Mycopathologia
https://doi.org/10.1007/s11046-019-00366-3

EDITORIAL

MycopathologiaGENOMES: The New 'Home' for the Publication of Fungal Genomes

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Received: 5 July 2019 / Accepted: 20 July 2019

Abstract The wider availability of information on genomes has become essential for future advances in fungal biology, pathogenesis and epidemiology, and for the discovery of new drugs and diagnostics. MycopathologiaGENOMES is designed for the rapid publication of new genomes of human and animal pathogenic fungi using a checklist-based, standardized format.

Keywords Pathogenic fungi · Genome sequence · Publication format

The generation of high-quality fungal genome sequences and their annotation remains a challenging but important mycological pursuit. While the global burden of fungal disease is increasingly recognized, many questions remain unanswered around the mechanisms of fungal pathogenesis and the clinical relevance of fungi as constituents of the human microbiome [1, 2]. Current shortfalls in the availability of high-quality fungal genomic data greatly restrict our study of fungal pathobiology, molecular epidemiology and metagenomics, which in turn impedes advances in fungal diagnostics, therapeutics and clinical mycology.

Genome-scale analysis of fungi lags significantly behind that of bacteria and viruses. This could be partly due to the larger and more complex fungal genomes and taxonomy [3, 4]. At the time of writing, prokaryotic (bacterial) entries in the National Center for Biotechnology and Information's 'Genomes' repository amount to more than fivefold that of fungi when cumulative megabases are considered. However, the true dichotomy of this figure is revealed when the number of database entries is considered: 821,234 prokaryotic (bacterial) entries to just 4727 fungi (a 174-fold difference). This disparity is recognized with efforts such as the 1000 fungal genomes project (http://1000.fungalgenomes.org) initiated in 2011 contributing significantly to the number of high-quality genomes available. The number of fungal genomes reported in the MycoCosm database currently stands above 1300 [5]. Availability of such high-quality genomes and their annotation allows powerful comparative analyses and advances the fields of molecular phylogenetics, mechanisms of fungal biology (sexual reproduction to virulence), secondary metabolite production and antifungal resistance

Handling Editor: Ferry Hagen.

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Published online: 10 August 2019

[6–11]. Still, most reports focus on the description of draft fungal genomes, while the description of completed high-quality genomes is progressing at a slower pace [12].

From a clinical context, advances in sequencing technology have heralded an era of genomic epidemiology. Whole-genome sequencing has replaced subgenome typing methods in favor of ultimate genetic resolution. Genomic studies of bacterial strains, analyzing large numbers of clinical isolates, are now reported in the literature enabled by advances in short-read sequencing technology and bioinformatic analysis [13]. More recently, we have witnessed fungal analyses approaching these scales, notably among pioneering studies of *Aspergillus fumigatus*, *Cryptococcus gattii* and *Candida auris* [10, 14, 15]. While consistent gains in short-read sequencing throughput undoubtedly enables such advances, the emergence of 'third-generation' long-read sequencing methods, such as single-molecule, real-time (SMRT) and nanopore, brings further gain in speed and cost reduction compared with alternative mate-pair and fosmid-based strategies [3]. Critically, longer reads and improved assembly including error correction software now allow larger contiguous sequences to be determined across troublesome repetitive regions of the genome, and, in combination with optical mapping methods, may even yield fully finished fungal genomes [16]. The increased availability of high-quality fungal genomes continues to advance our understanding of fungal biology and pathogenesis on numerous levels including the nascent area of fungal mycobiome research, a field that continues to highlight the important role of this fungal microbiome in health and disease [17–20]. In order to obtain valid mycobiome profiles, the selection of optimal marker genes for target amplicon sequencing is necessary and the availability of fungal genomes is crucial to this process. In addition, larger fungal genome datasets broaden the search space, allowing more accurate extraction of fungal profiles from whole-genome metagenomic shotgun data [2, 21]. Mycobiome research particularly suffers from current deficits in underpopulated fungal genomic databases and will greatly benefit from fungal genomic sequencing efforts.

The specialized journals such as Genome Announcements (Microbial Resource Announcements) and Standards in Genomic Sciences have focused on the publications of new bacterial genomes with the occasional inclusion of fungal genomes. There is still an unmet need for the publication of new fungal genomes in specialized mycology journals. Mycopathologia coverage of the fungal genomes dates as far back as 1999 carrying the information on a new community project for sequencing of the *Cryptococcus neoformans* genome [22]. A subsequent report described the community sequencing project on *Cryptococcus gattii* [23]. Similar articles also described the role of genomes in biology of *Aspergillus oryzae* and *Fusarium* species [24, 25]. The application of genome knowledge for addressing biological problems is exemplified in a recent article in the journal that used earlier published genomes of *Cryptococcus deneoformans* to highlight the accumulation of mutations in a pair of laboratory workhorse strains [26].

Against this aforementioned backdrop and during this exciting period of fungal genomics, we are pleased to announce a new section in Mycopathologia 'MycopathologiaGENOMES.' This new section will serve to announce novel fungal genome sequences, their genetic content, pathogenic attributes and pathological significance. It is our hope that the new section provides a platform to further catalyze interest in the area of fungal genomics as well as highlight the technical aspects and challenges of generating high-quality fungal genome assemblies. Through this new section, we aim to advance Mycopathologia's original mission to 'diffuse the understanding of fungal diseases in man and animals among mycologists' by focusing on the most fundamental unit of molecular mycology: the fungal genome [27].

MycopathologiaGENOMES welcomes submissions of high-quality draft and complete fungal whole-genome sequences that adhere to the guidance as specified below;

1. *Context* submissions must include a description of the fungus/fungi under investigation and their role in human and veterinary disease.
2. *Taxonomic analysis* taxonomic placement of the organism must be clearly demonstrated either by assessing the average nucleotide identity (ANI) relative to currently available genomes or in the absence of any close hit, by provision of other evidence to support taxonomic assignment (e.g.

phylogenetic placement by ITS/18S/28S sequence analysis, polyphasic approaches, etc.).

3. *Methodology* strain culture conditions, DNA extraction methods and library preparation and sequencing strategies must be detailed including bioinformatic methods that provide sufficient information to permit the analysis to be reproduced.
4. *Data availability* sequences and raw data must be made available and deposited in GenBank/EMBL/DDBJ with accession numbers to be provided on submission.
5. *Access to stock culture* authors must have access to original stock cultures of the sequenced fungus/fungi and deposit them at a recognized culture collection.
6. The manuscript format comprising 700 words or less should include the following sections: Title, authors and affiliations (no word limits); Abstract (50 words); Introduction and rationale (200 words); Methods: fungus, library, sequencing chemistry, platform, analysis pipeline (200 words; please include citation of this document here); Genome details: genome content, annotation, and accessions (200 words); Acknowledgments (50 words); References (20 maximum); and up to one table and/or figure.

MycopathologiaGENOMES submissions will be assigned to a specific group of journal editors, who will assess the manuscript content including scope and technical excellence as well as compliance with the standards set forth in this guidance document, which *must be cited* in all submissions in this category. Manuscripts will be peer-reviewed and a decision on acceptance made at the discretion of the editors. Multi-isolate comparative genomic studies as well as genomic epidemiology studies of novel genome sequences will also be considered, where a genuine contribution to knowledge in the field of fungal genomics is demonstrated. Fungal genome sequences generated as part of previously published works but which have not yet been made publicly available are also acceptable provided there is significant scientific progression. We earnestly hope the newly established 'home' for publication of high-quality fungal genomes will serve as an important academic and clinical resource for the scientific community.

Authors' Contribution MMA, VC and SHC wrote the manuscript.

Compliance with Ethical Standards

Conflict of interest The authors declare that they have no conflicts of interest.

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