Correlation between signal transduction domains and habitats in cyanobacteria

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1 Introduction

In living systems, the control of biological function occurs at the systematic, cellular and molecular levels. Such control mechanisms are often coupled with signal transductions that detect environmental changes and trigger the relevant components of the regulatory machinery, resulting in specific cellular responses. We considered that the diversity and evolution of signal transduction systems are influenced by habitat. Cyanobacteria was selected as our analysis model, and we investigated the correlation between habitats and signal transduction systems.

Cyanobacteria are a diverse group of prokaryotes known also as blue-green algae. They are either unicellular or filamentous, and perform plant-type oxygen-evolving photosynthesis. They are known to inhabit a variety of sea and freshwater habitats, and show many responses to changes in milieu exterior. Various signal transduction pathways in cyanobacteria have been investigated including light, pH, temperature, redox and nitrogen sensing systems [1]. Recently many cyanobacterial genome projects are ongoing, making available many genome sequences for analysis. Here we present results of the investigation into the correlation between habitats and evolution of signal transduction domains.

2 Results and Discussion

We used the hmmpfam (Pfam_ls version 14.0) program to search 14 cyanobacterial genomes (Table 1) and obtained 2016 Pfam domains. Then we used Manhattan distance hierarchical clustering and selected the result of the clustering analysis based on habitat (seawater or freshwater). Our results show interesting differences in signal transduction-related domains.

Table 1 Cyanobacteria strains used in this study.

species	abbr.	habitat	No. of ORF	No. of Pfam dmain
Nostoc punctiforme ATCC29133	npu	w	6873	5997
Anabaena variabilis	ava	w	6750	5083
Anabaena sp. PCC7120	ana	w	6129	5052
Gloeobacter violaceus PCC7421	gvi	w	4430	3833
Synechocystis sp. PCC6803	syn	w	3264	3142
Synechococcus sp. PCC6301	syc	w	2525	2475
Synechococcus elongatus PCC7942	sel	w	2876	2516
Thermosynechococcus elongatus BP-1	tel	w	2475	2452
Prochlorococcus marinus MED4	pmm	s	1712	1560
Prochlorococcus marinus SS120	pma	s	1882	1609
Prochlorococcus marinus MIT9313	pmt	s	2265	1933
Synechococcus sp. WH8102	syw	s	2517	2066
Crocosphaera watsonii WH8501	cwa	s	6751	3759
Trichodesmium erythraeum	ter	s	7713	3462

habitat) w, freshwater; s, seawater.

We focus on four domains: GAF (PF01590), PAS (PF00989), HisKA (PF00512) and Response_reg (PF00072). These domains function as external sensory domains [2] and two-component signal transduction systems in bacteria [3]. The number of domains was plotted against the number of ORFs in each species (Fig. 1A-D). These results show that the domain number increased in proportion to the ORF number. Interestingly, an approximately three-fold increase in the number of domains were observed in freshwater cyanobacteria compared to seawater species. Furthermore, we counted the kinds of transcriptional regulator (TR) domains that were part of the output in the signal cascade (Fig. 1E). This result also indicates that the number of TR domains of freshwater species is higher than that of seawater species.
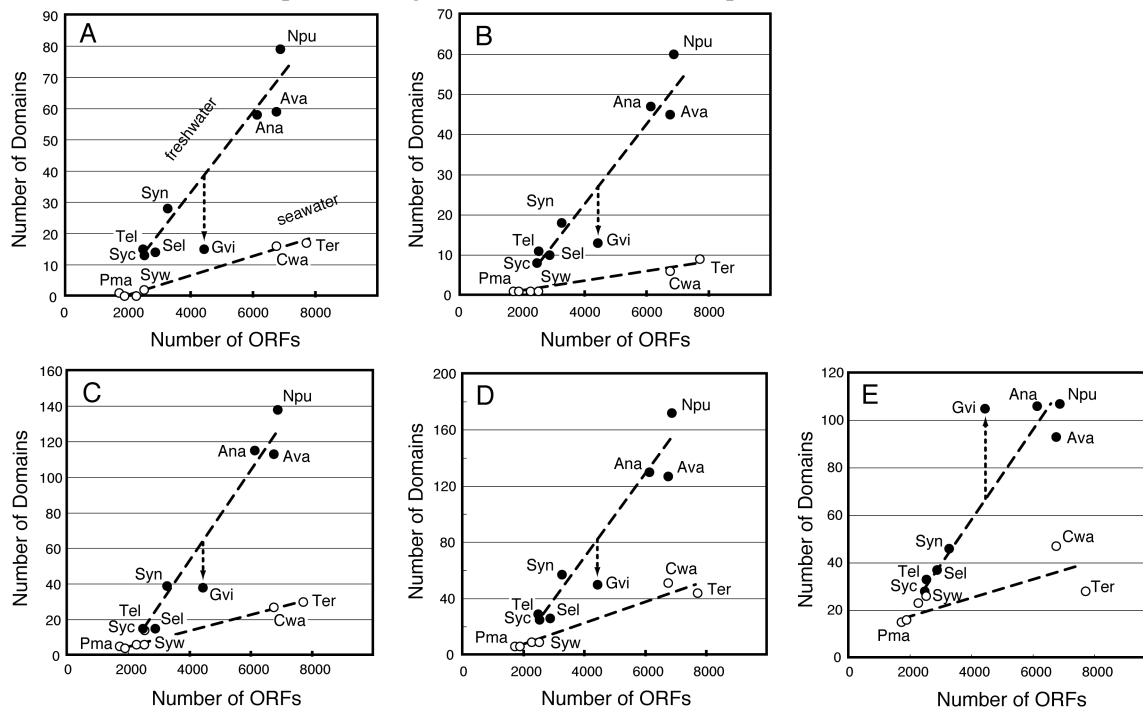

Figure 1: Relationship between the number of signal domains and genome size. Open circles indicate seawater species and closed circles indicate freshwater species. A) GAF, B) PAS, C) HisKA, D) Response_reg, E) Transcriptional regulator. "Transcriptional regulator" includes 20 transcription-related Pfam domains (GerE, HTH_8, Trans_reg_C, LytTr_DNA_binding, HSF-type_DNA_binding, HTH_1, CRP, FUR, HTH_5, MerR, GntR, PadR, DeoR, HTH_AraC, TetR_N, PemK, LexA, PhoU, AsnC_trans_reg). Arrows indicate shifts in the number of the domains in *Gloeobacter*.

These results show a significant positive correlation between habitats and functional domains of signaling pathways in cyanobacteria. Freshwater species probably developed signal transduction domains to adapt to external environmental changes due to the fact that freshwater conditions tend to change more than seawater. Surprisingly, *Gloeobacter*, exceptionally presents an opposite trend to that expected by comparison to other freshwater species. GAF, PAS, HisKA and Response_reg domains are lower, and TR domains are higher than other freshwater species. This has led to speculation that *Gloeobacter* is able to adapt to environmental stress, or this may be related to the ancestral characteristics of *Gloeobacter*, which requires further analysis.

References

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