

From: [Scott Allen Jackson](mailto:Scott.Allen.Jackson)
To: r.k.varshney@cgiar.org
Subject: Re: Invitation to Review for the The Plant Genome
Date: Thursday, December 18, 2014 1:40:31 AM

Rajeev, statistical modeling is way outside my comfort zone. You might try:

Jianming Yu (Iowa State)
Jason Wallace (jgw87@cornell.edu)
Justin Vaughn (jnvaughn@uga.edu)

Hope that helps.

scott

From: onbehalfof+r.k.varshney+cgiar.org@manuscriptcentral.com
<onbehalfof+r.k.varshney+cgiar.org@manuscriptcentral.com> on behalf of r.k.varshney@cgiar.org
<r.k.varshney@cgiar.org>
Sent: Thursday, December 18, 2014 12:53 AM
To: sjackson@purdue.edu
Cc: r.k.varshney@cgiar.org
Subject: Invitation to Review for the The Plant Genome

18-Dec-2014

Dear Dr. Jackson:

Manuscript ID TPG-2014-10-0078 entitled "Marker Imputation Prior to Genomewide Selection in Biparental Maize Populations" with Dr. Bernardo as contact author has been submitted to the The Plant Genome.

I invite you to review this manuscript. The abstract appears at the end of this letter, along with the names of the authors. Please let me know as soon as possible if you will be able to accept my invitation to review. If you are unable to review at this time, I would appreciate you recommending another expert reviewer. You may e-mail me with your reply or click the appropriate link at the bottom of the page to automatically register your reply with our online manuscript submission and review system.

Once you accept my invitation to review this manuscript, you will be notified via e-mail about how to access Manuscript Central, our online manuscript submission and review system. You will then have access to the manuscript and reviewer instructions in your Reviewer Center.

I realize that our expert reviewers greatly contribute to the high standards of the Journal, and I thank you for your present and/or future participation.

Sincerely,
Dr. Rajeev Varshney
The Plant Genome Associate Editor
r.k.varshney@cgiar.org

Agreed: https://mc.manuscriptcentral.com/plantgenome?URL_MASK=75ff837581d14746b5fd8a907d6fc2bf

Declined: https://mc.manuscriptcentral.com/plantgenome?URL_MASK=351162f9d1174f18987a4c57cb058d0b

Unavailable: https://mc.manuscriptcentral.com/plantgenome?URL_MASK=52ca87fd748b44d1b8b297e7b15f086b

MANUSCRIPT DETAILS

TITLE: Marker Imputation Prior to Genomewide Selection in Biparental Maize Populations

AUTHORS: Jacobson, Amy; Lian, Lian; Zhong, Shengqiang; Bernardo, Rex

ABSTRACT: Marker imputation increases the number of markers in genomewide selection. Our objectives were to determine: (i) if marker imputation increases the response to selection (R) and prediction accuracy (rMP) among the progeny of two maize (*Zea mays* L.) parental inbreds (A and B); (ii) the number of imputed single nucleotide polymorphism (SNP) markers needed to reach a plateau in rMP for grain yield, moisture, and test weight; and (iii) the lowest number of assayed SNP markers that can be used for imputation without a significant decrease in rMP. The progeny of 27 A/B crosses were assayed with 49 to 100 SNP markers, and imputation was conducted to increase the number of markers to 2911. For each A/B test population, the training population in the general combining ability (GCA) model consisted of 4 to 26 maize crosses with A and B as one of the parents, whereas the training population in the A/B model was the A/B population itself. Marker imputation made the GCA model as good as or better than the A/B model in terms of R and rMP for all the traits. The rMP values did not increase significantly beyond 500 imputed markers for grain yield, and beyond 1000 imputed markers for moisture and test weight. We recommend that maize breeders should assay a biparental cross with only around 50 polymorphic SNP markers, increase marker coverage to around 1000 markers by imputation, and use the GCA model with imputed markers for genomewide selection within a biparental cross.