

## **Ksenia V. Krasileva**

Department of Plant Sciences & Howard Hughes Medical Institute  
University of California, Davis CA 95616

**E-mail:** [krasileva@ucdavis.edu](mailto:krasileva@ucdavis.edu)

**Phone:** (858) 784-1376

### **RESEARCH INTERESTS**

---

My research program combines the areas of **comparative genomics, plant cell biology and plant-microbe interactions**. I will focus on wheat and its fungal pathogens to investigate the innate immunity of cereals. I will apply comparative genomics and next-generation sequencing together with biochemical, cell-biological, and classical genetics approaches to decipher the molecular mechanisms that control plant innate immunity. This work will be of central importance to the generation of sustainable crops for the future.

### **EDUCATION**

---

- PhD. Microbiology, Designated Emphasis in Computational Biology  
University of California, Berkeley. 2011.
- BS. Microbiology, Genetics and Plant Biology. Honors.  
University of California, Berkeley. 2005.

### **PROFESSIONAL TRAINING**

---

- 2011-present. Post-doctoral Fellow. University of California, Davis.

**Federal funding:** AFRI-NIFA Fellowship. USDA. \$130,000 2012-2014

Advisor: Jorge Dubcovsky.

Research topic: "Development of functional genomics tools for wheat"

From the very beginning of my post-doc, I focused on adopting **exome-capture** and **next generation sequencing technologies** to sequence 1,500 lines from an EMS-mutagenized population of durum wheat. The prediction of the wheat proteome is the first necessary step towards development of exome capture technology and efficient sequencing of large

collections of either natural or mutagenized wheat lines. As such, I sequenced the transcriptome of our wheat species and led the development of a novel strategy for assembling a tetraploid wheat transcriptome in which homeologous sequences are separated by phasing of mapped Illumina reads (Krasileva et al. 2013). This transcriptome was used to design a custom exome capture for sequencing wheat mutant lines. Exome capture technique allows the identification of several hundred mutations in the protein-coding sequences in each line and computational prediction of their effect on protein function. The resulting set of sequenced EMS lines comprises the first reverse genomics resource in wheat.

During 2012-2013, I conducted a forward genetics screen by exposing our mutagenized wheat population to natural disease pressure in the field and identified mutants with either **enhanced resistance** or **increased disease susceptibility** to stripe rust. Wheat exome capture technology has enabled me to rapidly map these mutations. The resulting collection of wheat mutant lines will serve as the foundation for my future lab's investigation of **wheat innate immunity**.

- 2005-2011. Graduate Student Researcher. University of California, Berkeley

Advisor: Brian J Staskawicz

Research topic: “The Molecular Basis for Recognition of Oomycete Effectors in *Arabidopsis*”

During my PhD work in the Staskawicz lab, I studied the **molecular basis of pathogen perception by *Arabidopsis***. Using an *in planta* co-immunoprecipitation assay, I showed a physical association between plant immune receptor and a pathogen-derived effector molecule; further analysis of the receptor uncovered the series of events leading to downstream immune activation (Krasileva et al. 2010). In collaboration with a structural biology group, I obtained a crystal structure of the effector molecule; mutagenesis of the effector revealed two non-overlapping surfaces recognized by two alleles of the plant immune receptor (Chou, Krasileva et al. 2011). By examining the natural variation in the *Arabidopsis* immune receptor alleles, I demonstrated that recognition of specific pathogen effectors arose independently in multiple plant lines – and this existing diversity can be harnessed to broaden recognition repertoire of plant immune receptors (Krasileva et al. 2011).

- 2002-2005. Undergraduate Student Researcher. University of California, Berkeley.

Advisor: Steven E Lindow

Research topic: “Mechanisms of quorum sensing inhibition by bacterial epiphytes”

## TEACHING

---

- **Mentorship** [2012-2013]

During my post-doctoral studies at University of California Davis, I have mentored a pre-PhD bioinformatics specialist Vince Buffalo providing guidance for software development, including peer reviewed and publicly available ‘findorf’ and ‘blast2cap3’ programs.

- **Undergraduate Research Mentor** [2007-2011]

During my PhD studies, I mentored three undergraduate students: Margie Payumo, Connie Cheng and Kelsie Morioka. Under my mentorship, both Margie and Connie received competitive undergraduate research awards and completed their Senior Thesis projects.

- **Guest Lecturer** [2008-2010]

I gave several guest lectures in the undergraduate course “Agriculture and Society” at the University of California, Berkeley.

- **Teaching Assistant** [2007]

I helped graduate students learn basic programming during a week-long course “Introduction to Programming for Bioinformatics” at University of California, Berkeley.

- **Graduate Student Instructor** [2006-2007]

As a graduate student instructor, I helped teach two undergraduate classes at UC Berkeley: a medium-sized class “Introduction to Comparative Virology” and a large undergraduate class “Introductory Biology 1A”. For this work, I received a teaching recognition award - a campus-wide **Outstanding Graduate Student Instructor Award**

- **Course Instructor** [2006]

I designed and taught “Summer Explorations in Microbiology”, a summer-course offered to 7-8<sup>th</sup> grade middle school students at University of California, Berkeley. I was responsible for designing and conducting this two-part course that consisted of a lecture and a laboratory exercise.

## PUBLICATIONS

---

11 publications (5 as first/co-first author)

**Krasileva KV**, Buffalo V, Bailey P, Pearce S, Ayling S, Tabbita F, Soria M, Wang S, Consortium I, Akhunov E, Uauy C, Dubcovsky J: “Separating homeologs by phasing in the tetraploid wheat transcriptome”. *Genome Biology* 2013, 14:R66. (2013)

Bart R, Cohn M, Kassen A, McCallum EJ, Shybut M, Petriello A, **Krasileva K**, Dahlbeck D, Medina C, Alicai T, Kumar L, Moreira LM, Neto JR, Verdier V, Santana MA, Kositcharoenkul N, Vanderschuren H, Gruissem W, Bernal A, Staskawicz BJ. “High-throughput genomic sequencing of cassava bacterial blight strains identifies conserved effectors to target for durable resistance.” *Proceeding of National Academy of Sciences U S A*, 109(28):E1972-9. (2012)

Goritschnig S, **Krasileva KV**, Dahlbeck D, Staskawicz BJ. “Computational prediction and molecular characterization of an oomycete effector and the cognate Arabidopsis resistance gene” *PLoS Genetics* 8(2):e1002502. (2012)

Win J, **Krasileva KV**, Kamoun S, Shirasu K, Staskawicz BJ, Banfield MJ. “Sequence divergent RXLR effectors share a structural fold conserved across plant pathogenic oomycete species” *PLoS Pathogens* 8(1): e1002400. (2012)

**Krasileva KV**, Zheng C, Leonelli L, Goritschnig S, Dahlbeck D, Staskawicz BJ. “Global analysis of *Arabidopsis* / downy mildew interactions reveals prevalence of incomplete resistance and rapid evolution of pathogen recognition” *PLoS One*, 6: e28765. (2011)

Zhao B, Dahlbeck D, **Krasileva KV**, Fong RW, Staskawicz BJ. “Computational and Biochemical Analysis of the Xanthomonas Effector AvrBs2 and Its Role in the Modulation of Xanthomonas Type Three Effector Delivery.” *PLoS Pathogens*. 12 :e1002408. (2011)

Chou S\*, **Krasileva KV\***, Holton J, Steinbrenner A, Alber T, Staskawicz BJ. “*Hyaloperonospora arabidopsidis* ATR1 effector is a repeat protein with distributed recognition surfaces” *Proceeding of National Academy of Sciences U S A*. 108(32): 13323-8. (2011)

**\*equal contribution**

Potnis N\*, **Krasileva K\***, Chow V, Almeida NF Jr, Patil PB, Ryan RP, Sharlach M, Behlau F, Dow JM, White FF, Preston JF, Vinatzer BA, Koebnik R, Setubal JC, Norman DJ, Staskawicz BJ, Jones JB. “Comparative Genomics Reveals Diversity among Xanthomonads Infecting Tomato and Pepper”. *BMC Genomics*, 12(1): 146. (2011)

**\*equal contribution**

**Krasileva KV**, Dahlbeck D, Staskawicz BJ. “Activation of an *Arabidopsis* Resistance Protein Is

Specified by the *in Planta* Association of Its Leucine-Rich Repeat Domain with Cognate Oomycete Effector”. *Plant Cell*, 22:1-16. (2010)

Dulla GF, **Krasileva KV**, Lindow SE. “Interference of Quorum Sensing in *Pseudomonas syringae* by Bacterial Epiphytes that Limit Iron Availability”. *Environmental Microbiology*, 12(6): 1762-74. (2010)

Win J, Morgan W, Bos J, **Krasileva KV**, Cano LM, Chaparro-Garcia A, Ammar L, Staskawicz BJ, Kamoun S. “Adaptive Evolution Has Targeted the C-terminal Domain of the RXLR Effectors of Plant Pathogenic Oomycetes”. *Plant Cell*, 19: 2349-69. (2007)

## AWARDS

---

**2012-2014 Federal Principle Investigator grant** through the United States Department of Agriculture AFRI-NIFA postdoctoral fellowship program.

**2007** Outstanding Graduate Student Instructor Award, UC Berkeley.

**2006** Honorable Mention, NSF Graduate Student Fellowship.

**2005** Plant and Microbial Biology departmental citation, UC Berkeley.

**2003-2005** Sponsored Projects for Undergraduate Research Fellowship, UC Berkeley.

**2004** Summer Undergraduate Research Fellowship, UC Berkeley.

## PRESENTATIONS

---

**2014** *Plant and Animal Genome Conference* | San Diego, CA | Invited Speaker

**2013** *Beyond the Genome Conference* | San Francisco, CA | Selected Speaker

**2012** *New Phytologist Conference* | Fallen Leaf Lake, CA | Poster

**2012** *Howard Hughes Medical Institute Conference* | Janelia Farm, VA | Poster

**2011** *Department of Plant Pathology Seminars, UC Davis* | Davis, CA | Invited Speaker

**2010** *Gordon Research Conference* | Holderness, NH | Poster

**2010** *International Congress MPMI* | Quebec, Canada | Selected Speaker

**2008** *Bay Area Microbial Pathogenesis Symposium* | San Francisco, CA | Selected Speaker

**2008** *Keystone Symposium in Plant Innate Immunity* | Keystone, Colorado | Poster

**2007** *Bay Area Microbial Pathogenesis Symposium* | San Francisco, CA | Poster

## **OUTREACH**

---

- **Invited Speaker** [2011]

Sally Ride Science Camp for girls, University of California Berkeley. Sally Ride camps encourage girls' interest and participation in sciences. I was invited to give a guest lecture for the girls telling about my positive experience in sciences from high school through Ph.D.

- **Panel Speaker** [2007-2008]

Biology Majors Fair, "Beyond the B.A.: Graduate and Professional Schools" at University of California, Berkeley

- **Volunteer in Community Outreach and Education** [2006]

Outreach course titled "Agriculture, Molecular Biology and Genetically Modified Organisms: GMOs in Food" that was part of the Advanced training of UCCE Master Gardeners in Santa Clara County. Directed by regional outreach specialist Dr. Peggy Lemaux.

## **SOCIETIES**

---

American Association for the Advancement of Science.

The International Society for Molecular Plant-Microbe Interactions.

## REFERENCES

---

**Dr. Jorge Dubcovsky**

UC Davis Professor & Howard Hughes Medical Institute researcher  
Department of Plant Sciences  
University of California | Davis, CA 95616, USA  
(530) 752-5159 | [jdubcovsky@ucdavis.edu](mailto:jdubcovsky@ucdavis.edu)

**Dr. Brian J. Staskawicz**

Maxine J. Elliot Professor  
Department of Plant and Microbial Biology  
University of California | Berkeley, CA 94720, USA  
(510) 642-3721 | [stask@berkeley.edu](mailto:stask@berkeley.edu)

**Dr. Gitta Coaker**

Associate Professor of Plant Pathology  
Department of Plant Pathology  
576 Hutchison Hall  
University of California | Davis, CA 95616, USA  
530-752-6541 | [glcoaker@ucdavis.edu](mailto:glcoaker@ucdavis.edu)

**Dr. Sophien Kamoun**

Senior Scientist and Head  
The Sainsbury Laboratory  
Norwich Research Park | NR4 7UH, UK  
44 (0) 1603 450410 | [sophien.kamoun@tsl.ac.uk](mailto:sophien.kamoun@tsl.ac.uk)