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EDITORIAL

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Readers of *Mitochondrial DNA* may have noticed several developments in the pages of the journal. We will start with some of the less obvious. First, we have begun to publish plastid genome announcements. This expansion to other organellar genomes is driven by our vision that the journal should be a logical and rapid way to announce the finishing of any organellar genome. We will include a specific reference to handling the plastid genome papers on our website and in our manuscript management system for the 2015 calendar year. In the meantime we encourage authors to submit plastid genome announcements following the same rules and restrictions of the Mitogenome Announcements that we will articulate below.

Second, readers may have noticed a proliferation of Next Generation or High Throughput Sequencing-generated Mitogenome Announcements. In anticipation of a major increase in the number of mitogenomes from this technique, *Mitochondrial DNA* will be very discerning of Mitogenome Announcements based on single mitochondrial genomes. Since the prevailing approach to sequencing animal mitogenomes with Next Generation Sequencing is to generate multiple mitogenomes at the same time, for the sake of brevity and citation issues, the editors have decided to prefer Mitogenome Announcements with multiple new mitogenomes starting from 1 January 2015. To compensate for the increase in minimal number of genomes in submitted Announcement manuscripts, we are increasing the word limit to 1000 words for such submisssions of multiple genomes. In this context we will no longer accept Mitogenome Announcements on model animal strains such as mice and rats. In addition, we will no longer accept Mitogenome Announcements that report the mtDNA genomes of strains or lines of domestic animals, such as geese, pigs, goats, etc.

Third, readers also may have noticed a proliferation of papers correlating mitochondrial DNA polymorphisms with disease state. Since these papers are concise and usually involve the reporting of three simple elements – the polymorphism, the study system, and the disease correlation – the editors have decided to limit such reports to 1000 words with one supporting item (i.e. a table or a figure).

Fourth, the Journal's new website (currently under construction) is able to host supplemental data only at the article level. It can also link through supplemental data in external repositories like Genbank, Dryad, etc. We will have a section in the Instructions for Authors regarding this. For Announcements we cannot accept Supplementary Data Files. We request that authors of Mitogenome Announcements place their data files in external, permanent websites or FTP sites, e.g. Dryad Digital Repository (http://datadryad.org).

Fifth, up until 2014, the journal's minimal requirements for Mitogenome Announcements consisted of (1) proper vouchering and storage of tissue and source DNA sample, and (2) proper submission to freely, publicly accessible nucleotide sequence database, e.g. GenBank, EMBL, DDBJ. As of 1 January 2015 we require that the submitted mitogenome sequences be accompanied by a phylogenetic analysis including at least ten of the most closely related mitogenome sequences in the database. The analysis should be presented as a tree figure for publication.

We will no longer accept tables with gene lists or figures with gene maps in them. Instead, we expect authors who submit Mitogenome Announcements to submit phylogenetic trees to validate their samples. To repeat, the only figure, and it is required, in Mitogenome Announcements will be a phylogenetic tree.

We hope that these new changes will streamline the submission and review of the ever-evolving nature of manuscripts submitted to *Mitochondrial DNA*.

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