Genome Announcement Publication

A genome announcement (GA) paper is a citable publication that ensures your NCBI/GenBank submissions are highlighted to the community in a wider research context. It is the best way to receive recognition for generating your genomic data. A GA paper should be written after GenBank submissions have been made and accessions generated, but before larger, primary research papers. These papers can cite your GA.

At GetGenome we collect metadata and provenance information from participants. Therefore, once you have generated your NCBI accessions, please do send them to us via email. Please do include the GG ID that corresponds to each deposit. Also please do send us drafts of your GA paper and we are always happy to review them and make suggestions.

Checklist

Before submission:

- ☐ Consider the implication of publishing – your DOI is forever – a permanent record.
- ☐ Draft your paper, send it to all authors at least one week before submission.
- ☐ Ensure you have submitted your sequence reads (SRA) and genome to NCBI/GenBank (you will need these accessions before you start your article submission)
- ☐ Create an account on Zenodo (https://zenodo.org/signup/).

During submission:

- ☐ Upload your paper as a **PDF**.
- ☐ *Ensure you link the GetGenome Community https://zenodo.org/communities/getgenome/ to your paper. To submit an **unpublished** record for review follow these instructions - https://help.zenodo.org/docs/share/submit-for-review/
- ☐ Copy and paste your abstract into the description box – it appears below your title on the publication page. It may help with searchability once the article is published.
- ☐ List your co-authors as **Creators**. See the paragraph from Zenodo below –

  "Creators/contributors: The full name has been split into *family name* and *given names*, and a new name type has been added to also support organisational names. Creators can now also have roles. The difference between creators and contributors is that creators are included in the citation, while contributors are not included".

* by submitting your article to the GetGenome Community page prior to submission you are effectively sending it for review by GetGenome. This is not a traditional peer review process but we will look over your paper. It should be in a publishable state before this point. A dialogue box will remind you that we (and you) can change the metadata of the paper before submission. We will not change any metadata unless there is a clear and obvious mistake or if you request it.

Title

Example: Whole-genome sequences of [number] [organism(s)] strains associated with [phenotype] isolated from [host] in [location]

[Author list] First Name1[1], Surname1[1]., First Name2[1], Surname2[1], First Name3[2], Surname3[2]

[1] Affiliation including department, institute and address.
[2] Affiliation including department, institute and address.

NOTE: No GetGenome staff should appear in the co-author list

Abstract

Key information within the abstract:

- What is/are the organism(s) sequenced?
- Why are they important (rationale for study / sequencing)? What is the unknown?
- How and from where were the organisms obtained?
- Any taxon classification conducted (e. g. 16S rRNA analysis)
- Key summary statistics for the genome(s) including:
    - Total size of the genome
    - Number of contigs the genome is assembled into
    - Contig N_{50}
    - GC content
- Final sentence highlighting the use of the study in the wider context.

  For example: "*These data will provide a useful resource for future studies into [Organism]...*"

Optional:

- *Genomic sequences were deposited in NCBI GenBank under the BioProject XYZ*

Introduction

Key information within the introduction:

- What is/are the organism(s) sequenced and why they are important to study?
- Statement of the challenge faced by stakeholder (pubic/researchers etc.).
- Use of genomic data in this field – What could the data be used to achieve?
- A statement of what you have done in this study.

Material and Methods

Bacterial Isolates

Where were your strains isolated from (environment, region, country)? Are they a part of an existing collection or donated by an individual, organisation or institute?

Mention any nomenclature previously assigned to these organisms.

Sequencing

As most projects will be processed via MicrobesNG protocols - https://microbesng.com/documents/39/Genome_Sequencing_Methods_V20231206.pdf

Important methods to report:

- Cell preparation and DNA processing was conducted following MicrobesNG (Birmingham, UK) strain submission procedures.

- Subsequent library preparation, DNA sequencing and bioinformatics was conducted by MicrobesNG, following in-house protocols.

- Genomic DNA libraries were prepared using the Nextera XT Library Prep Kit (Illumina, San Diego, USA) following the manufacturer's instructions with the following modifications: input DNA was increased 2-fold, and PCR elongation time increased to 45 seconds. Libraries were sequenced using the lllumina NovaSeq 6000 (Illumina, San Diego, USA) using a 250 bp paired-end protocol.

- Reads were adapter trimmed using Trimmomatic version 0.30 (Bolger et al., 2014) with a sliding window quality cutoff of Q15. *De novo* assembly was performed on samples using SPAdes version 3.7 (Bankevich et al., 2012), and contigs were annotated using Prokka 1.11 (Seemann, 2014).

Results

Trimmed sequence read data and genome assembly data of the xyz strains has been deposited in NCBI/GenBank under the BioProject XYZ.

A summary of the genomic features of xyz is listed in Table 1.

Summarize the following statistics both in tabular form and important features may also be written in a results paragraph:

- Organism (taxon classification)
- Host
- Genome size
- Number of contigs
- Contig N_{50}
- Mean coverage
- GC content
- BioSample IDs
- GenBank accession (Assembly)
- GenBank accession (Reads)

Table 1: Summary statistics of xyz strains isolated from [environment, region, country].

Acknowledgements

Since our incorporation in late 2022, we do not co-author on GA papers. We are grateful if you would consider mentioning the assistance we have offered via the acknowledgements. For example,

The sequencing of the bacterial strains was supported by GetGenome and The Sainsbury Laboratory, Norwich, UK, with support from the Gatsby Charitable Foundation and the Biotechnology and Biological Sciences Research Council (BBSRC).