**Genomic traits associated with transcription and *in situ* growth rates of soil bacteria during rewetting.**

**OR**

**Growth of soil bacteria during rewetting is related to genomic traits.**

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ABSTRACT

Genomic traits are informative metrics for assessing life-strategies of soil microorganisms; however, their relationship to growth remains unclear. In soil bacteria, traits such as codon usage bias and genome size have been linked to growth, yet often through indirect measurements or modeling approaches. Here, we utilize metagenome-assembled genomes in combination with metatranscriptomics and 18O-water stable isotope probing to track traits associated with the activity and growth of soil microorganisms over the course of one week following rewetting after a prolonged dry period. One week after rewetting, we observed higher growth rates in bacteria with smaller genomes, indicating that reduced genome size may play an important role in bacterial growth in response to sudden pulses of nutrients. However, we found that the predominant trait of fast-growing bacterial taxa was high levels of codon bias in ribosomal protein genes and lower GC content. Similarly, we found that high levels of codon bias corresponded to higher upregulation of ribosomal protein genes. Cheaper nucleotides were more common at synonymous sites in fast-transcribing taxa, and weakly related to faster growth. Together, these results provide *in situ* evidence for the influence of genomic characteristics on growth rate and transcription, and provide insight into the selection of these characteristics in soil bacteria.

INTRODUCTION

Rewetting represents an ecologically important phenomenon where traits associated with growth and activity may play an important role for stabilizing soil carbon. In ecosystems characterized by dry and wet seasons, the first rain event following the dry season results in the rapid mineralization of soil carbon (known as the Birch Effect) (1), which can account for a large portion of the annual soil respiration (2). The rapid stimulation of activity is driven by both the release of water stress as well as an influx in the bioavailability of carbon compounds sourced from osmolytes (3–5), microbial necromass (6, 7), slaking of microaggregates (8), and increased connectivity in the soil matrix (9, 10). The microbial response to rewetting therefore has important consequences for the fate of soil organic carbon; however, we lack an understanding of which traits control the growth and activity of this response.

Trait-based frameworks have long-been used in ecology to help understand complex community structures (11, 12), and this approach has naturally has gained considerable attention in microbial ecology (13, 14), where advancements in sequencing technology have greatly expanded the ability to probe previously unexplored microbial community structures. Traits help uncover the evolutionary forces which dictate when and how traits emerge (15), as well as serve as valuable metrics for assessing community dynamics across scales (16, 17) and with ecosystem function (14). Traits associated with growth are of particular importance, as growth is often central in life-strategy frameworks (14, 18, 19), functional metrics such as carbon use efficiency (20), and understanding changing community dynamics.

Trait-based analyses using genomic data can generally be separated intro two broad categories: functional traits (those which describe specific function) and genomic traits (those which do not describe a specific function; e.g., GC-%, genome size, codon usage, etc.). Functional traits are often observed through functional gene composition and the expression of these genes under a specific set of environmental conditions. During growth, expression of specific genes varies considerably depending on function (21) and environmental constraints (22). Ribosomal genes are highly upregulated during growth, and the number of rRNA gene copies in a genome increases with maximum growth rate. Although the link between rRNA levels and both growth (cite) and activity (23) are inconsistent, the tendency for fast-growing bacteria to have a greater number of rRNA gene copies is a useful trait dimension used in several trait-based frameworks in microbial ecology (18, 19, 24). Although other genes have been shown to be associated with growth, this is often under a specific set of conditions that could favor specific nutrient acquisition strategies or metabolic pathways, and therefore might not be predictive outside of that environment.

However, genomic traits (such as genome size, nucleotide frequency, and codon usage), may provide more generalized metrics that could be compared across systems. For example, codon usage has also been indicated as a strong determinant of both transcription and growth rate. A high alignment of gene codon frequencies to the anticodons of the tRNA pool increases the rate of both transcription and translation (25)—commonly referred to as codon optimization. The level of codon optimization of a transcript has important consequences for translation; affecting the rate of elongation, protein folding, initiation, and termination (26–28). Codon usage is also a strong determinant of mRNA abundance, as a high abundance of optimized codons generally increases mRNA stability (29, 30) and has also been shown to be independently related to higher levels of transcription (31, 32). Codon bias describes codon redundancy in the genetic code for a particular gene or genome, and generally correlates to the degree of codon optimization (33). High levels of codon bias in ribosomal proteins is associated with rapid growth in bacteria (34, 35) and has been increasingly used as a predictor of maximum growth rate (36, 37).

Outside of an intrinsic relationship between GC content and codon usage (25), there appears to be no direct relationship between doubling time and GC content in prokaryotes (38), and the link between GC content and growth in soil bacteria specifically remains unclear. The cost of nucleotide synthesis has been shown to influence transcription, where rapidly transcribed genes often use cheaper nucleotides at synonymous sites to reduce the cost of transcription, but more expensive nucleotides at nonsynonymous sites (39)—as there is an inverse relationship between nucleotide cost of codons and the cost of their encoded amino acid.

Genome size is also thought to influence growth; however, the relationship is less clear than codon usage or rRNA copy number. In oligotrophic marine environments, extremely small genomes are thought to arise in response to nutrient limitation to curb the cost of reproduction (termed genomic streamlining; 30), and often have slower growth rates than copiotrophs with larger genomes (18). Although streamlined genomes have been documented in soils (41), the majority of soil bacterial genomes tend to be large relative to other systems (42)—a potential result of the increased metabolic diversity required to utilize a complex substrate (43). It’s been hypothesized that these large genomes might come at the expense of growth rate (44), as the increased energy required for reproduction in large genomes may slow growth. However, the evidence of the relationship between genome size and growth rate in soil bacteria is mixed (45, 46), and requires further study.

In soils, a major hurdle in assessing how traits relate to growth rate has been our inability to effectively measure these traits ­*in situ*. Much of the work linking genomic traits to growth in soils has been conducted using isolate data from databases where the growth rate is often assessed from culture. It has been shown that traits associated with growth of microbes on media might not translate to free-living microbes in their natural environments (46), making it difficult to rely on these trends when assessing the functional potential of soil bacteria. Further, it is unclear how these traits translate to growth during real-world phenomena. Recent methodological and technological advancements have created new opportunities to track the growth of microbes *in situ*. Quantitative stable isotope probing (qSIP) uses the incorporation of added stables isotopes into DNA to track the growth rate of microbes based on sequence (47). This approach has provided valuable insights into metagenomic features and metagenome-assembled genomes (MAGs) associated with growth (7, 48, 49), and shows promise for linking measured microbial traits and growth. In this study, we pair metagenomic, metatranscriptomic, and qSIP data to assess how genomic traits are associated with activity and growth during the rewetting of dry soil at the end of the dry season in a Mediterranean grassland. Specifically, we investigate how traits such as genome size, nucleotide selection, codon usage, and ribosomal protein gene frequency relate to growth and transcription.

METHODS

The field study was located at Hopland Extension and Research Center (HERC), Hopland, California, USA (39.00092, -123.07962), which resides on the ancestral home of the Shóqowa and Hopland people. The region has a Mediterranean climate, with warm dry summers and cool wet winters. The field site was in a field dominated by *Avena barbata* (wild oat grass). This study consisted of 16 plots 3.24 m2 in a randomized block design across X. Rain out shelters were constructed around each plot, either allowing full or 50% precipitation. A full description of the field experimental set-up can be found in *[Rina’s future paper]*

Soils were collected in August 2018 before the first rain event at the end of the dry season. At the time of collection the soil gravimetric water content was approximately 3%. Soil was taken from 8 randomly selected plots (4 full and 4 reduced precipitation) with 0-15 cm cores. Samples were transported to Lawrence Livermore National Laboratory where they were pooled by plot, run through a 2 mm sieve, and picked of roots and large debris.

*Wet-up experiment*

Details of the H218O labeling can be found in Nicolas et al., 2022 and Sieradzki et al., 2022. Soils from each of the 4 plots were separated into 12 chambers containing 5 g of soil each, for 48 samples in total. Soils were brought to 22% gravimetric water content either with natural abundance water or with 98-at% H218O. A pair of labeled and unlabeled samples from each plot were destructively harvested at 0, 3, 24, 48, 72, and 168 h post wet-up. Samples were immediately frozen in liquid-N2 and stored in a -80°C freezer.

*Metagenomic qSIP*

A full description of the DNA extraction, sequencing, assembly, binning, and qSIP calculations can be found in Sieradzki et al., 2022. Briefly, DNA was extracted in triplicate using a phenol chloroform extraction and then pooled. Samples were then spun on an ultracentrifuge in a cesium chloride solution to create a density gradient. The contents of the ultracentrifuge tube were then separated into 36 fractions, each of which was assessed for DNA density. Fractions were combined into 5 groups along the density gradient, purified and concentrated, and then sequenced on an Illumina Novaseq platform.

Adapters were trimmed and reads were QC filtered using bbduk (50) and Sickle (51). QC filtered reads were assembled into contigs using MEGAHIT (v1.2.9; (52), binned with MaxBin 2.0 (53) and MetaBAT2 (54), and refined with MetaWrap (55). We combined this set of MAGs with another set binned from a study at a nearby site at HERC (48) and dereplicated MAGs using dRep (56). Reads from each fraction were then mapped against the set of MAGs using BBMap (50). DRAM (57) was used to identify open reading frames (ORFs) using Prodigal (58) and annotate functional genes against the KEGG database (59).

*RNA Extraction and sequencing*

Since no isotopic work was conducted with the RNA samples, we randomly selected 4 samples from each precipitation treatment to track RNA transcription at all timepoints. RNA was extracted from soils using a RNeasy PowerSoil Total RNA kit (Qiagen) according to manufacturer instructions. Extracted RNA was treated with RNase-free DNase (Qiagen) and stored at -80°C. RNA concentration was determined using a Qubit fluorometer (Invitrogen, Carlsbad, CA, USA) and quality was assessed using a Nanodrop One Spectrophotometer (Thermo Scientific Invitrogen). Samples were sent to the Joint Genome Institute (JGI; Berkeley, California, USA), for sequencing. Paired-end 2 x 151 bp libraries were sequenced on an Illumina NovaSeq platform. Metatranscriptomes were run through the JGI Integrated Microbial Genomes (IMG) pipeline v.5.1.5 (60) and can be found under the GOLD project ID Gp0612223. Although IMG assemblies are not included in this analysis, a more detailed description can be found in the data release (DOI: and citation).

*Metatranscriptome analysis*

Raw reads were downloaded from the JGI genome portal in September 2022. Reads were QC filtered using bbduk (50) and Sickle (51). BBmap was then used to map QC filtered reads to a concatenated reference mag file (minid=0.95). FeatureCounts (61) was then used to extract the number of reads mapped to genes identified by DRAM. Expression and normalization values of mapped transcripts for each annotated gene (excluding rRNA genes) were generated using DESeq2 (62). Nonannotated genes were not included in the normalization, as some of these may represent rRNA genes—the abundance of which would be representative of the efficiency of rRNA depletion, as opposed to any biologically meaningful mechanism.

*Genomic traits*

Genome size was calculated for medium to high quality mags by multiplying the total base pairs assembled by the completeness of the genome. For each gene in each MAG we calculated the nucleotide frequencies and effective number of codons considering the genomic background nucleotide frequency (ENC’), as described by *Novembre 2002* (63). We also calculated the ENC’ of the ribosomal proteins, which was used to calculate ΔENC’ (35):

Where ENC’all is the ENC’ for the whole genome, and ENC’ribo is the ENC’ of the ribosomal protein genes. Higher ΔENC’ values represent greater codon bias in ribosomal protein genes.

Nucleotide frequencies and skews were determined at synonymous and non-synonymous substitution sites on ribosomal protein genes according to nucleotide degeneracy detailed in Chen et al. 2016. Synonymous site nucleotide frequencies were calculated from fourfold degenerative sites, and nonsynonymous frequencies from sites where any substitution would change the encoded amino acid. The cost of amino acid synthesis—measured at the total number of phosphate bonds used for synthesis—was derived from Akashi & Gojobori 2002 (64).

*Analysis and model selection*

MAGs were grouped by transcriptional response according to when each MAG was most transcriptionally active, as measured by the total number of upregulated genes. We divided these responses into 4 groups: early responders (most active 3 h post wet-up), middle responders (most active 24, 48, 72 h), late responders (168 h), and sensitive (down-regulated post wet-up). Differences in genomic traits between transcriptional response groups were determined using an analysis of variance (ANOVA). Tukey’s HSD was used for pairwise comparison between groups. Relationships between traits and growth rates were determined using multiple linear regression. Model comparison was conducted using Akaike information criteria (AIC)—with a threshold of -Δ 4 indicating an improvement of a model with the addition of a parameter. All statistical analyses were conducted in R version 4.2.1 (65) and visualized with the ggplot2 package (66).

RESULTS AND DISCUSSION

*Codon bias, GC content, and genome size*

A diagram of ribosome protein

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Description automatically generated with medium confidenceWe initially conducted model comparisons of traits most often associated with growth, specifically, codon bias, genome size, and GC content. R2 and AIC values indicated that ENC’ribo better predicted AFE values than ΔENC’ or genome ENC’. ENC’ribo predicted growth better than estimated genome size, GC content, or ribosomal GC content (Supplemental Table 1). This result—while not especially surprising considering the well-established link between codon usage and growth—shows that codon bias as a good predictor of growth even in complex soil microbial communities in response to a natural pulse phenomenon. Further, this result demonstrates that codon bias is crucial for wet-up responses. Although no broad-scale analysis of codon usage bias has been conducted in soils, previous work has found that in soils with lower C, higher pH, and less rainfall, there tends to be a higher redundancy in the codon usage in the bacterial population (67). High codon bias could be a fundamental life-strategy trait for soil communities subject to ephemeral water and nutrient supply, allowing for faster responses to pulse evens. This highlights the importance of codon usage as a critical trait-dimension when considering the adaptation of soil bacteria to changing precipitation regimes with climate change.

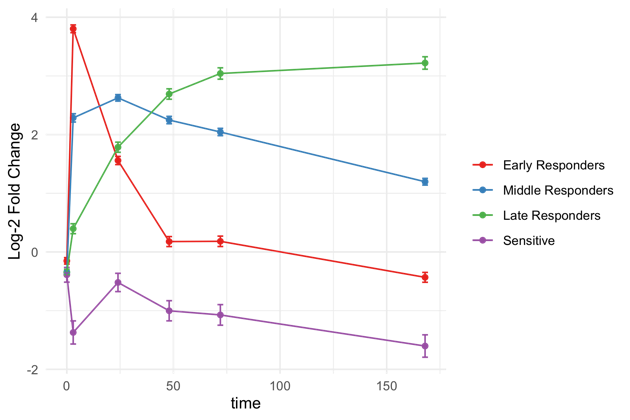
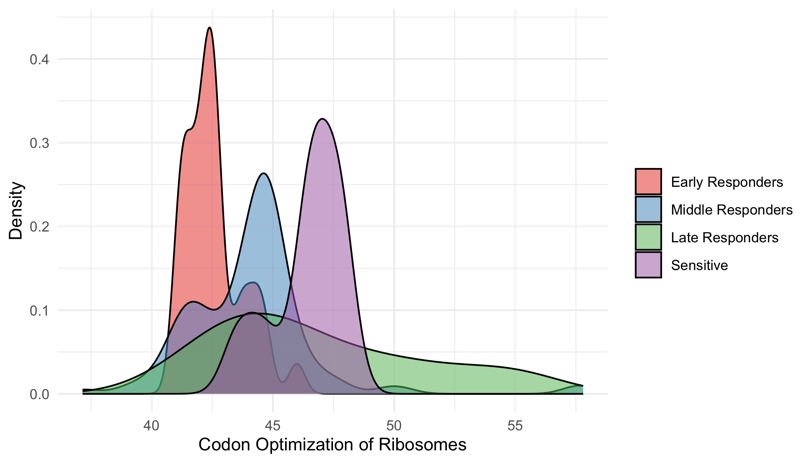
**a**

**b**

*Figure 1: Atom fraction excess (AFE) values as they related to effective number of codons in ribosomal protein genes (ENC`) and estimated genome size (Mbp) at each time point* ***(A)*** *as well as the GC content of ribosomal protein genes at 72 h post wet-up, with color indicating ENC values* ***(B).*** *Lower ENC values indicate a higher level of codon bias.*

Although ENC’ribo explained the most variance of any single metric, a multiple regression model incorporating ENC’ribo, genome size, and ribosomal GC content performed better than ENC’ribo alone (Supplemental Table 1, R2 = 0.49). GC content was negatively correlated with growth rate when codon bias has high (i.e., lower ENC`; Figure 1b). We believe this could be attributed to the higher metabolic cost of GC base pairs vs AT base pairs. We found that early growth at 24 h was predominantly driven by codon bias and GC content, and that the influence of genome size increased over time (Figure 1a). Smaller genomes were associated with higher growth rates at later timepoints, particularly 72 and 168 h post wet-up. Smaller genomes may reduce the cost of reproduction, and thus might be key in responding to sudden pulses of nutrients. This idea compliments the hypothesis that large genomes with metabolic diversity come at the expense of growth rate (44), and poses a trade-off where smaller genomes are therefore better adapted to pulse-driven systems where carbon is limited. This would also explain why smaller genomes are highly prevalent in arid and carbon poor soils (67–69), since the ability to quickly respond to the momentary availability of water and nutrients may be fundamental to survival and persistence.

The influence of codon bias was also observed in transcription. Where early responding taxa had a higher level of codon bias (Fig 2a), and a greater upregulation of ribosomal protein genes early on (Fig 2b). The peak time of transcription followed a logical pattern with growth response, where early transcribing taxa were represented more during early growth and late transcribing taxa were more often growing later (Supplemental Figure Xa); however, we did not find a strong relationship between the expression of ribosomal protein genes and growth rate (Supplemental Fig Xb). These results demonstrate that although the transcription of ribosomal proteins may be required for growth, they do not serve as a quantitative proxy for growth rate. This mirrors previous work indicating rRNA as a poor metric for activity (23) and highlights important limitations in the use of metatranscriptomics for quantitatively assessing certain metrics between organisms in microbial communities.



a

b

*Figure 2:* ***(A)*** *Codon usage bias of ribosomal protein genes colored by transcriptional response type.* ***(B)*** *Ribosomal protein gene expression over time, averaged by response type*

*Nucleotide selection*

Nucleotide cost was tied transcriptional response, were early responding organisms tended to have a higher AT and GC skew at synonymous sites for ribosomal protein genes (Fig 3 A&B). This is in line with results from Chen et al. (2016) (39), which showed that the lower cost U and C at nonsynonymous sites were associated with higher levels of gene transcription. This trend did not translate cleanly to growth rate. GC skew of synonymous substitutions on ribosomal protein genes was weakly negatively correlated to growth (R2 = 0.12, p < 0.01; Fig 3C) and AT skew was not significantly negatively correlated with growth (R2 = 0.01, p = 0.06; Fig 3D), further showing points of disconnect between those traits which impact transcription and those which more strongly influence growth.

There was no relationship between nonsynonymous nucleotide usage and transcription (Fig 3 A&B). We found a slight positive relationship between GC skew and growth (Fig. 3E), and a surprisingly positive relationship between AT skew and growth (Fig. 3F). This could potentially be reflecting the inverse relationship between nucleotide cost and amino acid cost. More expensive nucleotides tend to encode for less expensive amino acids (39), and this relationship could reflect this cost conservation. However, we did not find that amino acid cost is associated with growth (Supplemental Fig X). When we examined the amino acid composition as it relates to these nonsynonymous substitutions, we found that AT skew was most closely correlated with the abundance of lysine (encoded for by AAG and AAA)—yet it is unclear what specifically about lysine would be causing this relationship. Lysine is not notably cheaper to make and has elemental ratios similar to other amino acids. This relationship might therefore be due to features of the ribosomal protein structure, the analysis of which is beyond the scope of this study. Alternatively, the correlation could also be caused by correlations between AT skew and other genomic features, especially GC content (linear regression R2= X.XX). Further, the addition of nonsynonymous AT skew to the model outlined in Supplemental Table 1 did not explain much more variation as opposed to the base model.

A collage of diagrams

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*Figure 3: Nucleotide skew as it relates to transcriptional responses and growth rate. The synonymous and non-synonymous GC (****A****) and AT* ***(B)*** *skew by transcriptional response, with color indicating site-type. Growth rate as a function of synonymous nucleotide skew for GC-skew* ***(C)*** *and AT skew* ***(D)****, and nonsynonymous GC* ***(E)*** *and AT skew* ***(F)****.*

*Limitations and future directions*

These traits may be particularly relevant in pulse-driven systems, but it is still unknown how they may relate to growth in soils where water and nutrients are either less variable or more available. For example, the frequency of cycles of drying and rewetting are known to influence microbial community responses to rewetting . Although this may be tied to shifts in community composition, it does not preclude plasticity in the physiological response of individual taxa. More or less frequent rain events could potentially influence the response of these traits to rewetting events.

How genomic traits relate to growth in environments where change is gradual is also not well understood. A complete picture of the relationship between genomic traits and activity of soil bacteria requires assessing these relationships across environments and stimuli. Although the growth rates of soil bacteria under stable conditions is often difficult to measure—recent advancements in isotopic vapor labeling provide allow for the study the growth rates of bacteria without the addition of water or nutrients (70, 71) and provides a promising avenue to study growth in undisturbed environments.

It is also important to highlight the limitations of these traits for predicting growth and transcription. The most predictive traits combined only explained ~50% of the variance for growth. Together with the limited sample size and potential bias from metagenomic binning—it is unclear how much predictive power these traits might have for predicting growth in response to real world phenomena, and additional studies and data will clarify these relationships. This result—in conjunction with the fact that these traits may not correlate with growth in non-pulse-driven systems—should be carefully considered when drawing conclusions about growth potential of microbial communities.

*Conclusion*

These results highlight trait dimensions that correspond with growth rate and bacteria in soil microbial communities. Specifically, we found that fast growth was related to high codon usage bias, lower GC content, and smaller genome sizes. We also found that transcription was associated with nucleotide synthesis cost as well as codon usage bias. These relationships offer important perspective for examining the broad scale ecological distribution of these traits, as the importance of short-term responses may play a vital role in systems characterized by pulses of nutrient availability.

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