Introgression of Disease Resistance into *Phaseolus vulgaris* variety OAC Rex from *Phaseolus acutifolius*

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The white navy bean variety OAC Rex was developed from an interspecific cross with a wild relative *Phaseolus acutifolius* (tepary bean). The interspecific cross was made to introduce resistance to common bacterial blight (CBB), caused by *Xanthomonas axonopodis* pv. phaseoli and its fuscan variant. *X. fus*cans subsp. fuscans into cultivated beans. The complete genome sequence for OAC Rex was obtained by Illumina HiSeq sequencing to give 136x coverage and supplemented by long-read PacBio™ data, resulting in a pseudochromosome-level draft genome. The genome coverage of OAC Rex comprises approximately 97% of G19833 and it contains partial or complete representations for 96% of the CEGMA conserved data set [1]. A comparison of a contig-stage assembly for the *P. acutifolius* accession in the pedigree of OAC Rex, with the OAC Rex and G19833 genome sequences, showed that there are regions on every chromosome that are shared between the *P. acutifolius* and OAC Rex but are missing from G19833. The regions of introgression from *P. acutifolius* include self-incompatibility, disease resistance, regulation of disease resistance, and Niemann Pick-like sterol transporter genes. A comparison of the OAC Rex sequence with the G19833 reference genome, which is susceptible to CBB, identified differences in gene content and structure on chromosome 8 near a marker (SU91) associated with CBB resistance. This region includes an introgression from *P. acutifolius* containing a Niemann Pick sterol transporter gene with a unique structure shared with *P. acutifolius* that has features of executor genes described previously in *Xanthomonas* resistant rice and pepper.

References

[1] http://www.ncbi.nlm.nih.gov/sra/?term=OAC+Rex; Accession: PRJNA237957 ID: 237957