

OCTOBER 17, 2014

Dear Editor,

We are writing a pre-submission enquiry regarding a manuscript entitled “Persistence of sub-genomes in paleopolyploid cotton after 60 million years of evolution.” We would very much appreciate your feedback regarding a possible submission to *Genome Research*. We believe the manuscript will be of interest to your broad readership, particularly those interested in evolution and paleogenomics.

The role of gene duplication as an evolutionary force has long been recognized, and in this manuscript we examine the role of duplicate gene retention and loss in shaping the modern genome of cotton. We demonstrate that despite 60 million years of evolution the sub-genomes of paleopolyploid cotton are still easily distinguishable via several genomic characteristics including transposable element (TE) content, GC content, targeting by siRNAs, and a bias in the rate of gene fractionation (duplicate gene loss after whole genome duplication). Our data stand in contrast to other reports by extending the evolutionary time over which these signatures can be detected, suggesting that hitherto, the long term impact of bias fractionation has not been fully appreciated.

Furthermore, and contrary to previous hypotheses and analyses, we demonstrate that positional down-regulation of genes by transposable elements is unlikely to be the primary driver of biased fractionation in cotton. This advance is important to the field of plant genome evolution and paleogenomics as our data suggest a modification to current understanding of gene loss following ancient whole genome duplication is needed. Indeed, our observations lead us to suggest an alternative mechanism driving biased fractionation.

We hope that you will consider our manuscript suitable for consideration in *Genome Research* and we look forward to hearing your thoughts.

Thank you for your time and consideration.

Sincerely,



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