

SHAHIDEH NOURI
Assistant Professor
Department of Plant Pathology
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APPOINTMENT

Kansas State University, Department of Plant Pathology, Manhattan, KS USA

Assistant Professor (90% research and 10% teaching) 2018-present

Laboratory of Prof. Bryce Falk, University of California, Davis, CA USA

Project Scientist 2017- 2018

Postdoctoral Scholar 2013- 2017

EDUCATION

Department of Plant Pathology, University of Wisconsin, Madison, WI 2007-2012

Doctor of Philosophy (Plant Virology)

Department of Plant Pathology, Isfahan University of Technology, Iran 2002-2005

Master of Science (Plant Pathology: Bacteriology)

Department of Plant Pathology, Isfahan University of Technology, Iran 1998-2002

Bachelor of Science (Plant Protection)

PROFESSIONAL SOCIETY AFFILIATION

American Society of Virology (ASV): Full member

American Phytopathological Society (APS): Full member

TEACHING EXPERIENCE

- *Plant virus-insect vector interactions Guest Lecturer*
- Department of Entomology, Kansas State University April 2022

- *Plant Virology Guest Lecturer*
- Department of Bio Ag Sciences, Colorado State University September 2021

- *PLPTH835: Plant Virology*
- Department of Plant Pathology, Kansas State University Fall 2019-present

- **Workshop instructor for ~ 30 female 6-8th graders**
KAWSE-GROW: Kansas State University Office for the Advancement of Women in Science & Engineering – Girls Researching Our World February 2019
- **Bioinformatics for pathogen identification guest lecturer for undergraduates in general plant pathology**
Department of Plant Pathology, University of California October 2016

MENTORING EXPERIENCE

- **M.S. program, Kansas State University** 2018-2021
Mentoring Ms Carla Bianca Redila, a Master`s student at the Department of Plant Pathology. Carla joined my lab in August 2018. In her project, she investigated viral communities associated with field collected wheat samples in KS using metagenomics. Carla is now employed by the USDA-ARS (Manhattan, KS) since completing her M.S. degree last year.
- **Postdoctoral scholar, Kansas State University**
 - Dr. Ferdinand Nanfack Minkeu Ferdinand joined my lab in summer 2019 and he studied interactions between an insect-specific virus and its insect host.
 - Dr. Maryam Rastegar joined my lab in Summer 2020 and she studied the mechanism(s) of tolerance to wheat viruses in wild wheat relatives.
 - Dr. Ved Prakash joined my lab in Summer 2021 and he has continued studying the mechanism(s) of tolerance to wheat viruses in wild wheat relatives.
- **Undergraduate program, Kansas State University** 2018-present
 - Ms. Savannah Phipps - REEU student: Plant Science, Montana State University
 - Ms. Madi Leierer: Microbiology, Kansas State University
 - Ms. Theresa Quintana: Microbiology, Kansas State University
 - Ms. Savannah Pipper: Entomology, Kansas State University
 - Ms. Emma Woodworth: Architecture, Kansas State University

RESEARCH EXPERIENCE

Assistant Professor June 2018-present
Plant-Virus-Insect Interactions Laboratory, Kansas State University

My research program focuses on different aspects of plant virology at the basic and translational levels. My basic research focuses on identifying and characterizing emerging viruses, virus evolution, and studying host-virus-vector interactions. My research uses traditional and molecular virology along with genomics and system biology to understand these interactions. I am also building my translational research program by developing new control strategies for plant pests by using new plant and insect-specific viruses (ISVs) as RNA/gene delivery vectors.

My research program focus on the following research themes:

A) *New Emerging Viruses: Are we prepared?* Viruses are the most abundant biological entities on earth, and many are undiscovered. Wheat viruses cause significant yield loss annually and WSM is considered as one of the major diseases in the Great Plains and other wheat growing regions around the world. Three viruses including WSMV, TriMV and HPMoV have been documented in association with WSM so far. Despite good breeding programs, WSM is still one of the major issues for farmers causing significant yield loss. One of my research questions is “Is it the whole story?”, “Is it possible that other viruses are related to this disease

complex, but they have not been identified yet?” To address this research question, my lab used NGS and Bioinformatics to study all viral communities associated with field wheat samples. We studied the distribution and evolution of wheat known viruses in KS fields (Redila *et al.* 2021a). The results of this study help breeders to have a better understanding of the status of the related viruses in the field for developing more effective and long-lasting control strategies including new resistance genes. Our study was able to identify not only known wheat viruses but also novel putative viruses. *Wheat associated-vipo virus* (WaVPV), which shares low but significant similarities to both plant and fungus-associated viruses, is one of these newly identified viruses. Additionally, we identified a new umbravirus-like associated RNA (ulaRNA) tentatively named *Wheat umbra-like virus* (WULV) in our field-collected wheat samples. This was the first report of this group of viruses in cereals (Redila *et al.* 2021b).

As new viruses, many questions have arisen about the biology of these putative viruses that my research group have identified in wheat. There is little known about the biological significance of ulaRNAs as well as their transmission mode and potential helper virus(es). Interestingly, all our WULV positive field samples were co-infected with WSMV suggesting WSMV as the potential helper virus. As a newly emerging viral RNA infecting wheat, several research questions regarding the evolution and epidemiology of WULV, its biological significance and host range, and its transmission mode have raised. To address these knowledge gaps, we attempt to characterize WULV by following these aims: 1) Evaluating the distribution of WULV in Great Plains fields and studying the genetic variations of field isolates; 2) Studying the relationship between WULV and WSMV in co-infections and the impact of this interaction on symptom severity; 3) Determining WULV host range; 4) Studying the potential of WSMV as the helper virus; and 5) Determining Wheat curl mite as the potential vector. Although, umbra-like viruses are considered as pathogens, they have also received attention for their potential to be used as a delivery tool (engineered virus) for inducing silencing of target genes of plant pathogens through RNA interference (RNAi) antiviral mechanism. Therefore, my lab is also interested in evaluating WULV for translational applications as a new gene delivery tool.

B) Molecular mechanisms associated with plant tolerance to virus infections: My research aims to explore viral tolerance as a breeding tool. From an evolutionary perspective, tolerance is an evolutionary mechanism for both viruses and their hosts for adaptation. One of the best examples that we hear a lot these days is bat tolerance to many viruses including Coronaviruses. Because viruses are allowed to persist, the selection pressure for emergence of virulent strains is reduced in tolerant hosts compared to resistant. Using tolerance instead of resistance in the field to impose less selection pressure on plant viruses has recently received attention. However, the molecular mechanisms of tolerance are not clear. My research aims to address this research gap using wheat wild ancient relatives (*Ae. tauschii*) mainly grew in Middle East (Iran, Afghanistan, and Turkey) around thousand years ago and wheat viruses. Our preliminary observations and data showed tolerance to WSMV in some genotypes of *Ae. tauschii* despite high virus titers. Our hypothesis is that the virus not only changes the gene expression profile of the host, but also the host epigenetics (non-coding RNAs including miRNAs pattern) as well as proteomic and metabolic profiles.

The first step to address the knowledge gaps is screening *Ae. tauschii* for virus tolerance based on both phenotype (symptoms and virus titer) and genotype. This project has been supported by NSF-IUCRC (Industry–University Cooperative Research Centers) and USDA-NIFA. This an international collaborative project with me as the lead PI and Dr. Jesse Poland at KAUST as the Co-PI who is conducting genotyping of the screened lines.

C) Developing New Plant and Insect-specific viruses (ISVs) Viral Vectors For Translational Applications: Virus induced gene silencing (VIGS) has been successfully applied for induction of silencing of genes of interests in plants via RNA interference (RNAi). In this method, viral vectors (engineered viruses) are used as gene delivery tools. A viral vector has been also recently successfully used for the delivery of the guide RNA for the genome editing in wheat. The potential of this approach as a new environmentally safe control strategy of insect vectors of plant pathogens has also raised particular interest from the biotechnological viewpoint. For this purpose, my lab has recently constructed a cDNA infectious clone for WULV (a new ulaRNA) to study plant-virus interactions. Although, ulaRNAs are considered as pathogens, they have also received attention for their potential to be used as a delivery tool (engineered virus) for inducing silencing of target genes of plant pathogens through RNA interference (RNAi) antiviral mechanism. Therefore, my lab is also interested in evaluating WULV for translational applications.

Additionally, ISVs which only replicate in their insect hosts without causing any pathogenicity, have gained increasing attention in their potential use for translational applications for manipulating traits in insect vectors. Since this group of viruses are transmitted vertically, any inserted gene of interest in the genome of ISVs can be spread in the population easily. My research is interested to explore this potential using ISVs of the selected aphid species which are natural vectors of plant viruses as well as the Asian citrus psyllid.

Assistant Project Scientist

2017- 2018

Department of Plant Pathology, University of California

I focused on the newly discovered insect-specific viruses associated with *D. citri*. I evaluated cDNA clones made for one of the *D. citri* viruses under the control of different promoters in cell lines and *D. citri*. This research was done within the BSL3 facility located at the University of California-Davis. I also used genomics and high-throughput screening together with in vitro (cell line) and in vivo (insect) trials, to gain novel insights into the interactions between some of these novel viruses and the insect host. I led a research group studying the molecular and cellular aspects of the interactions between DcACV, DcFLV and *Diaphorina citri reovirus* (DcRV) as a part of the insect virome with their insect host and citrus plant, mechanisms/strategies applied by the new viruses to establish persistent infections in their host, and the possible involvement of these new specific viruses in natural regulation of infection and transmission of insect pathogens including *C. L. asiaticus*, and potential interactions between the viral and bacterial communities in the gut.

Postdoctoral Associate

2013- 2017

Department of Plant Pathology, University of California

My primary research focused on discovering and manipulating viruses associated with *Diaphorina citri*, the Asian citrus psyllid which might be useful for virus-based biological control strategies. *D. citri*, the most important recent invasive insect vector of a plant pathogen in U.S., is the natural vector of the bacterial causal agent of citrus greening or Huanglongbing. Since our knowledge about insect viruses in general, and in particular of *D. citri*, is very limited, discovering insect specific viruses and evaluating their potential to be used as bio-pesticides was needed. I used Next Generation Sequencing (NGS) technology for viral metagenomic studies. My analysis led to the discovery of novel putative RNA and DNA viruses from different taxa, including the Picorna-like virus superfamily, *Reoviridae*, *Parvoviridae*, *Bunyaviridae*, *Flaviviridae* and an unclassified positive sense single-stranded RNA virus. I identified these new viruses in both native geographic regions, including China and Taiwan, and also from Brazil and the United States in which the insect and disease has newly emerged. Our ultimate goal was to select the best viral candidates to be used as biological control agents either in the form of wild type virus or as a delivery vehicle to knock down vital target genes in the insect host via the RNAi pathway to prevent transmission of the pathogen.

PROFESSIONAL SERVICE

- Co-Editor for a Special Issue “Ecology, evolution and biodiversity of plant and fungal associated viruses” in *Frontiers in Microbiology (Virology)*
- Editor for a Special Issue “Plant Virus Pathogenesis and Disease Control” in *Viruses*
- Referee of 15 manuscripts for several peer-reviewed journals
- Referee of 3 grant proposals for French National Research Agency (ANR) and US-Israel Binational Science Foundation (BSF)
- Served on the USDA-NIFA Pest and Beneficial Species in Agriculture Production System panel and reviewed 10 assigned grant proposals
- Served on the NSF-NIFA Plant-Biotic Interactions panel and reviewed 8 assigned grant proposals
- Professional affiliations: American Society for Virology (full member) and American Phytopathological Society (full member).

RESEARCH SUPPORT/AWARDS

- **Lead PI:** PLANT BREEDING PARTNERSHIP: Exploring resistance and tolerance to wheat streak mosaic complex in wheat wild relative, *Aegilops tauschii* **supported by USDA-NIFA** (\$560K#/\$380K*) 12/01/2021-11/30/2024
- **Lead PI:** Evaluating Resistance and Tolerance to *Wheat Streak Mosaic Virus* in Single and Mixed-infections With *Triticum Mosaic Virus* in Wild Relative, *Aegilops tauschii* **supported by NSF-IUCRC**(\$115K#/\$115K*) 10/01/2021-12/31/2022
- **Lead PI:** Understanding Interactions of the Wheat Virome, Mite Vector Genome and Wheat Cultivar Composition in Kansas **supported by the Kansas Wheat Commission** (\$55K#/\$31K*) 07/01/2019-06/30/2020
- **CO-PI:** Integrative and Innovative Approaches to Diminish Barley Yellow Dwarf Epidemics in Kansas Wheat **supported by the Kansas Wheat Commission**(\$99K#/\$48K*) 07/01/2018-06/30/2019

#Total funded budget

*Nouri's lab share

PEER REVIEWED JOURNAL PUBLICATIONS

*Corresponding Author

#Co-corresponding Author

&Co-first Author

Redila C, Prakash V, Nouri S*. 2021. Metagenomics analysis of the wheat virome identified novel plant and fungal-associated viruses. *Viruses*. doi.org/10.3390/v13122457

Redila C, Phipps S, Nouri S*. 2021. Full Genome Evolutionary Studies of Wheat Streak Mosaic-associated Viruses Using High-throughput Sequencing. *Front. Microbiol.* 12:699078. doi: 10.3389/fmicb.2021.699078

Falk BW and Nouri S#. 2020. Special Issue: "Plant Virus Pathogenesis and Disease Control". *Viruses* 12, 1049; doi:10.3390/v12091049

Chen Q, Nouri S, Zhang Y, Erickson A, Falk BW. 2020. Diaphorina citri reovirus is most closely related to fijiviruses. *Virology*, 547: 20-26

Nouri S, Matsumura EE, Kuo YW, Falk BW. 2018. Insect-specific viruses: From discovery to potential translational applications. *Current Opinion in Virology*, 33: 33-41

Matsumura EE, Coletta-Filho HD, Machado MA, Nouri S, Falk BW. 2018. Rescue of Citrus sudden death-associated virus in *Nicotiana benthamiana* plants from cloned cDNA: insights into mechanisms for expression of the three capsid proteins. *Molecular Plant Pathology*, 20(5): 611-625, DOI: 10.1111/mpp.12780

Matsumura EE, Nouri S, Falk BW, Machado MA. 2017. Deep Sequencing Analysis of RNAs from Citrus Plants Grown in a Citrus Sudden Death-affected Area Reveals Diverse Known and Putative Novel Viruses. *Viruses*, 24: 9 (4); doi: 10.3390/v9040092

Nouri S, Salem N, Nigg JC, Falk BW. 2016. A diverse array of new viral sequences identified in worldwide populations of the Asian citrus psyllid (*Diaphorina citri*) using viral metagenomics. *Journal of Virology*, 90: 2434-2445

Nouri S, Salem N, Falk BW. 2016. Complete genome sequence of Diaphorina citri-associated C virus, a novel putative RNA virus of the Asian citrus psyllid, Diaphorina citri. *Genome Announcement*, 4(4):e00639-16. doi: 10.1128/genomeA.00639-16

Matsumura EE, Nerva L, Nigg JC, Falk BW, Nouri S*. 2016. Complete genome sequence of the largest known "flavi-like virus", Diaphorina citri flavi-like virus (DcFLV), a novel virus of the Asian citrus psyllid, Diaphorina citri. *Genome Announcement*, 4(5):e00946-16. doi:10.1128/genomeA.00946-16

Stenger DC, Krugner R, Nouri S, Ferriol I, Falk BW, Sisterson MS. 2016. Sequence polymorphism in an insect RNA virus field population: A snapshot from a single point in space and time reveals stochastic differences among and within individual hosts. *Virology*, 498: 209-217

Matsumura EE, Dorta SO, Filho HDC, Nouri S, Machado MA. 2016. Genetic Structure and Molecular Variability of Citrus sudden death associated virus isolates from Infected Plants Grown in Citrus Sudden Death Affected Regions in Brazil. *Viruses*, 8: 330; doi: 10.3390/v8120330

Nandety RS, Kuo Y, Nouri S&, Falk BW. 2014. Emerging strategies for RNA interference (RNAi) applications in insects. *Bioengineered*, 6(1): 8-19

Nouri S, Aarevalo R, Falk BW, Groves RL. 2014. Genetic structure and molecular variability of Cucumber mosaic virus isolates in the United States. *PLOS ONE*, 9(5): e96582. Doi: 10.1371

NON-PEER-REVIEWED PUBLICATION

Kuo Y, Matsumura EE, Nigg JC, Chen Q, Henry E, Nouri S, Godfrey KE and Falk BW. 2020. ACP Are Full of Viruses. Can We Use Them Against HLB? Citrograph Magazine

INVITED ACADEMIC SEMINARS

- March 1st, 2022 Iowa State University, Department of Plant Pathology
- November 4, 2021 University of Missouri-Kansas City (UMKC), School of Biological Sciences
- February 26, 2020 Oklahoma State University, Dept of Entomology and Plant Pathology (cancelled because of COVID-19)
- April 9, 2019 KSU Dept Entomology
- April 12, 2019 University of Tulsa Dept of Biological Science
- October 9, 2019 Colorado State University Dept of Bio Ag Sciences

INVITED CONFERENCE/SCIENTIFIC MEETINGS SPEAKER

- June 7 2022 International Symposium of Plant Virus Epidemiology, Madrid, Spain
- March 2022 Joint ESA/APS-CD Meeting, San Juan, PR
- June 2019 12th Arthropod Genomics Symposium, Manhattan, KS
- July 2019 KSU Ecogen Summer Research Meeting
- August 2017 APS annual meeting: the hot topic session, San Antonio, TX

ORAL/POSTER PRESENTATIONS AFTER JOINING KSU

Nouri S., Redila C, Prakash V. (2022). Identification and Characterization of New Umbra-like Associated RNA in Wheat. American Society of Virology, Madison, WI.

Nouri S., Chen Q., Matsumura E.E., Kuo Y., Nigg J., Falk, B.W. (2022). Insect-specific viruses of the Asian citrus psyllid: From discovery to evolution to potential translational application. 2022 Joint SEB and APS-CD Meeting, San Juan, Puerto Rico.

Redila C., Phipps S., **Nouri S.** (2020). Studying the genetic variation of wheat streak mosaic-associated viruses in Kansas fields through high-throughput sequencing. APS Annual Meeting (virtual meeting)

Redila C., **Nouri S.** (2020). Characterizing the wheat virome: Discovery of novel plant and fungal-associated viruses. APS Annual Meeting (virtual meeting)

Phipps S., Redila C., Quintana T., **Nouri S.** (2019). Inquiries into *Wheat Streak Mosaic Virus* and Other WSM Associated Viruses. 1st Plant Pathology REEU Poster Symposium, Summer. Kansas State University, Manhattan, KS.

Piper S., Marshall J., **Nouri S.** (2018). *Cricket Paralysis Virus* Threatens Cricket Farm Business. 3rd Entomology Undergraduate Research Poster Symposium. Kansas State University, Manhattan, KS.