

UC Riverside, Department of Nematology

Faculty Recruitment Candidate Seminars - *Assistant Professor of Nematology*

Monday, February 26, 2024, 10:30 AM – 11:30 AM (Hybrid)

Utilizing Classical Breeding and Advanced Genomics Approaches to Design Sustainable Nematode Management Strategies



Pawan Basnet

Research Scientist, AgriPlex Genomics

In-Person Location: Genomics Auditorium 1102A

Zoom Meeting Link: <https://ucr.zoom.us/j/91029793165>

Brief Biography:

Pawan Basnet is a research scientist at agriplex genomics working toward advancing R&D of next-generation sequencing techniques to assist animal and plant breeders for their genomic-assisted selection. He holds a PhD in Plant, Insect and Microbial Sciences from the University of Missouri-Columbia, and a PhD Minor in Statistics. Prior to this current role, Pawan worked as a postdoctoral research associate at the University of Wisconsin-Madison, where his research focused on the genetics of pathogen resistance traits in alternative crops. His expertise lies in utilizing classical breeding, field-based methodologies, and advanced genomics to explore and design sustainable nematode management strategies.

Brief Seminar Abstract:

A single mode of genetic resistance derived from PI88788 (*rhg1-b*) has dominated the \$57.5 B US soybean market for almost three decades. The breakdown of resistance and selection of virulent nematode population poses a significant threat to soybean production, estimated at a \$1.5 billion loss annually. Breeding for soybean cyst nematode (SCN) resistant soybeans to effectively combat the widespread increase in virulent populations presents a significant challenge. Utilizing classical breeding and advanced genomic approaches, we identified an epistatic interaction of two nematode resistance genes, *rhg1-a*, and *rhg2*, in a highly resistant but underutilized soybean accession, PI90763. Concurrently, we also utilized resistant cultivars with unique resistance genes/QTL in continuous and rotated schemes to understand their effects on population density and

virulence through a 4-year microplot field study. Results from this study highlighted the importance of rotating resistant sources as a crucial nematode management strategy.

With SCN already being a single major pathogen in soybean, newer prospects of incorporating pennycress, an alternative SCN host, as an oilseed cover crop in the Midwest's corn-soybean production system could be counterproductive. To facilitate successful pennycress domestication, we developed a nematode screening strategy in pennycress and identified susceptible checks and resistant lines. A follow-up GWAS analysis further identified unique resistance genes, unlike soybeans' predominant *SNAP* gene family. Recent advancements in genetics and genomics could provide a broader understanding of plant-nematode interactions and the genetic architecture of resistance mechanisms, which are crucial for designing sustainable nematode management approaches.