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LETTER TO THE EDITOR

Letter to Professor Currie

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Dear Professor Currie,

As the current longest-serving Senior Editor responsible for environmental articles submitted to Cell Stress & Chaperones, I felt it was important to bring to your attention a couple of worrying trends in recent submissions to our journal in this field:

1) **No pre-publication submission of sequence data.** Genomics has a long and proud history of open access. This dates back to the Bermuda Principles (1996), whereby leaders of the scientific community agreed to rapid and pre-publication release of all sequence data in publicly accessible databases, namely the International Nucleotide Sequence Database Collection (https://www.insdc.org/), which comprises DDBJ, NCBI and ENA (see Marshall, 2001; https://doi.org/10.1126/science.291.5507.119). This practise was reinforced by the Fort Lauderdale Agreement in 2003 (https://www.genome.gov/10506537/reaffirmation-and-extension-of-nhgri-rapid-data-release-policies), which emphasized the free and unrestricted use of sequencing data by the scientific community. Thus, genomics has lead the way in open access of data, long before Open Access Publishing and FAIR (Findability, Accessibility, Interoperability, and Reuse of digital assets) (https://www.go-fair.org/fair-principles/). However, at least 50% of recent environmental submissions fail to include any data submission statement and are returned to the authors to ensure compliance. This includes explicit requests for any genome or transcriptome data from which candidate genes were data-mined to be submitted to the INSDC alongside the specific genes, which were the main subject of the publication.

2) **Minimal publishing unit or "salami" publication.** We receive numerous publications where one or two candidate genes have been data-mined from either transcriptome or genome data. These are subjected to the usual range of minimal bioinformatics characterisation with a minor element describing either tissue-specific expression or the expression pattern after the application of an acute stress, which invariably does not reflect actual field conditions. Occasionally the same candidate genes appear in different submissions with a different stressor applied and slightly different text. Whilst technically these studies may be within the scope of our journal, they represent only very small incremental increases in knowledge.

My main concern here are environmental submissions, which rely heavily on genome or transcriptome data. It is essential that we maintain those early guiding principles and provide leadership in the field, especially to young researchers, who are likely unaware of the agreements mentioned above. Hence, can I suggest that we explicitly state in our instructions to authors that all environmental submissions must include a full open access data statement to be eligible under the reviewing process. Furthermore, that manuscripts received describing the characterisation and expression patterns of only one or two genes will not be sent out for review and will be returned to the authors with the encouragement to resubmit with a more a substantial experimental component.

Yours sincerely,
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