



Common bean (*Phaseolus vulgaris* L.) is an important legume in many developing countries throughout the world. It is most useful for its high protein content as well as dietary fiber. With the advent of full genome sequencing, we are now able to better understand the relationship between host resistance genes and pathogen virulence genes by analyzing transcriptional changes in common bean.

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## Characterization and Isolation of candidate genes responsible for fungal rust *Uromyces appendiculatus* resistance in common bean *Phaseolus vulgaris*

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### Who cares and why?

The fungal rust pathogen *Uromyces appendiculatus* is virulent on susceptible cultivars of common bean, causing the formation of rust pustules. In many countries around the world, common bean is a staple part of the diet, important mainly for its protein content. Recent advances in common bean genome sequencing have allowed researchers to examine how resistance genes in host and avirulence genes in pathogens interact with each other to prevent signs and symptoms of disease. The

research that is being performed will provide better insight into how to prevent disease in important food crops such as common bean. The specific aim of the current research seeks to identify the *Crg* gene, located in a 250kb stretch on chromosome 10. Through our research, we would also like to locate the *Ur-3* gene, which is believed to be contained at the distal end of chromosome 11 and confers resistance more than 40 of the 89 curated races of fungal rust at USDA-ARS in Beltsville, Maryland.

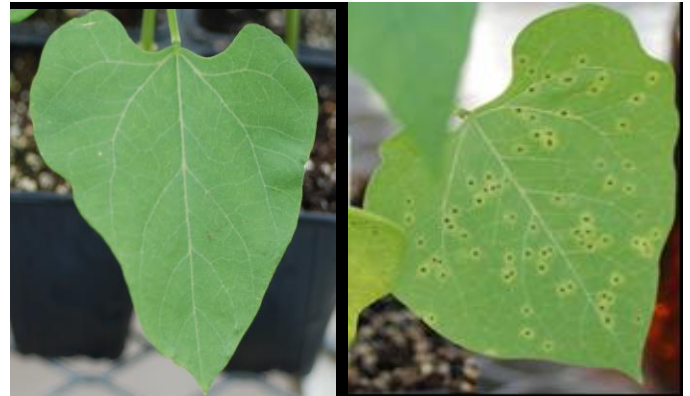
### What has the project done so far?

Thus far, we have made advances in transcriptomics in resistant varieties and susceptible mutants of common bean. Information generated from Illumina RNA-Seq has allowed us to generate sequence data for two wild type cultivars 'Sierra' and 'Olathe', race 53 resistant and susceptible, respectively, and race 53-susceptible mutants *crg*, *ur3-Δ2* and *ur3-Δ3*. We have been able to identify the location of a major molecular marker in common bean and characterize it as part of a gene. We have been able

to delineate the region of deletion on chromosome 10 of mutant *crg*, possibly leading us to isolation of the *Ur-3* complementary resistance gene, *Crg* (Complements resistance gene.) We now know that the 250kb deletion region contains approximately 20 genes, one of which may be the *Crg* gene. Currently, bioinformatic analysis is being carried out to locate the deletion region in mutants *ur3-Δ2* and *ur3-Δ3* which may help us locate the *Ur-3* gene on chromosome 11.

Along with new genetic discovery, this project has provided training and learning experiences to undergraduate and graduate students, as well as visiting faculty and staff from several collaborating

colleges, universities, and institutes. Several of the undergraduate students who have participated in the past and current research have gone on to complete their bachelor's degrees and attend graduate school.



## Impact Statement

With the availability of the genome sequence of common bean cultivar G19833, we are now able to use a global approach to understanding genes responsible for rust resistance in common bean. In order to better understand the correlation between hosts and pathogens, we treated several common bean cultivars, including resistant cultivar 'Sierra', with race 53 rust and isolated their transcriptomes. Information generated from Illumina RNA-Seq has allowed us to produce sequence data for two wild type cultivars, Sierra and 'Olathe', a race 53-susceptible cultivar, and race 53-susceptible mutants *crg*, *ur3-Δ2* and *ur3-Δ3*. One mutant, *crg*, is missing a previously identified gene, *Complements resistance gene*, which co-segregates with the resistance gene analog SB1, and has been mapped to chromosome 10.

### What research is needed?

New time course experiments need to be executed to find out when the gene or genes responsible for disease resistance begin to express. This requires

inoculations on resistant and susceptible genotypes of bean, collecting samples at shorter time points, and the sequencing of more transcriptomes.

### Want to know more?

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Strategic Priority: Plant health; biotechnology

Additional links: <http://www.umes.edu/ard/Default.aspx?id=46285>

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### Funding

This research was made possible by the National Science Foundation EPSCoR Grant No. IIA-1301765, Delaware EPSCoR with funds from the National Science Foundation Grant EPS-0814251, and the State of Delaware.