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Letter to the Editor

Comments on Smith (2015)—'The past, present and future of mitochondrial genomics: have we sequenced enough mtDNAs'

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In his carefully written review, Smith [1] asks the question of mitochondrial DNA (mtDNA) genomes—'Have we sequenced enough mtDNAs?' This is a question I have asked myself often during my entire tenure as Editor in Chief of mtDNA, one of the journals Smith [1] mentions in his review. Since starting the journal in 2008, mtDNA has published nearly 2000 Mitogenome Announcements, most of which are animal genomes, and there is no doubt that the steep incline in Smith's Figure 2 is this journal's doings. Smith [1] suggests that publications on mtDNA genomes are not advancing science and in fact may be holding the science back by tying up resources and editors' time (the latter is a very accurate statement, as I know all too well myself).

However, there are some inaccuracies and points of contention in Smith's [1] paper that I would like to address. First he suggests that the journal mtDNA (now published by Taylor Francis) 'is devoted entirely to the description of mitochondrial genomes'. While the journal does publish Mitogenome Announcements (short 500-word reports on whole mtDNA genomes) the journal is hardly 'entirely' devoted to description of mitochondrial genomes. mtDNA has published papers on human mtDNA pathology, many organisms' phylogeography, human population genetics based on mtDNA, DNA barcoding using Cytochrome Oxidase I sequences and on novel methods for detection of mtDNA polymorphisms in a wide variety of organisms to name a few categories with non-genomic focus. The trend in increase of genome announcements at mtDNA is interesting though and supports Smith's [1] contention that there is an inordinate rise in these kinds of reports. From 2009 to the present the rise in percent of announcements in the journal goes from 50% to 80%. The percentage of pages in the journal dedicated to announcements rises from 25% to 50% over the same period. This steep incline in interest in publishing announcements by researchers has prompted the editors at mtDNA to create a 'resources' publication specifically for genome announcements.

Second, Smith suggests that publishers of journals devoted to reporting mtDNA genome information 'are not complaining, charging fees as high as $2000 USD per paper'. While I am sympathetic to the disdain Smith [1] appears to have for the practice of charging huge page charges, I would point out that the journal mtDNA does NOT have page charges, unless open access is requested by an author, and for announcements, open access is an order of magnitude less than what Smith [1] suggests above.

Third, while I completely agree with Smith's [1] suggestion that 'the most important thing is depositing the mtDNA into GenBank and annotating it correctly', I suggest that publications announcing mtDNA genomes serve an important purpose in science. Access to information should be enhanced whenever we can and it seems to me that having the information about a newly sequenced mtDNA genome in the literature is an enhancing element. More importantly, an announcement can link the specimen's archival data to a sequence and clarify the provenance of a sequence. In addition, if phylogenetic analysis of the generated sequence is required (as the journal mtDNA requires) then the validity of the sequence can be determined by its phylogenetic placement with other known sequences.

I am sure the face of mitochondrial genomics will be very different in a decade. For instance, I would bet that all of the 1.8 million named eukaryotic species that are available on the planet will have either a mitochondrial genome or a chloroplast genome sequence generated for it. But I do hope that this does not mean we will have 1.8 million mtDNA genome announcements. On the other hand, incentive is a big driving force in science. If the incentive of publishing the findings from a novel mtDNA genome is removed as Smith [1] suggests, then I fear that the generation of these genomes will be severely slowed and in essence a reachable goal of a mitochondrial/chloroplast DNA genomic database for all organisms on the planet with these genomes will not be realized. One alternative is to increase the incentive to submit directly to GenBank, and make such submissions recognizable as valid publications. I suspect this latter route is not a palatable approach to many scientists. We will need to think of better ways to handle this problem of reporting and making this information available in the literature. While I have some disagreements, Smith's [1] review is a great starting place to think about the problem.

Reference

1. Smith DR. The past, present and future of mitochondrial genomics: have we sequenced enough mtDNAs? *Brief Funct Genomics*, 2015, 1–8; doi: 10.1093/bfgp/elv027.

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