



Cong Feng

Bioinformatics · Genomics · Population genetics

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"Be the change that you want to see in the world."

Summary

As an **Assistant Researcher** at the Agricultural Genomics Institute, Chinese Academy of Agricultural Sciences for 6 years, I've immersed myself in the realms of genomics and population genetics. My pivotal roles have spanned from the development of bioinformatics tools, conducting population genetic analyses on wheat/pea, to gene mining. My contributions have been published in top-tier international journals, including *Nature*.

Proficient in crafting bioinformatics analysis tools, workflows, and setting up specialized websites. Love to contribute to open sources and tech communities by sharing knowledge and experience. I have an innate interest in devising innovative problem-solving methodologies for intricate tasks and am always on the hunt to learn and implement new technologies and tools.

Education

College of Basic Medical Sciences, Chongqing Medical University

Chongqing, China

B.S. in Bioinformatics

Sept. 2015-Jul. 2019

Activities: Student Union External Relations Officer (1 year); Head, Discipline Inspection Department (1 year)

Honors & Awards

- Provincial & Municipal**
2018 — Finalist, Microsoft Imagine Cup — "Code with Purpose" (Chongqing Regional)
- University**
2018 — First Prize, Chongqing Medical University Entrepreneurship Competition
- Faculty & Department**
2017 — Outstanding Student
2016 — Outstanding Student Cadre
2016 — Third Prize, "Ying Yao Plan" Research Project, College of Basic Medical Sciences

Work Experience

Agricultural Genomics Institute, Chinese Academy of Agricultural Sciences

Shenzhen, China

Assistant Researcher

Jul. 2019 - Present

Wheat population genomics (Watkins landraces & Worldwide Wheat G2B; published in *Nature*)

- Led large-scale variant discovery (SNPs, SVs, CNVs) for 1,051 Watkins accessions; built QC and joint-calling workflows.
- Developed an LD-aware haplotype matrix construction pipeline; derived TagSNP panels capturing population diversity.
- Designed NAM imputation and NAM-GWAS methodologies to enhance power in complex trait mapping.
- Built community resources: Global Grain Genomics Research Program (<https://g3rp.com>) and WWWG2B (<https://wwwwg2b.com>); engineered an interactive Manhattan-plot viewer for GWAS.
- Authored and maintained HAPPE for Excel-based population haplotype visualization (<https://github.com/fengcong3/HAPPE>).

Pea genetics (Mendel Pea G2P; published in *Nature*)

- Resolved/validated causal haplotypes for three previously undecoded classical traits (pod colour, pod shape, flower position).
- Performed comprehensive haplotype analyses for four cloned genes (seed shape, cotyledon colour, plant height, flower colour).
- Led multi-omics integration (RNA-seq, methylation, RT-PCR) to support gene-to-phenotype decoding.
- Contributed to the MendelPeaG2P data portal (<https://mendelpea.com>).

BGI Group

Shenzhen, China

Bioinformatics Engineer Intern

Jun. 2018 - Aug. 2018

- Performed *de novo* genome assembly for *Lycium ruthenicum* and *L. barbarum*, contributing to medicinal-plant genomics.
- Developed components of a pipeline to identify and characterize cysteine-rich peptides with pharmaceutical potential.

Conferences

- 2025/05/08-11, **Attendee**, The 3rd Conference on Biotech Wheat Breeding, Taian, China.
- 2024/08/19-22, **Attendee**, Plant Genomics in China XXIII, Haikou, China, <http://www.plantgenomics.cn/>
- 2024/07/21-27, **Attendee**, XX International Botanical Congress, Madrid, Spain, <https://ibcmadrid2024.com/>
- 2024/06/05-07, **Workshop organizer and speaker**, Crop Genomics to Breeding: Decode, Discover, Design and Deliver, the Plant

5. 2022/07/17-29, **Attendee**, Peking University Institute of Modern Agriculture 2022 Molecular Breeding Training Program, Shandong, China.

Publications

(Note: * the first author; † the corresponding author. For briefing, not all authors are listed)

1. **Cong Feng***, Baizhi Chen*, Julie Hofer*, Yan Shi, Mei Jiang, et al., Claire Domoney, Noel Ellis, Noam Chayut, Shifeng Cheng†. Genomic and Genetic Insights into Mendel's Pea Genes. **Nature**, DOI: 10.1038/s41586-025-08891-6. April 23, 2025. <https://www.nature.com/articles/s41586-025-08891-6>. **IF: 50.5**
2. Shifeng Cheng†*, **Cong Feng***, Luzie U. Wingen*, et al., Simon Griffiths†. Harnessing landrace diversity empowers wheat breeding. <https://doi.org/10.1038/s41586-024-07682-9>. 2024 June. **Nature**. **IF: 50.5**
3. Hafeez, Amber N., Laetitia Chartrain, **Cong Feng**, et al., James K. M. Brown. Septoria Tritici Blotch Resistance Gene Stb15 Encodes a Lectin Receptor-like Kinase. doi:10.1038/s41477-025-01920-2. 2025. **Nature Plants**. **IF: 13.6**
4. Petros P Sigalas, Peter R Shewry, Andrew Riche, Luzie Wingen, **Cong Feng**, et al., Shifeng Cheng, Simon Griffiths, Malcolm J Hawkesford. Improving wheat grain composition for human health by constructing a QTL atlas for essential minerals. **Commun Biol** 7, 1001 (2024). <https://doi.org/10.1038/s42003-024-06692-7>. **IF: 5.2**
5. Tom O'Hara, et al., **Cong Feng**, Mei Jiang, Shifeng Cheng, Susanne Dreisigacker, Beat Keller, Brande BH Wulff, Cristóbal Uauy, Paul Nicholson. The wheat powdery mildew resistance gene Pm4 also confers resistance to wheat blast. **Nat. Plants** 10, 984–993 (2024). <https://doi.org/10.1038/s41477-024-01718-8>. **IF: 13.6**
6. **Cong Feng***, Xinwei Wang, Shishi Wu, Weidong Ning, Bo Song, J Yan, S Cheng†. HAPPE: A tool for population haplotype analysis and visualization in editable excel tables. **Frontiers in Plant Science**, 2298. 2022. **IF: 5.3**
7. Djivan Prentout, Olga Razumova, Bénédicte Rhoné, Hélène Badouin, Hélène Henri, **Cong Feng**, Jos Käfer, Gennady Karlov, Gabriel AB Marais. An efficient RNA-seq-based segregation analysis identifies the sex chromosomes of Cannabis sativa. **Genome Research** 30 (2): 164–72. <https://doi.org/10.1101/gr.251207.119>. **IF: 5.5**