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Bogotá, August 15st, 2020

Dear Editorial Board,

We would like to submit our manuscript entitled "MultiGWAS: An integrative tool for Genome Wide Association Studies (GWAS) in tetraploid organisms" for consideration for publication as a computer program in Molecular Ecology Resources.

The Genome-Wide Association Studies (GWAS) are essential to determine the genetic basis of ecological or economic phenotypic variation across individuals within populations of wild and domesticated species, many of them polyploids. But, despite the importance of polyploidy and the increasing availability of new genomic data, GWAS tools for polyploids are scarce. Therefore we have developed the MultiGWAS tool that deals with the whole GWAS process in tetraploid species by running , integrating, and analysing the results of four software packages designed for GWAS in polyploids and diploid species.

MultiGWAS includes the input and pre-processing of genomic data in different formats; association analysis by running the GWAS software in parallel; post-processing and summarizing of their results; reporting using graphical and tabular views; and in particular replicating the results by identifying both the highest-scoring and shared associations between the four software packages which helps users to decide more intuitively on possible true or false associations. In addition, MultiGWAS offers both an easy-to-use graphical user interface and a command line interface for advanced users, and the tool has been well evaluated with several real data sets.

We believe that this manuscript is appropriate for publication in your journal because it presents a novel software that would be of great interest to researchers studying genetic associations in plant and animal breeding and conservation, furthermore polyploidy is a prominent feature of plant genomes, and currently there is no other tool for GWAS in tetraploides that integrates and analyzes results from multiple sources.

Thank you in advance for your consideration,

Best regards.











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## **Sede Central**

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