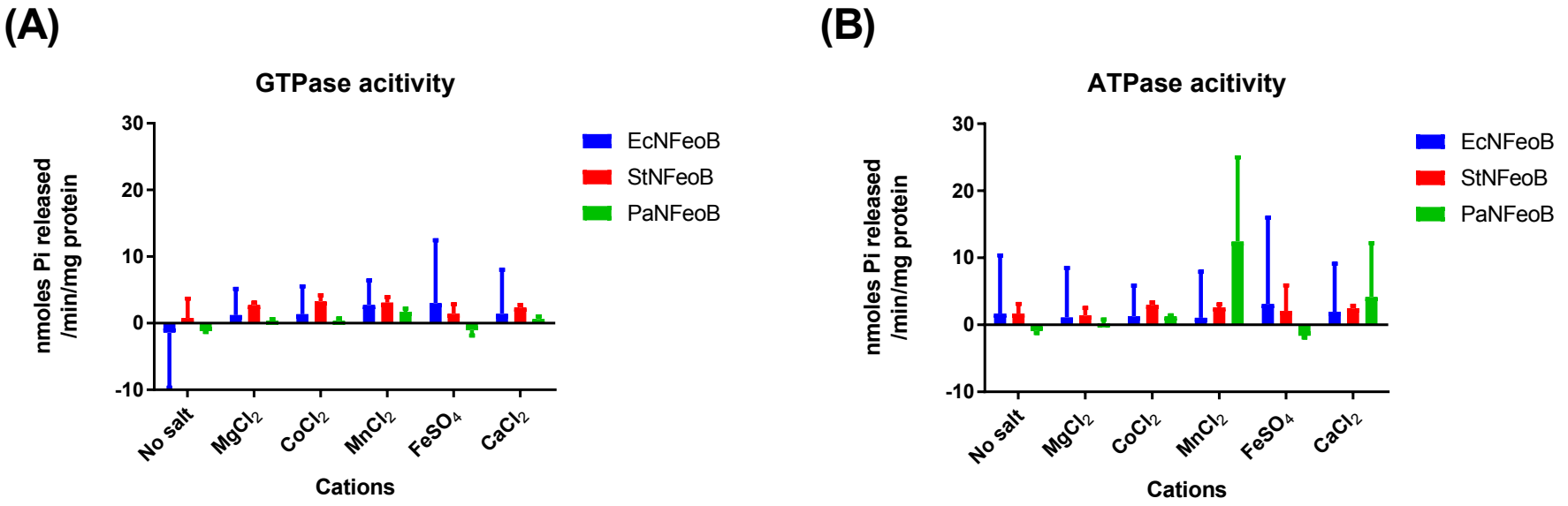
Running head: Bacterial FeoBs with two distinct nucleotide specificities

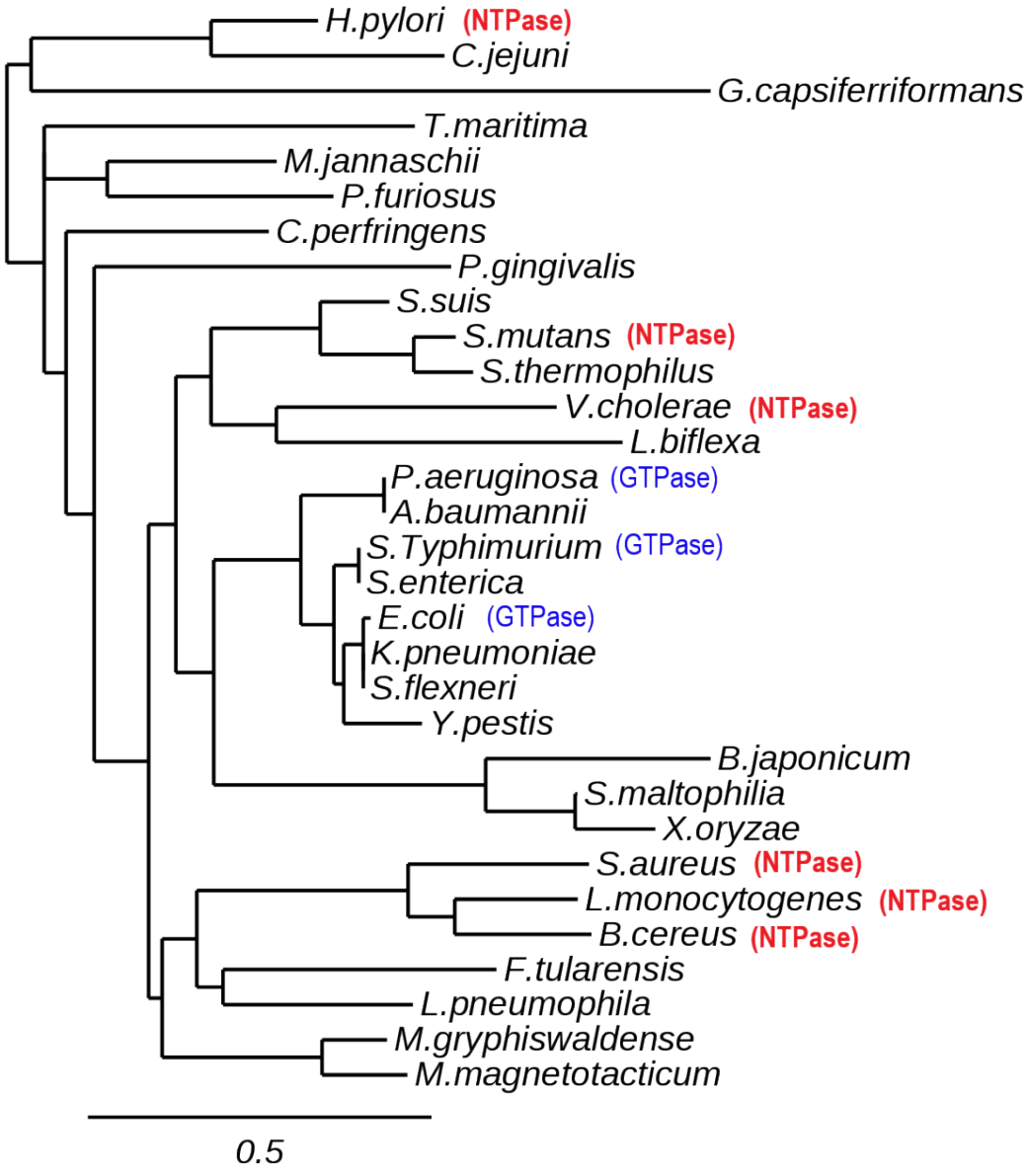
Keywords: Feo, ferrous iron transport, GTPase, ATPase, Potassium

Supplementary Fig. S1. Without addition of potassium, the GTPase (A) or ATPase (B) activity in the group of GTP-specific NFeoBs was not stimulated by any metal ions. The enzyme reaction buffer contained 10 mM NaCl. The error bars represent the standard deviation.

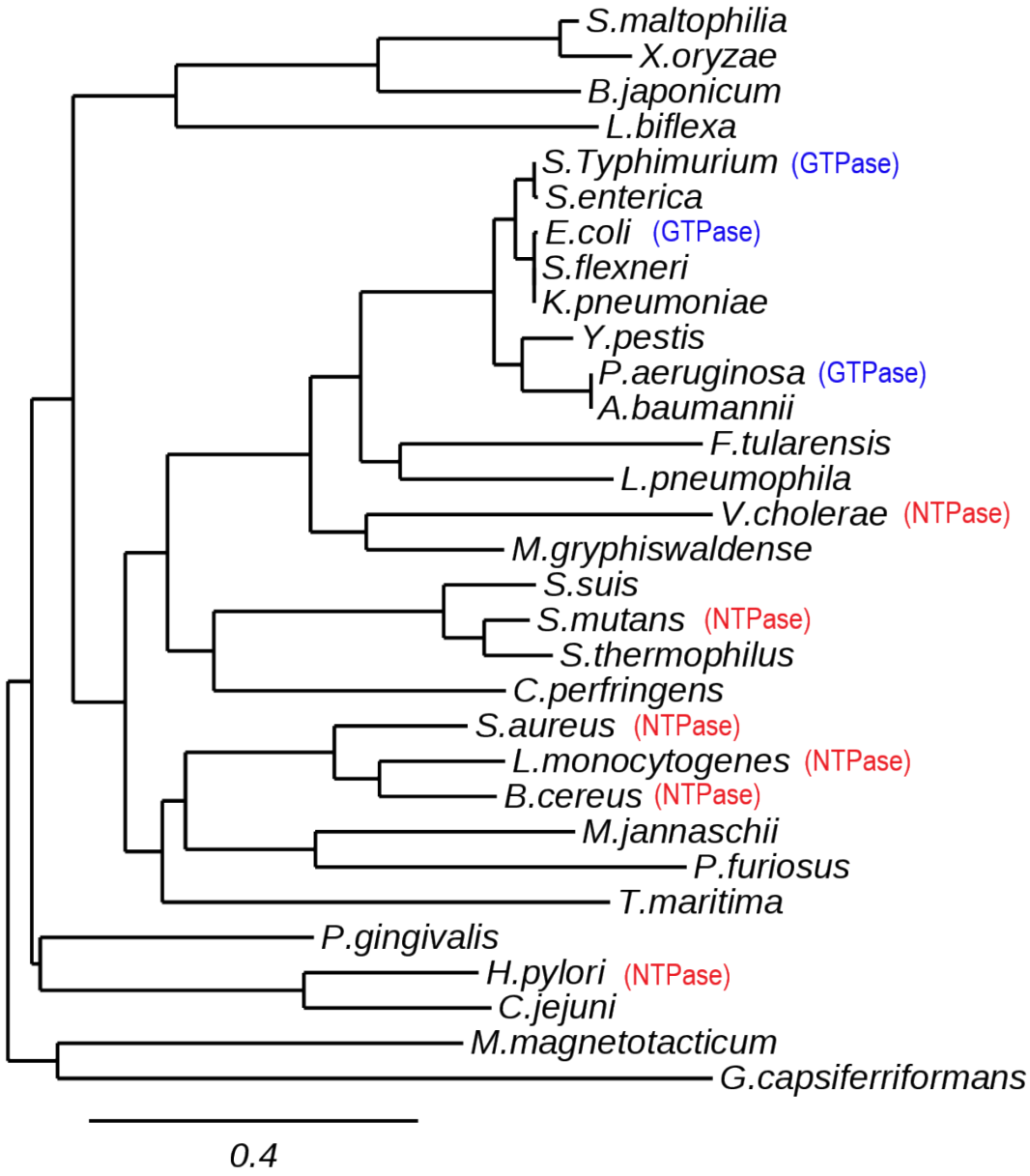


Supplementary Fig. S2. Both the cytosolic domain and whole FeoB sequences of GTP-specific bacteria were grouped as gamma-proteobacteria, while NTP-specific bacteria were present in various bacterial phyla. Phylogenetic analysis of cytosolic domains (A) and full-length (B) sequences of FeoB indicates clear separation of bacterial strains into either GTP-specific or NTP-specific groups. Bacterial strains in the analysis were selected based on publications where their FeoB was studied. Bacterial strains studied were represented as GTPase or NTPase. Phylogenetic assay was conducted using Phylogeny.fr (http://www.phylogeny.fr/index.cgi).

(A) NFeoB



(B) Whole FeoB


S.maltophilia
X.oryzae
B.japonicum
L.biflexa
S.Typhimurium (GTPase)
S.enterica
E.coli (GTPase)
S.flexneri
K.pneumoniae
Y.pestis
P.aeruginosa (GTPase)
A.baumannii
F.tularensis
L.pneumophila
V.cholerae (NTPase)
M.gryphiswaldense
S.suis
S.mutans (NTPase)
S.thermophilus
C.perfringens
S.aureus (NTPase)
L.monocytogenes (NTPase)
B.cereus (NTPase)
M.jannaschii
P.furiosus
T.maritima
P.gingivalis
H.pylori (NTPase)
C.jejuni
M.magnetotacticum
G.capsiferriformans
0.4