Rajeev, I'm in conflict with Phil, Jane and Jeremy:)

I will suggest Justin N Vaughn <jnvaughn@uga.edu>

Scott

> On Oct 25, 2015, at 1:20 PM, r.k.varshney@cgiar.org wrote:
>
> 25-Oct-2015
>
> Dear Dr. Jackson:
>
> Manuscript ID TPG-2015-09-0092 entitled "Sequence-Based Introgression Mapping Identifies Candidate Genes Within WM7.1 and WM8.3, Two Major QTL Affecting White Mold Tolerance in Common Bean (Phaseolus vulgaris L.)" with Dr. McClean 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=eb8c0a1d8b69465bb32021a94a6cca33
>
> Declined: https://mc.manuscriptcentral.com/plantgenome?URL_MASK=c3a67d8494d345169d87e4ca1d0537d8
>
> Unavailable: https://mc.manuscriptcentral.com/plantgenome?URL_MASK=c67b9e3825bd401b8f1caf6717bc679d
>
>
> MANUSCRIPT DETAILS
>
> TITLE: Sequence-Based Introgression Mapping Identifies Candidate Genes Within WM7.1 and WM8.3, Two Major QTL Affecting White Mold Tolerance in Common Bean (Phaseolus vulgaris L.)
>
> AUTHORS: McClean, Phillip; Mamidi, Sujan; Miklas, Phillip; Trapp, Jennifer; Felicetti, Erin; Grimwood, Jane; Schmutz, Jeremy; Lee, Rian
>

> ABSTRACT: White mold disease, caused by the necrotrophic fungus Sclerotinia sclerotiorum (Lib.) de Bary, is a major pathogen of common bean (Phaseolus vulgaris L.). Two QTL, WM7.1 and WM8.3, with major effects on tolerance to the pathogen were previously mapped using single marker analysis but have not been placed within narrow genetic or physical intervals. Here a combination of traditional genetic mapping and a new approach called sequence-based introgression mapping were used to place the QTL within narrow intervals each with a relatively small number of genes. Advanced back-cross populations segregating individually for either of the two QTL, and a recombinant inbred (RI) population segregating for both QTL were used to fine-map and confirm the genetic location of the QTL. The QTL intervals were physically mapped using the common bean reference genome. The physical intervals were further confirmed by sequence-based introgression mapping. Using whole-genome sequence data (12-19x) from susceptible and tolerant DNA pools, introgressed regions were identified as those with significantly high numbers of SNPs relative to the whole genome. Combining the QTL and SNP data located WM7.1 to a 660 kb region that contained 41 gene models on the proximal end of chromosome Pv07, while the WM8.3 introgression was narrowed to a 1.36 Mb region containing 69 gene models. The most polymorphic candidate gene in the WM7.1 region encodes a BEACH-domain protein associated with apoptosis. Within the WM8.3 interval, a receptor-like protein with the potential to recognize pathogen effectors was the most polymorphic gene. The utilization of gene and sequence-based mapping identified two candidate genes whose putative functions are consistent with the current model of Sclerotinia pathogenicity.