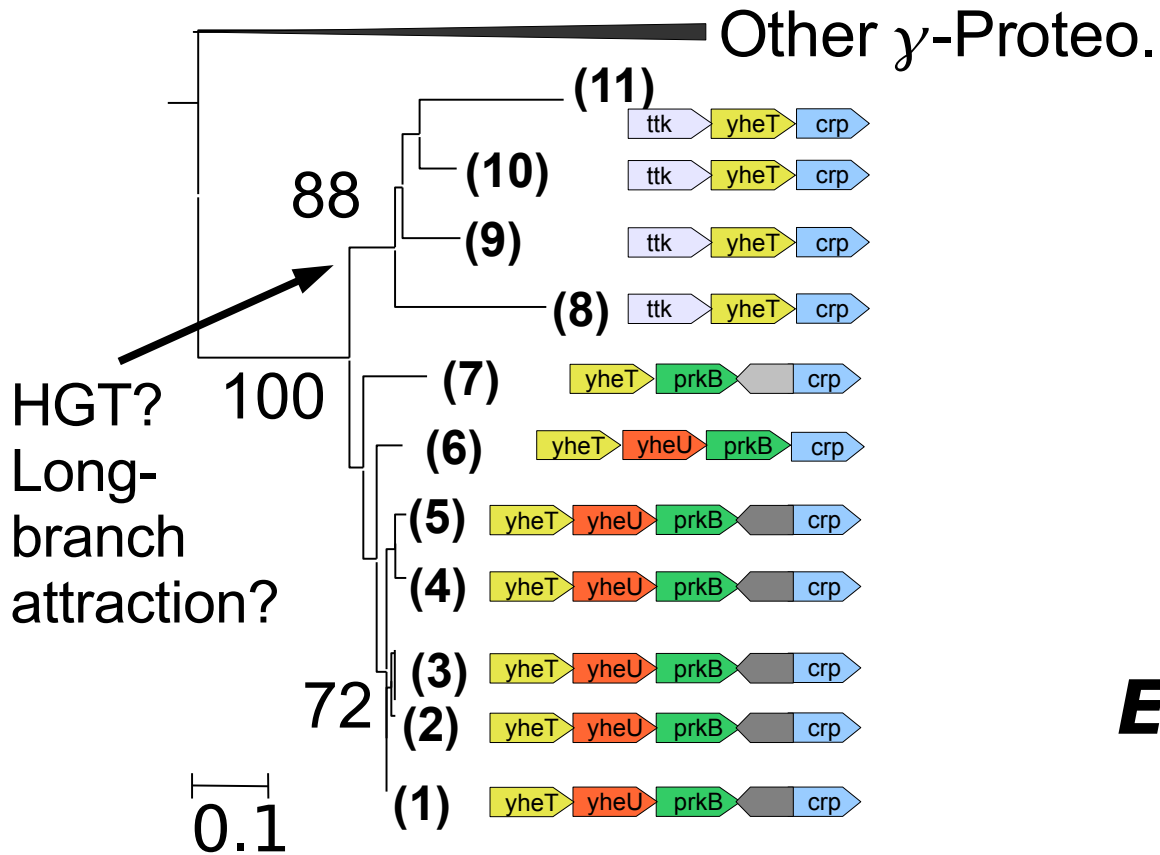


Rapid Evolution of Gene Regulation

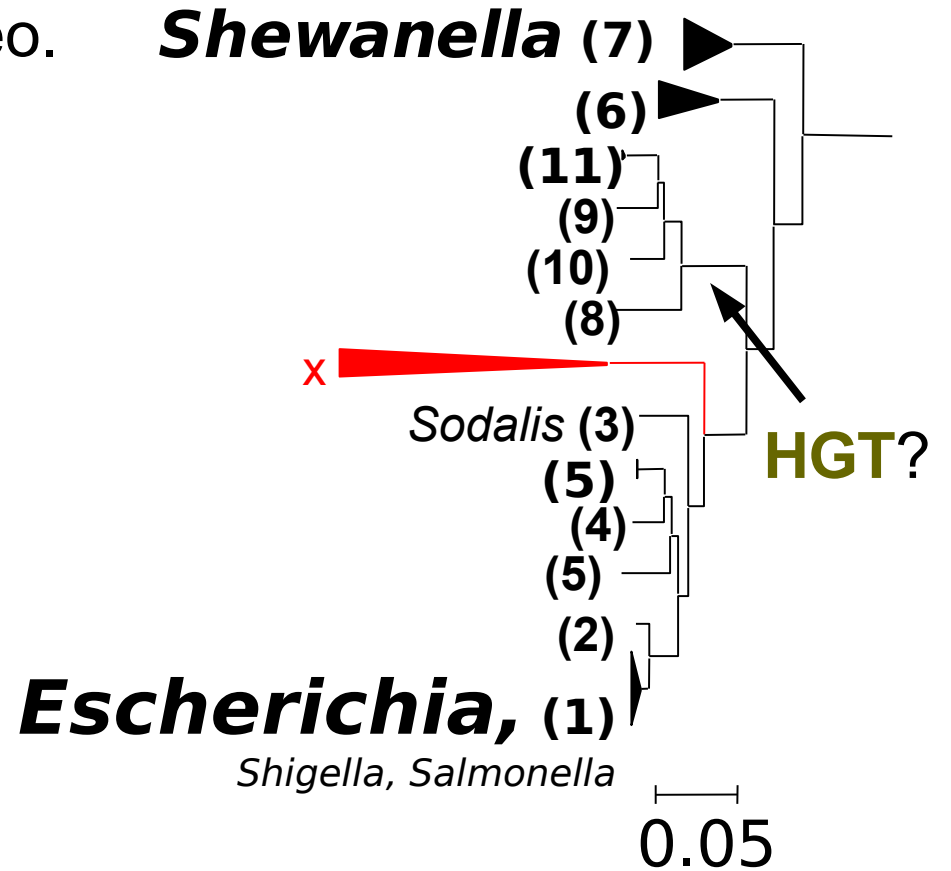
- Transcription factors (TF) have complex histories
 - Rampant transfer (not duplication)
 - “Orthologs” are problematic
 - Annotations are usually incorrect
 - “Neighbor regulation”
 - driven by horizontal gene transfer, aids annotation
 - Global regulators are more conserved
 - but we can predict little about other divisions
- Regulatory interactions not highly conserved

Vertical Inheritance of Global Regulators in *E. coli*

Gene tree for *crp*



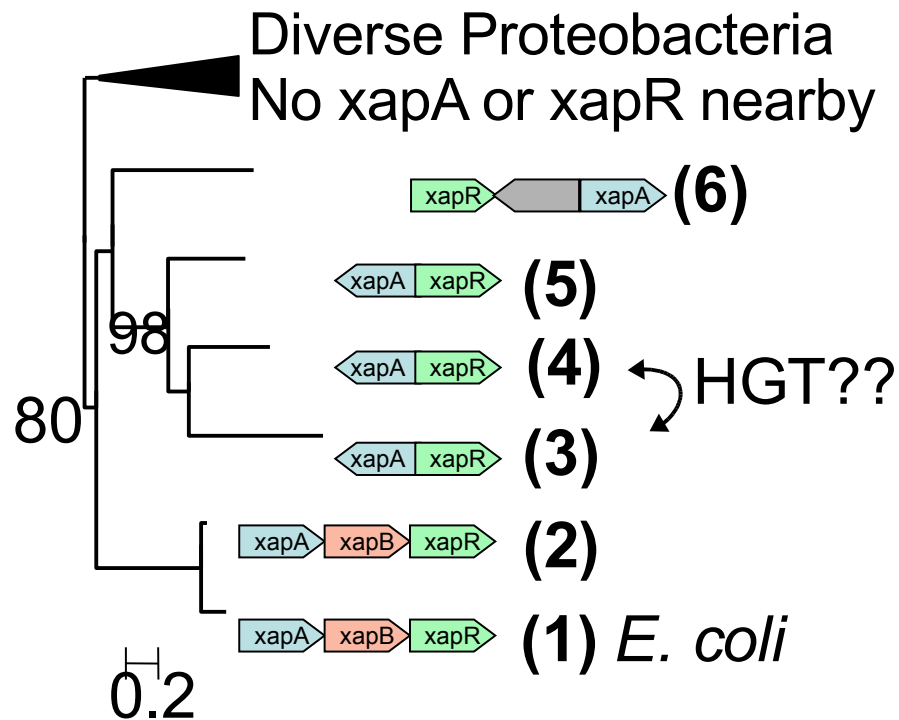
Distribution of *crp*



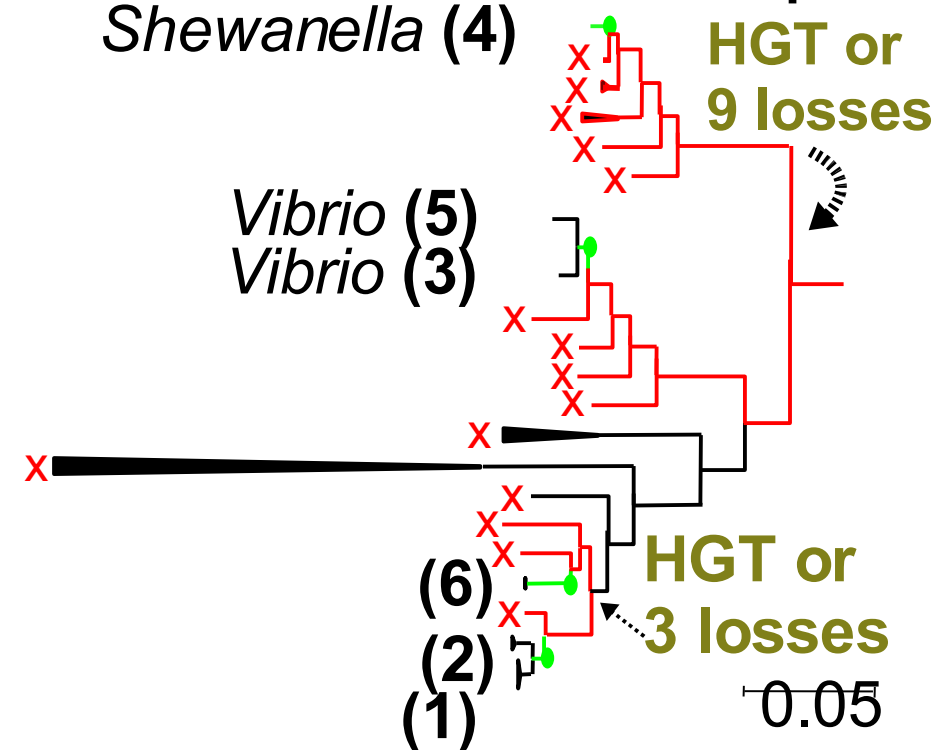
17/20 top global regulators are native

Complex Histories of Neighbor Regulators in *E. coli*

Gene tree for xapR



Distribution of xapR

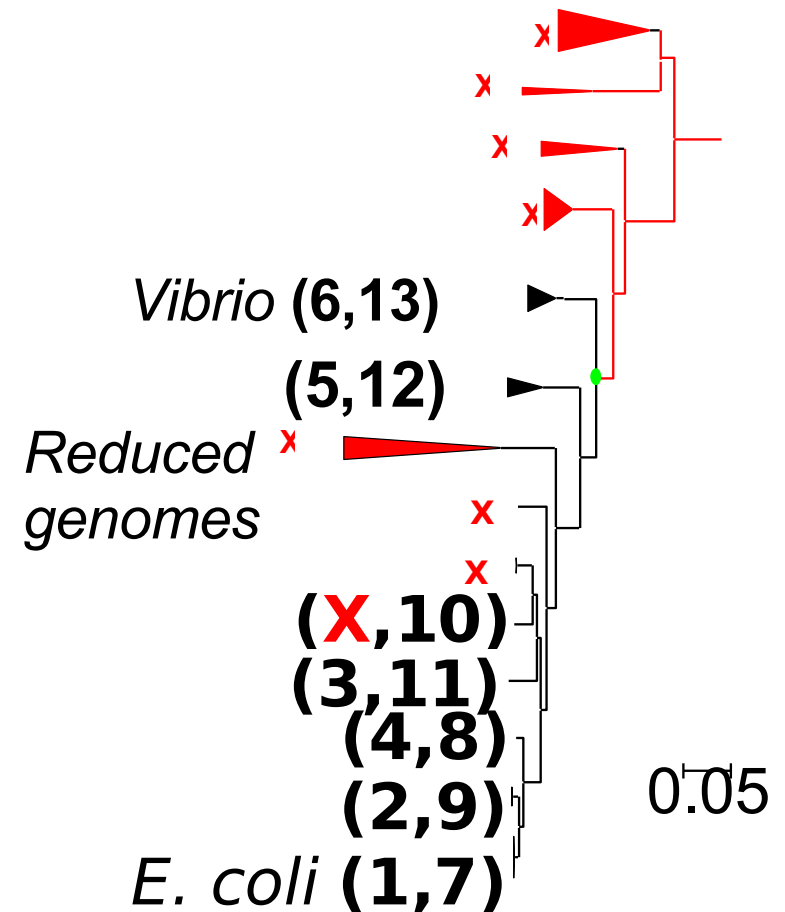
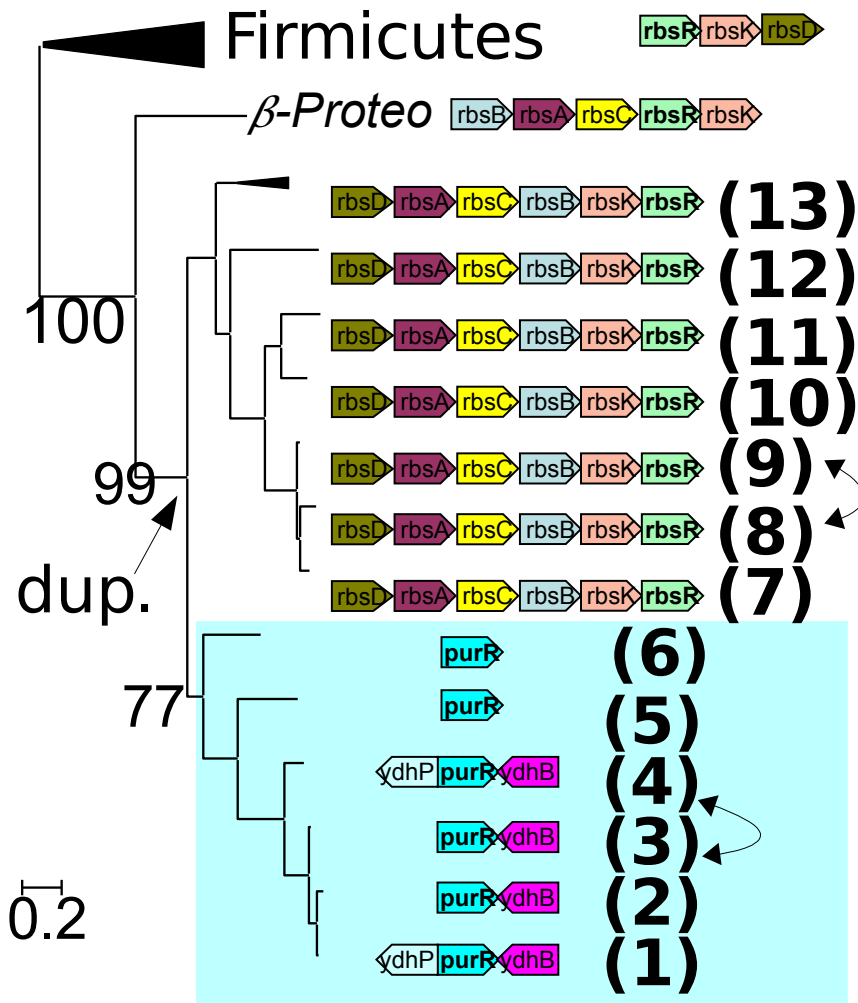


- Co-transfer: ~60% of neighbor regulators, 45% of putative regulators => predictions
- Repeated HGT: ~40% of neighbor reg.

Duplication of rbsR/purR

Gene tree for rbsR, purR

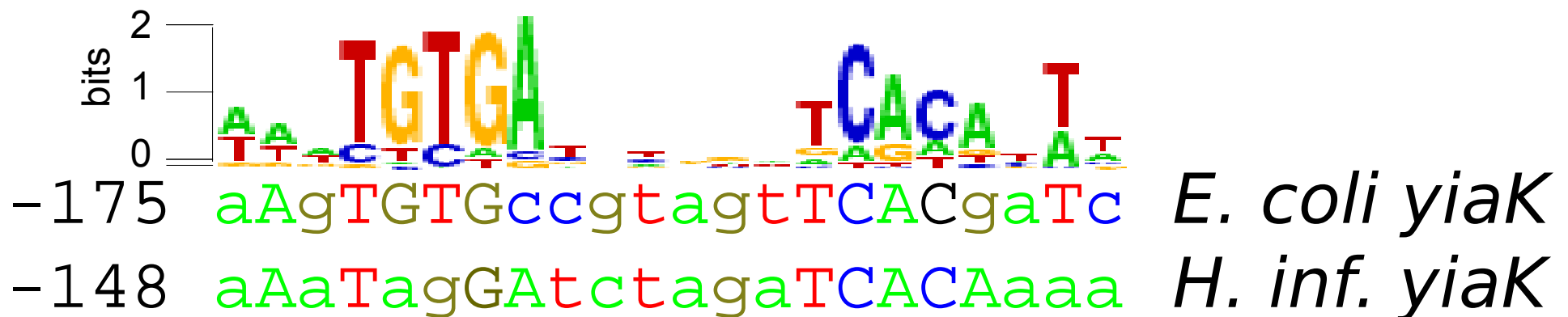
Distribution of rbsR, purR



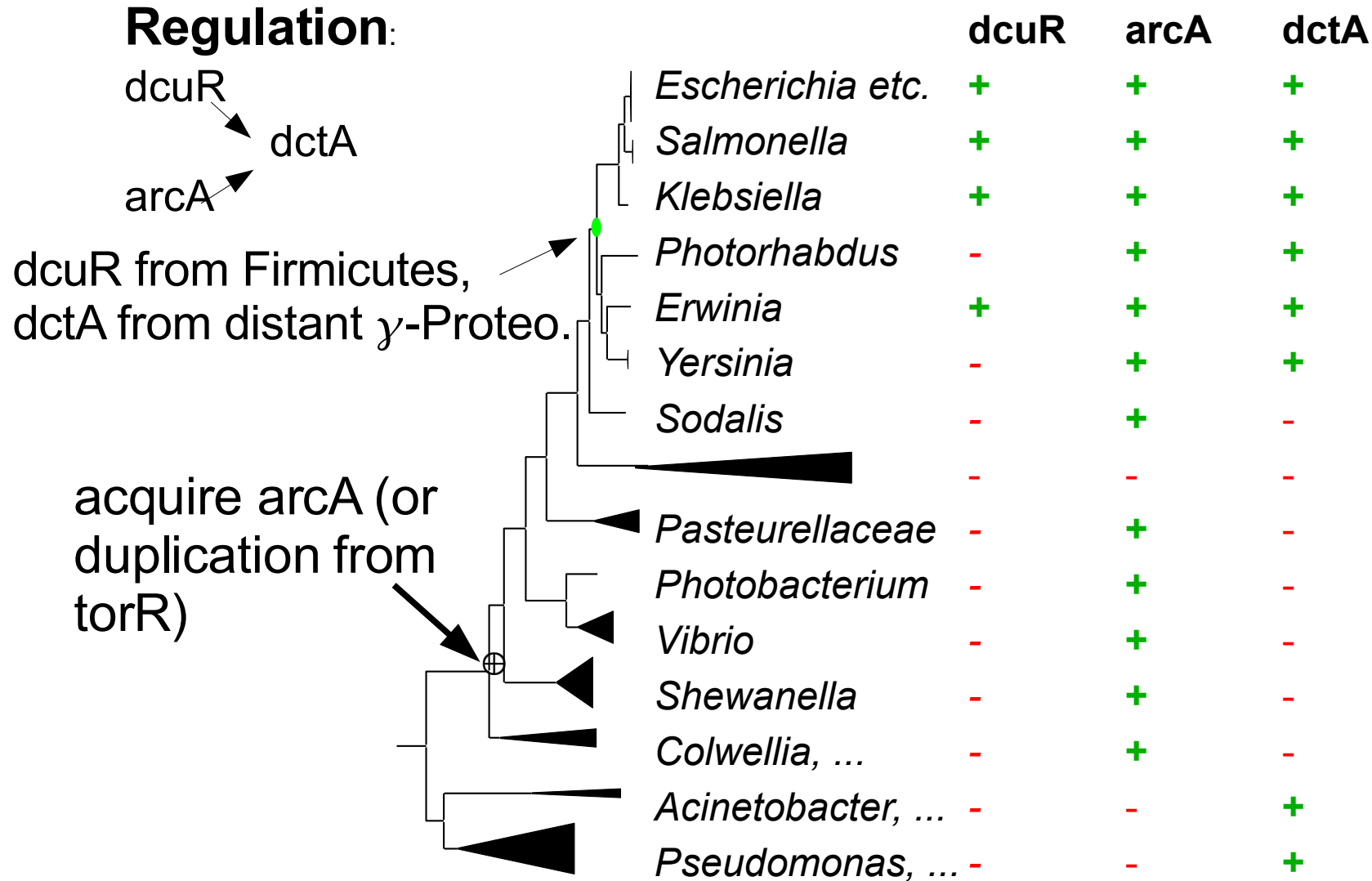
- Dups are rare (13% of *E. coli* TFs)
- Non-overlapping functions (~half of dups)

Sources of the CRP Regulon

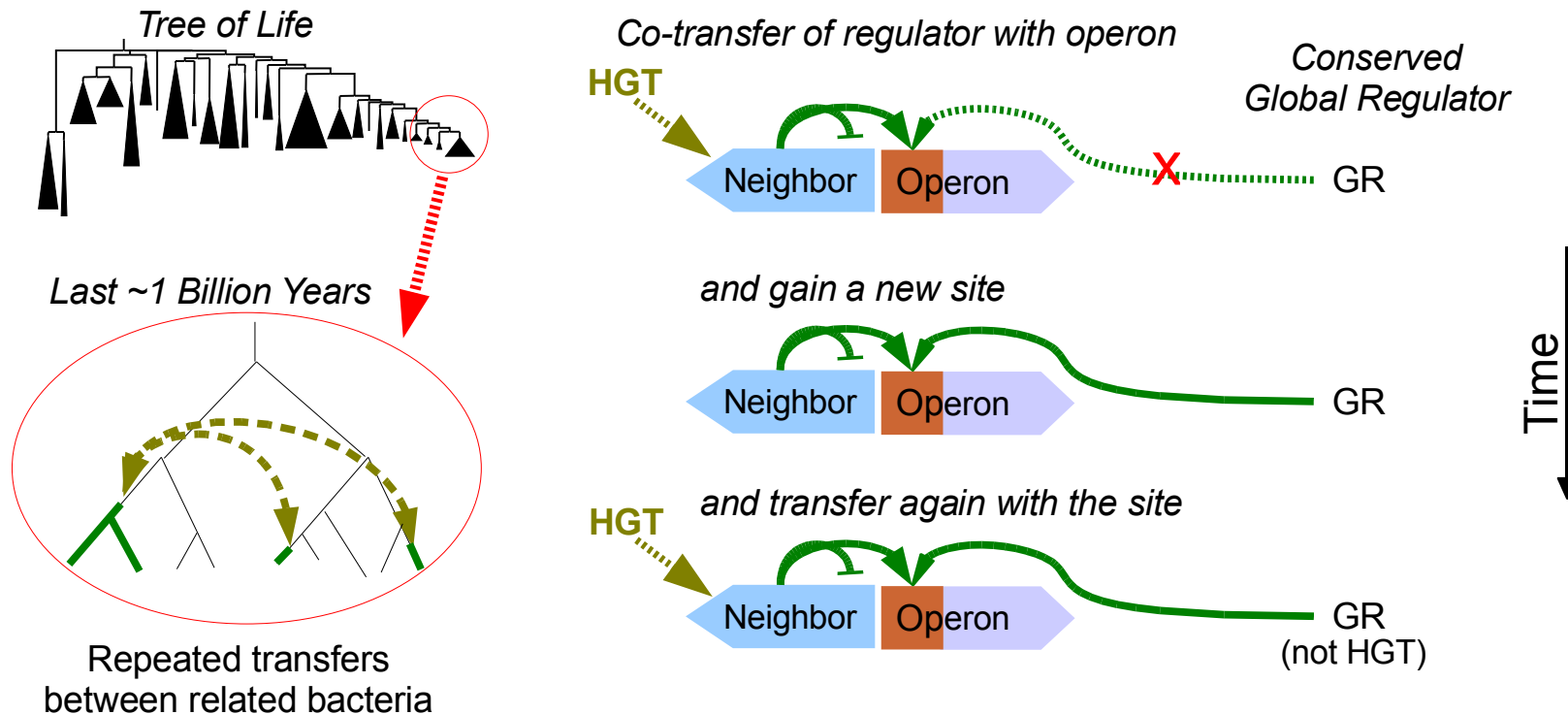
- From distant bacteria w/o CRP (~80%)
- From related bacteria with CRP (~20%)
 - CRP site conserved across HGT in 4/12
- Sites usually not conserved across HGT (6/20 for global regulators)
 - except for co-transfer (presumably)



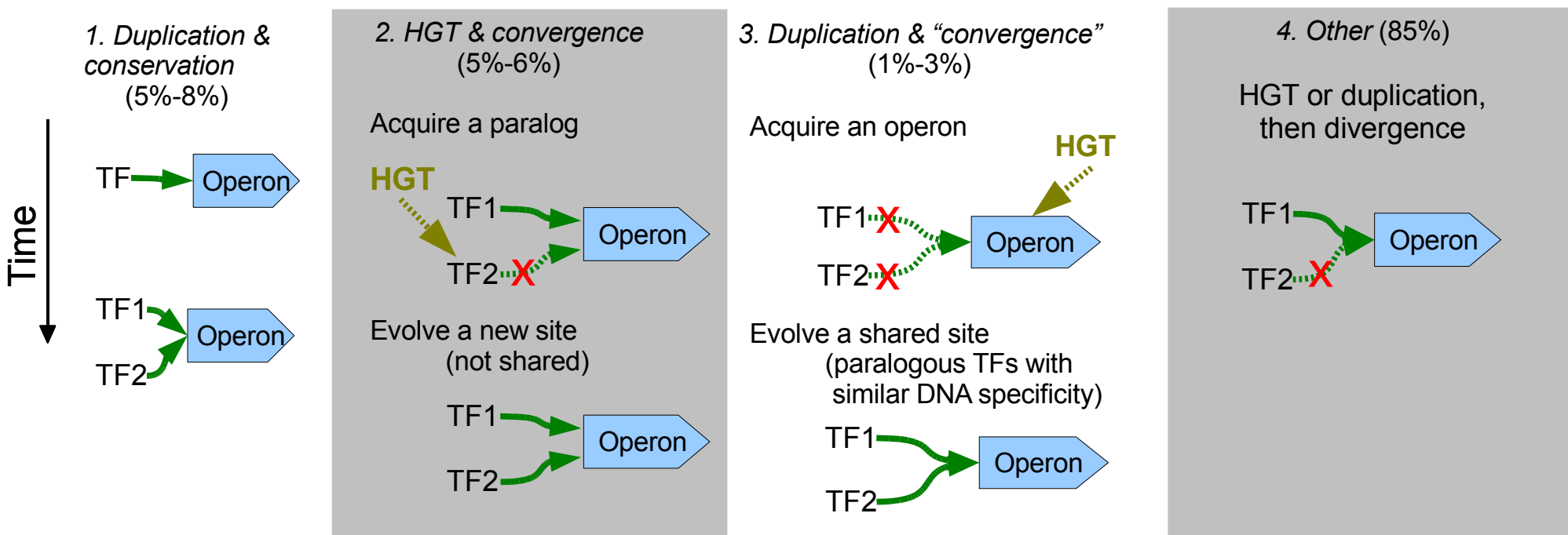
Apparent Evolution of Regulation by Duplication is Convergent



(A) Niche-Specific Neighbor Regulators vs. Conserved Global Regulators



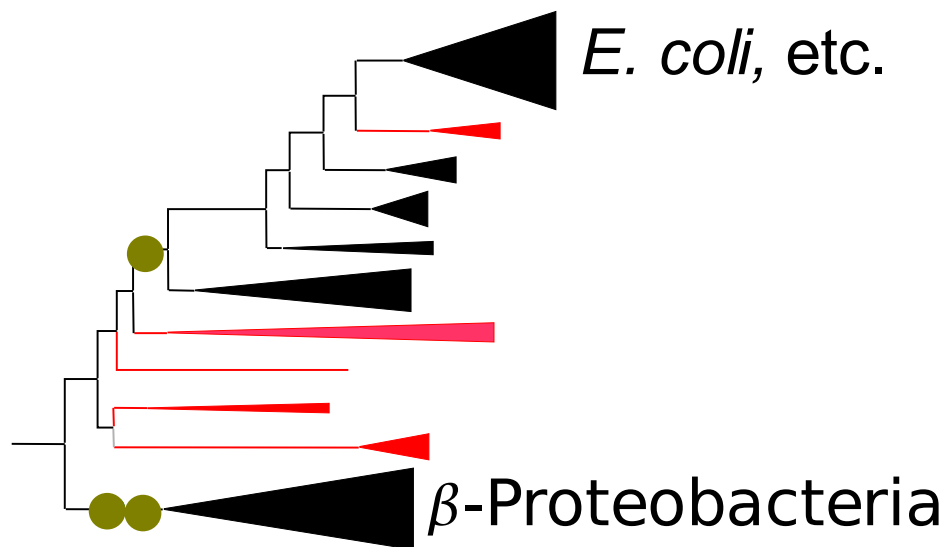
(B) Rapid & Convergent Evolution of Regulatory Interactions



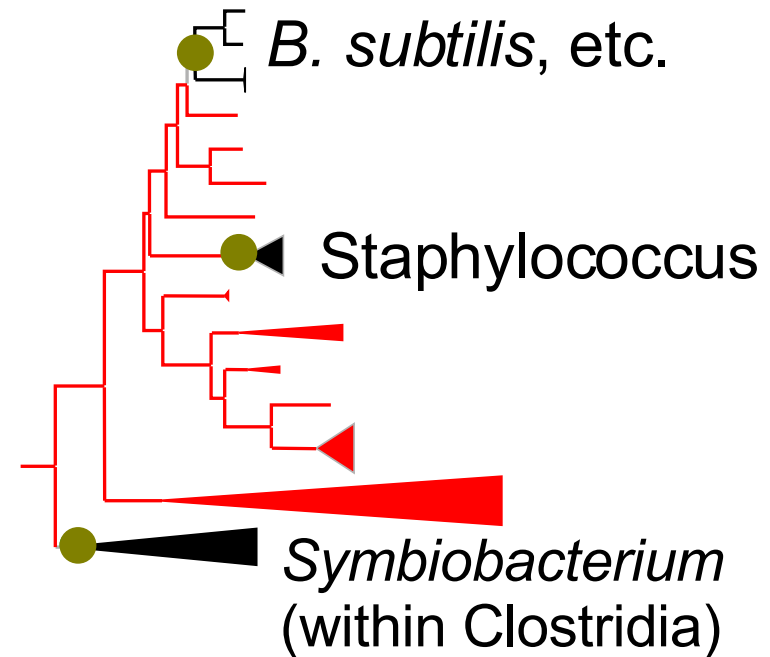
BBHs of TFs Have Different Functions

- Different pathways & stimuli
 - *E. coli* *betI*: choline -> osmotic stress
 - *B. subtilis* *pksA*: polyketide synthase

***betI*: HGT or 3 losses**



***pksA*: 2 HGT or >5 losses**



17/26 different functions between *E. coli*, *B. subtilis*

9/20 different between *E. coli* and other divisions of Proteobacteria