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Core Genome of Deinococcota Phylum from 72 Strains Across 40 Species Consist of Only One Gene, Beta Subunit of DNA-Directed RNA Polymerase

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Abstract

Deinococcota, or Deinococcus-Thermus, is a phylum of highly environmentally tolerant extremophiles with value in industrial applications and evolution studies. Phylogenetics using core genome is an important aspect of evolutionary studies. However, the core genome of Deinococcota phylum has not yet been identified. In this study, we report 6 species-specific core genomes of Deinococcota. However, the core genome of Deinococcota from 72 strains across 40 species consist of only one gene - beta subunit of DNA-directed RNA polymerase. This surprisingly small core genome may be the result of tolerance to diverse environments and may suggest that sequence similarity alone may not be sufficient enough to identify core genomes.

Introduction

Deinococcota [1], also known as Deinococcus-Thermus, is a phylum of highly environmentally tolerant extremophiles [2]. This includes *Deinococcus radiodurans* - first isolated by Anderson et al. 1950s [3] and is currently the most radioresistant micro-organism known [4] with the potential for extended outer space travel given the appropriate conditions [5], supporting the panspermia hypothesis [6]. Another notable member is *Thermus aquaticus*, isolated by Brock and Freeze in the 1960s [7], which is the source of the Taq DNA polymerase used in polymerase chain reactions [8, 9]. Hence, the evolution of extremophiles is of interest [10-12] as it may be central to the evolution of eukaryotes [13].

Phylogenetics is a crucial tool used to study evolution [14] and core genomes are important sources of sequence data for phylogenetics [15-17]. The core genome for a set of related genomes represents a set of orthologous genes within that set of related genomes [18], which may be from different strains of a species [19] or different species of a genus [20]. Hence, a core genome represents the intersection of the set of genomes under study. Recently, a study suggests that phylogenetic analysis requires the complete set of orthologs as phylogenies from single orthologs may differ from that of multiple single orthologs [21]. In this study, we aim to identify the core genome of Deinococcota from 72 strains of Deinococcota across 40 species using a taxonomy pruning approach where intermediate core genomes, such as species-specific core genomes were identified from strains, followed by core genome identification from species-specific core genomes. Using an E-value of more than 1E-5 in BLAST as the threshold for orthologs, only the beta subunit of

DNA-directed RNA polymerase is common between the 72 strains under study; thus, the core genome.

Materials and Methods

Complete coding sequences of 72 strains of Deinococcota across 40 species were downloaded from GenBank as FASTA files and used to identify the core genome of Deinococcota (see supplementary materials for details). For strains with more than one replicon, coding sequences from multiple replicons were concatenated into a single FASTA file. This resulted in only one FASTA file per strain. Due to the large number of source genomes, a taxonomy pruning approach was proposed. For example, several intermediate core genomes, such as species-specific core genomes, were first identified from strains. This was followed by core genome identification from species-specific core genomes. The procedure of identifying core genome by genome intersection was based on that of previous studies [22, 23] using NCBI BLAST [24] version 2.12.0, where the E-value of more than 1E-5 in BLASTN was used as the threshold for orthologs, which was consistent with that of recent studies on core genomics [18, 23, 25].

Results and Discussion

This study uses a taxonomy pruning approach where intermediate core genomes, such as species-specific core genomes, were identified from strains, which was followed by core genome identification from species-specific core genomes. The advantage of this approach over previous studies [18, 22, 23, 25] is the availability of intermediate core genomes, such as species-specific core genomes, which may have further applications. Using this approach (Figure 1), the following 6 species-specific core genomes were identified; namely, (a) *Deinococcus actinosclerus* consisting of 2877 genes, (b) *Deinococcus radiodurans* consisting of 3149 genes, (c) *Deinococcus wulumuqiensis* consisting of 2733 genes, (d) *Thermus antranikianii* consisting of 2082 genes, (e) *Thermus brockianus* consisting of 2192 genes, and (f) *Thermus thermophilus* consisting of 1803 genes.

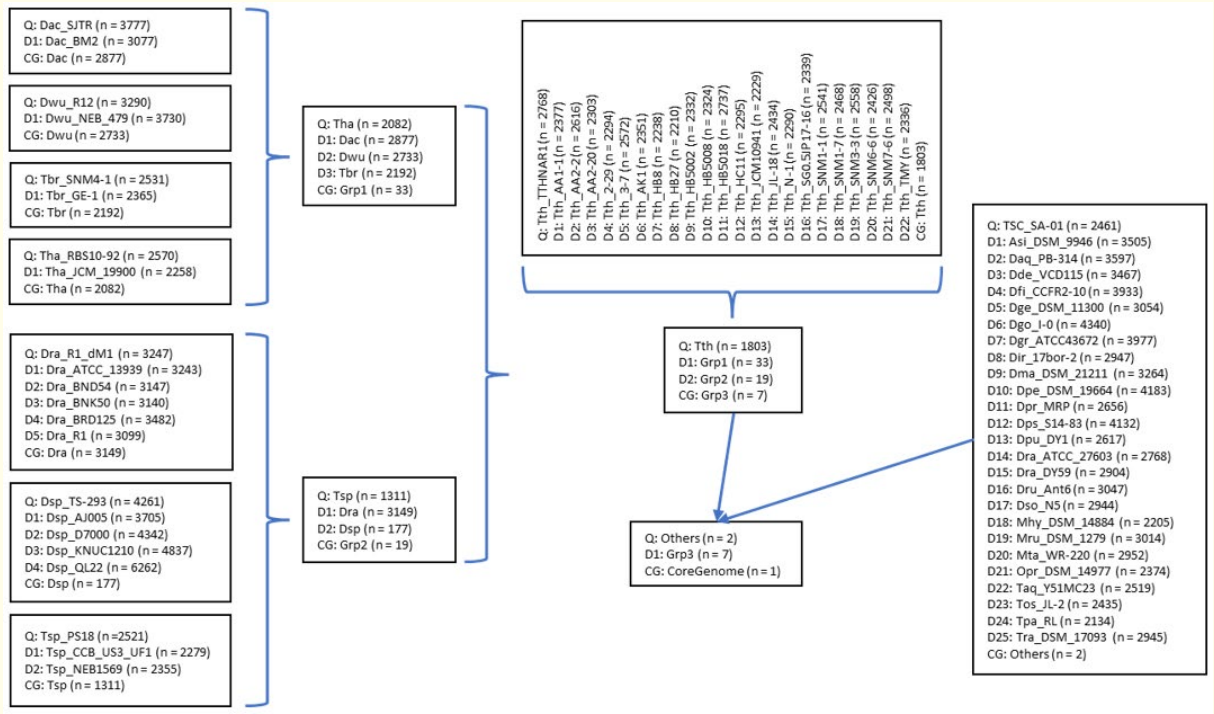

Figure 1: Taxonomy pruning approach to core genome identification via intermediate core genomes.

The following 6 species-specific core genomes were identified - (a) *Deinococcus actinosclerus* (Dac), (b) *Deinococcus radiodurans* (Dra), (c) *Deinococcus wulumuqiensis* (Dwu), (d) *Thermus antranikianii* (Tha), (e) *Thermus brockianus* (Tbr), and (f) *Thermus thermophilus* (Tth).

However, the identified core genome of *D. actinosclerus* (Dac), *D. wulumuqiensis* (Dwu), *T. antranikianii* (Tha), and *T. brockianus* (Tbr) consists of only 33 genes. More crucially, the identified core genome of 26 species with only 1 strain (Others) consists of only 2 genes. This resulted in the final identified core genome of Deinococcota phylum consisting of only 1 gene; namely, Beta subunit of DNA-directed RNA polymerase (Accession ADW21061.1).

This surprisingly small core genome may be the result of highly diverse environmental tolerance of this phylum [26, 27]. This is supported by findings from Jamandre et al. [28] showing high mitochondria sequence variations in different populations of flathead mullets. Rainey et al. [29] also shows a high diversity of Deinococcus species within a single soil sample. This is further supported by de Groot and Blanchard suggesting a high diversity in DNA repair and oxidative stress responses in radiation-resistant Deinococcus species [30]. More importantly, this also suggests that sequence similarity alone may not be a sufficient enough tool to identify core genomes, and additional methods may need to be considered.

Conclusion

Using a taxonomy pruning approach, we identified 6 species-specific core genomes of Deinococcota phylum. However, the core genome of Deinococcota phylum only consists of 1 gene - Beta subunit of DNA-directed RNA polymerase (Accession ADW21061.1). This may be the result of high environmental diversity of this phylum. In addition, this may suggest that sequence similarity alone may not be sufficient enough to identify core genomes.

Supplementary Materials

The sequences and identified core genomes can be downloaded at https://bit.ly/CG_Deinococcota. Supplementary material for this study can be downloaded at https://bit.ly/CG_Deinococcota_SM.

Conflict of Interest

The authors declare no conflict of interest.

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