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© The Society of Nematologists 2017.**Introduction to Nematode Genome and Transcriptome Announcements in the *Journal of Nematology***DEE R. DENVER,¹ ERIK J. RAGSDALE,² W. KELLEY THOMAS,³ AND INGA A. ZASADA⁴

Abstract: The *Journal of Nematology* now offers publication of Nematode Genome Announcements (NGA) and Nematode Transcriptome Announcements (NTA). These brief reports announce the sequencing and assembly of a nematode genome or transcriptome resource, along with basic technical information on DNA sequencing and bioinformatic methods used. This publishing initiative offers a new avenue to openly and concisely communicate the availability and relevance of genome and transcriptome sequence resources to the broader scientific community.

Key words: bioinformatics, DNA sequencing, genomics, scientific publishing, transcriptome.

Nematodes played a central role in catalyzing the genomics revolution. The famous laboratory model *Caenorhabditis elegans* was the first animal species to have its complete genome sequenced in the late 1990s (*C. elegans* Sequencing Consortium, 1998). This foundational achievement inspired many subsequent nematode genome sequencing efforts targeting more laboratory model species (Stein et al., 2003; Dieterich et al., 2008), animal-parasitic species (Ghedini et al., 2007; Hunt et al., 2016), entomopathogenic species (Bai et al., 2013; Dillman et al., 2015), and plant-parasitic species (Abad et al., 2008; Cotton et al., 2014). These efforts provided unprecedented scientific community resources leading to a diversity of new advances in biological disciplines ranging from ecology and evolution to human medicine to parasitology to nematology.

Scientific publications associated with new nematode genome sequences have typically been lengthy and complicated affairs. Such papers generally involve extensive monetary costs and effort in gene annotation, comparative and functional genomic investigations, and other analyses. Author lists are often very long, reflecting the extensive collaboration usually required for such endeavors. From initial sequencing to published product, these “Genome of . . .” articles generally take years to complete.

Publishing trends in genome sciences, however, are changing. Over the last decade, a quantum leap in

genome and transcriptome sequence production has resulted from new high-throughput DNA sequencing technologies and broader training of scientists and students in bioinformatic methodology. Genome biologists now churn out genomic resources at a dizzying pace; the paradigm of “Genome of . . .” articles simply cannot keep up. This phenomenon has elicited alternative strategies for communicating the availability of genomic resources. One approach is to share nematode genomes and transcriptomes as basic components of more standard research articles. Another alternative strategy is to directly deposit ‘omic resources into public sequence repositories (e.g., the NCBI Short Read Archive) without associated citable publications. This latter approach results in the most rapid path to sharing such resources with the scientific community, but also results in the data remaining hidden to many potential “end-user” scientists. These directly deposited resources, without accompanying scientific publications, do not benefit from peer review and are not citable.

Over the last few years, very short (~500–1,500 word) genome reports and announcements have arisen as novel outlets for scientists to rapidly communicate and share their ‘omic resources (Smith, 2016). These brief publication units serve to simply announce the availability of new genome or transcriptome sequences, and provide simple overviews of the project methodology and rationale. An increasing number of publishers offer these simple genome announcements, sometimes as special sections in the journal (e.g., the Genome Reports offered by *Genome Biology and Evolution*). The journal *Genome Announcements* is entirely dedicated to this category of scientific communication, and published more than 1,000 announcements in 2015 (Smith, 2016). The American Society for Microbiology sponsors this journal, which predominantly announces genomes for bacteria, unicellular eukaryotes, and viruses. These announcements are commonly published as open-access, and offer a balanced strategy allowing genome scientists

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to rapidly share their work while also providing a reliable and citable publication unit. Most journals offering genome announcements or reports, however, require high publication cost, usually in the range of US\$300 to \$1,500 per unit. These prohibitive costs hold some scientists back from pursuing this strategy.

At the 2015 annual meeting of the Society of Nematologists in East Lansing, Michigan, conversations among us and other attendees precipitated the idea for genome announcement-style publications in the *Journal of Nematology*. This initial concept percolated and matured through the course of a year, followed by the submission of a published abstract and oral presentation pitching this idea to the broader Society of Nematologists community at the 2016 annual meeting in Montreal, Quebec. The feedback was uniformly positive and enthusiastic about this new direction for the *Journal of Nematology*.

Starting with this issue, the *Journal of Nematology* now offers publication of NGA and NTA. Announcements reporting the sequencing of nematode genomes (nuclear and/or mitochondrial) and transcriptomes are welcome, as are those focused on microbial associates of nematodes (e.g., bacterial endosymbionts). Submissions are encouraged from a diversity of nematode groups including free-living, entomopathogenic, plant-parasitic, animal-parasitic, and marine species. Special instructions for authors submitting NGA and NTA are provided on the *Journal of Nematology* website: <http://journals.fcla.edu/jon>.

We aim for this new venture to provide nematode genome biologists an effective outlet for rapidly sharing new genome and transcriptome resources with the scientific community. The *Journal of Nematology* offers free and open-access publication for authors, setting it apart from other genome announcement publishers where author fees are often prohibitive. We are optimistic that integrating genomic publications into the *Journal of Nematology* might foster new collaborations and interactions between genome biologists and nematologists. Send us your genomes and transcriptomes!

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