

## Publications acknowledging WheatCAP support

WheatCAP 2022 in [Google Scholar](#)

### 2022 ( publications)

1. Alarcón-Reverte R, Xie Y, Stromberger J, Cotter JD, Mason RE, Pearce S (2022) Induced mutations in *ASPARAGINE SYNTHETASE-A2* reduce free asparagine concentration in the wheat grain. *Crop Science* 62:1484–1496. <https://doi.org/10.1002/csc2.20760>
2. Baenziger PS, Frels KA, Boehm J, Belamkar V, Rose DJ, Xu L, Wegulo SN, Regassa T, Easterly AC, Creech CF, Santra DK, Klein RN, Jin Y, Kolmer J, Chen MS, Guttieri MJ, Bai G, El-Basyoni Salah I, Masterson SD, Poland J (2022) Registration of ‘Epoch’ hard red winter wheat. *Journal of Plant Registrations* 16:613–621. <https://doi.org/10.1002/plr2.20247>
3. Chen H, Su Z, Tian B, Liu Y, Pang Y, Kavetskyi V, Trick HN, Bai G (2022) Development and optimization of a Barley stripe mosaic virus-mediated gene editing system to improve Fusarium head blight resistance in wheat. *Plant Biotechnology Journal* 20:1018–1020. <https://doi.org/10.1111/pbi.13819>
4. Chen H, Su Z, Tian B, Hao G, Trick HN, Bai G (2022) TaHRC suppresses the calcium-mediated immune response and triggers wheat Fusarium head blight susceptibility. *Plant Physiology* 190:1566–1569. <https://doi.org/10.1093/plphys/kiac352>
5. Chen Y, Liu Y, Zhang J, Torrance A, Watanabe N, Adamski NM, Uauy C (2022) The *Triticum ispahanicum* elongated glume locus P2 maps to chromosome 6A and is associated with the ectopic expression of SVP-A1. *Theor Appl Genet* 135:2313–2331. <https://doi.org/10.1007/s00122-022-04114-y>
6. Chu C, Wang S, Rudd JC, Ibrahim AMH, Xue Q, Devkota RN, Baker JA, Baker S, Simoneaux B, Opena G, Dong H, Liu X, Jessup KE, Chen MS, Hui K, Metz R, Johnson CD, Zhang ZS, Liu S (2022) A new strategy for using historical imbalanced yield data to conduct genome-wide association studies and develop genomic prediction models for wheat breeding. *Mol Breeding* 42:18. <https://doi.org/10.1007/s11032-022-01287-8>
7. Dang C, Zhang J, Dubcovsky J (2022) High-resolution mapping of *Yr78*, an adult plant resistance gene to wheat stripe rust. *The Plant Genome*, 15: e20212. <https://doi.org/10.1002/tpg2.20212> .

8. Debernardi JM, Woods DP, Li K, Li C, Dubcovsky J (2022) MiR172-APETALA2-like genes integrate vernalization and plant age to control flowering time in wheat. *PLoS Genetics*, 18: e1010157. <https://doi.org/10.1371/journal.pgen.1010157>.
9. DeWitt N, Guedira M, Murphy JP, Marshall D, Mergoum M, Maltecca C, Brown-Guedira G (2022) A network modeling approach provides insights into the environment-specific yield architecture of wheat. *Genetics* 221(3) iyac076. <https://doi.org/10.1093/genetics/iyac076>
10. Fan M, Zhang X, Nagarajan R, Fan M, Zhang X, Nagarajan R, Zhai W, Rauf Y, Jia H, Ma Z, Yan LL (2022) Natural variants and editing events provide insights into routes for spike architecture modification in common wheat. *The Crop Journal*. <https://doi.org/10.1016/j.cj.2022.04.009>
11. Gill HS, Halder J, Zhang J, Rana A, Kleinjan J, St. Amand P, Bernardo A, Bai G, Sehgal SK (2022) Whole-genome analysis of hard winter wheat germplasm identifies genomic regions associated with spike and kernel traits. *Theor Appl Genet* 135:2953–2967. <https://doi.org/10.1007/s00122-022-04160-6>
12. Glenn P, Zhang J, Brown-Guedira G, DeWitt N, Cook JP, Li K, Akhunov E, Dubcovsky J (2022) Identification and characterization of a natural polymorphism in *FT-A2* associated with increased number of grains per spike in wheat. *Theor Appl Genet* 135:679-692. <https://doi.org/10.1007/s00122-021-03992-y>
13. He F, Wang W, Rutter WB, KW Jordan, Ren J, Taagen E, DeWitt N, Sehgal D, Sukumaran S, Dreisigacker S, Reynolds M, Liu S, Chen J, Fritz A, Cook J, Brown-Guedira G, Pumphrey M, Carter A, Sorrells M, Dubcovsky J, Hayden MJ, Akhunova A, Morrell PL, Szabo L, Rouse M, Akhunov E (2022) Genomic variants affecting homoeologous gene expression dosage contribute to agronomic trait variation in allopolyploid wheat. *Nat Commun* 13:826. <https://doi.org/10.1038/s41467-022-28453-y>
14. Jiang D, Hua L, Zhang C, Li H, Wang Z, Li J, Wang G, Song R, Shen T, Li H, Bai S, Liu Y, Wang J, Li H, Dubcovsky J, Chen S 2022. Mutations in the miRNA165/166 binding site of the HB2 gene result in pleiotropic effects on morphological traits in wheat. *The Crop Journal*. Online first. <https://doi.org/10.1016/j.cj.2022.05.002> .
15. Kissing Kucek L, Dawson JC, Darby H, Mallory E, Davis M, Sorrells ME (2021) Breeding wheat for weed-competitive ability: II—measuring gains from selection and local adaptation. *Euphytica* 217:203. <https://doi.org/10.1007/s10681-021-02905-w>
16. Kissing Kucek L, Mallory EB, Darby HM, Dawson JC, Sorrells ME (2021) Breeding wheat for weed-competitive ability: I. Correlated traits. *Euphytica* 217:202. <https://doi.org/10.1007/s10681-021-02930-9>
17. Kuzay S, Lin H, Li C, Chen S, Woods D, Zhang J, Dubcovsky J (2022) WAPO-A1 is the causal gene of the 7AL QTL for spikelet number per spike in wheat. *PLOS Genetics* 18:e1009747. <https://doi.org/10.1371/journal.pgen.1009747>
18. Larkin DL, Mason RE, Moon DE, Holder AL, Ward BP, Brown-Guedira G (2021) Predicting Fusarium Head Blight Resistance for Advanced Trials in a Soft Red Winter Wheat

- Breeding Program With Genomic Selection. *Frontiers in Plant Science* 12.  
<https://doi.org/10.3389/fpls.2021.715314>
19. Li H, Zhang F, Zhao J, Bai G, St. Amand P, Bernardo A, Ni Z, Sun Q, Su Z (2022) Identification of a novel major QTL from Chinese wheat cultivar Ji5265 for Fusarium head blight resistance in greenhouse. *Theor Appl Genet* 135:1867–1877.  
<https://doi.org/10.1007/s00122-022-04080-5>
  20. Lopez SR, Wiersma AT, Strauss NM, Watkins T, Baik BK, Zhang G, Sehgal SK, Kolb FL, Poland JA, Mason RE, Carter AH, Olson EL (2022) Description of U6719-004 wheat germplasm with YrAS2388R stripe rust resistance introgression from *Aegilops tauschii*. *Journal of Plant Registrations*: <https://doi.org/10.1002/plr2.20226>
  21. Luo J, Rouse MN, Hua L, Li H, Li B, Li T, Zhang W, Gao C, Wang Y, Dubcovsky J, Chen S (2022). Identification and characterization of *Sr22b*, a new allele of the wheat stem rust resistance gene *Sr22* effective against the Ug99 race group. *Plant Biotechnology Journal*. 20: 554–563. <https://doi.org/10.1111/pbi.13737>.
  22. Morales N, Ogbonna AC, Ellerbrock BJ, Bauchet GJ, Tantikanjana T, et al. (57 co-authors including Jean-Luc Jannink, Clay Birkett, and David Waring) 2022. Breedbase: a digital ecosystem for modern plant breeding. *G3*. <https://doi.org/10.1093/g3journal/jkac078>
  23. Moriconi JI, Silva M, Zhang J, Tranquilli GE, Santa-María GE (2022) A genome-wide association study unveils key chromosome regions involved in determining sodium accumulation in wheat under conditions of low potassium supply. *Journal of Plant Physiology* 275:153739. <https://doi.org/10.1016/j.jplph.2022.153739>
  24. Peters Haugrud AR, Zhang Q, Green AJ, Xu SS, Faris JD (2022) Identification of stable QTL controlling multiple yield components in a durum × cultivated emmer wheat population under field and greenhouse conditions. *G3 Genes|Genomes|Genetics* jkac281. <https://doi.org/10.1093/g3journal/jkac281>
  25. Prather S, Schneider T, Gaham Godoy J, Odubiyi S, Bosque-Perez NA, Rashed A, Rynearson S, Pumphrey MO (2022) Reliable DNA Markers for a Previously Unidentified, Yet Broadly Deployed Hessian Fly Resistance Gene on Chromosome 6B in Pacific Northwest Spring Wheat Varieties. *Frontiers in Plant Science* 13.  
<https://doi.org/10.3389/fpls.2022.779096>
  26. Rivera-Burgos LA, Brown-Guedira G, Johnson J, Mergoum M, Cowger, C (2022) Accounting for heading date gene effects allows detection of small-effect QTL associated with resistance to *Septoria nodorum* blotch in wheat. *PLoS one* 17(5) e0268546.
  27. Rooney TE, Kunze KH, Sorrells ME (2022a) Genome-wide marker effect heterogeneity is associated with a large effect dormancy locus in winter malting barley. *The Plant Genome*:e20247. <https://doi.org/10.1002/tpg2.20247>
  28. Rooney TE, Sweeney DW, Sorrells ME (2022b) Time series barley germination is predictable and associated with known seed dormancy loci. *Crop Science* 62:100–119.  
<https://doi.org/10.1002/csc2.20638>

29. Sandhu KS, Merrick LF, Sankaran S, Zhang Z, Carter AH (2022) Prospectus of Genomic Selection and Phenomics in Cereal, Legume and Oilseed Breeding Programs. *Frontiers in Genetics* 12. <https://doi.org/10.3389/fgene.2021.829131>
30. Sandhu KS, Mihalyov PD, Lewien MJ, Pumphrey MO, Carter AH (2021) Genomic Selection and Genome-Wide Association Studies for Grain Protein Content Stability in a Nested Association Mapping Population of Wheat. *Agronomy* 11:2528. <https://doi.org/10.3390/agronomy11122528>
31. Sandhu KS, Patil SS, Aoun M, Carter AH (2022) Multi-Trait Multi-Environment Genomic Prediction for End-Use Quality Traits in Winter Wheat. *Frontiers in Genetics* 13. <https://doi.org/10.3389/fgene.2022.831020>
32. Sandro P, Kucek LK, Sorrells ME, Dawson JC, Gutierrez L (2022) Developing high-quality value-added cereals for organic systems in the US Upper Midwest: hard red winter wheat (*Triticum aestivum* L.) breeding. *Theor Appl Genet.* <https://doi.org/10.1007/s00122-022-04112-0>
33. Sweeney DW, Kunze KH, Sorrells ME (2022) QTL x environment modeling of malting barley preharvest sprouting. *Theor Appl Genet* 135:217–232. <https://doi.org/10.1007/s00122-021-03961-5>
34. Sweeney DW, Rooney TE, Sorrells ME (2021) Gain from genomic selection for a selection index in two-row spring barley. *The Plant Genome* 14:e20138. <https://doi.org/10.1002/tpg2.20138>
35. Sweeney DW, Rooney TE, Walling JG, Sorrells ME (2022) Interactions of the barley SD1 and SD2 seed dormancy loci influence preharvest sprouting, seed dormancy, and malting quality. *Crop Science* 62:120–138. <https://doi.org/10.1002/csc2.20641>
36. Taagen E, Jordan K, Akhunov E, Sorrells ME, Jannink JL (2022) If It Ain't Broke, Don't Fix It: Evaluating the Effect of Increased Recombination on Response to Selection for Wheat Breeding. *G3 Genes | Genomes | Genetics* jkac291. <https://doi.org/10.1093/g3journal/jkac291>
37. Venegas J, Guttieri MJ, Boehm Jr. JD, Graybosch R, Bai G, St. Amand PC, Palmer N, Hussain W, Blecha S, Baenziger PS (2022) Genetic architecture of the high-inorganic phosphate phenotype derived from a low-phytate mutant in winter wheat. *Crop Science* 62:1228–1241. <https://doi.org/10.1002/csc2.20738>
38. Wu J, Qiao L, Liu Y, Fu B, Nagarajan R, Rauf Y, Jia H, Yan LL (2022) Rapid identification and deployment of major genes for flowering time and awn traits in common wheat. *Frontiers in Plant Science* 13. <https://doi.org/10.3389/fpls.2022.992811>
39. Xu Y, La G, Fatima N, Liu Z, Zhang L, Zhao L, Chen MS, Bai G (2021) Precise mapping of QTL for Hessian fly resistance in the hard winter wheat cultivar 'Overland.' *Theor Appl Genet* 134:3951–3962. <https://doi.org/10.1007/s00122-021-03940-w>
40. Zhang G, Martin TJ, Fritz AK, Li Y, Seabourn BW, Chen RY, Bai G, Bowden RL, Chen M-S, Rupp J, Jin Y, Chen X, Kolmer JA, Marshall DS (2022) Registration of 'KS Hamilton' hard red winter wheat. *Journal of Plant Registrations* 16:73–79. <https://doi.org/10.1002/plr2.20190>

41. Zhang J (2022) Check CRISPR editing events in transgenic wheat with next-generation sequencing. In: Wani SH, Kumar A (eds) Genomics of Cereal Crops. Springer US, New York, NY, pp 95–106
42. Zhang J, Gill HS, Brar NK, Halder J, Ali S, Liu X, Bernardo A, St. Amand P, Bai G, Gill US, Turnipseed B, Sehgal SK (2022) Genomic prediction of Fusarium head blight resistance in early stages using advanced breeding lines in hard winter wheat. The Crop Journal. <https://doi.org/10.1016/j.cj.2022.03.010>
43. Zhang J, Gill HS, Halder J, Brar NK, Ali S, Bernardo A, St. Amand P, Bai G, Turnipseed B, Sehgal SK (2022) Multi-locus genome-wide association studies to characterize Fusarium Head Blight (FHB) resistance in Hard Winter Wheat. Frontiers in Plant Science 13. <https://doi.org/10.3389/fpls.2022.946700>
44. Zhang L, Xu Y, Chen M-S, Su Z, Liu Y, Xu Y, La G, Bai G (2022) Identification of a major QTL for Hessian fly resistance in wheat cultivar ‘Chokwang.’ The Crop Journal 10:775–782. <https://doi.org/10.1016/j.cj.2021.08.004>
45. Zhang XY, Jia HY, Li T, Wu JZ, Nagarajan R, Lei L, Powers C, Kan CC, Hua W, Liu ZY, Chen C, Carver BF, Yan LL (2022) TaCol-B5 modifies spike architecture and enhances grain yield in wheat. Science 376:180–183. <https://doi.org/10.1126/science.abm0717>
46. Zhao L, Ge W, Lyu Z, Xu S, Xu Y, Bernardo A, Zhang Q, Xu S, Wang H, Kong L, Bai G (2022) Development and validation of diagnostic markers for the wheat Fusarium head blight resistance gene *Fhb7*. Crop Science 62:1903–1911. <https://doi.org/10.1002/csc2.20754>
47. Zhao L, Su P, Hou B, Wu H, Fan Y, Li W, Zhao J, Ge W, Xu S, Wu S, Ma X, Li A, Bai G, Wang H, Kong L (2022) The Black Necrotic Lesion Enhanced Fusarium graminearum Resistance in Wheat. Frontiers in Plant Science 13. <https://doi.org/10.3389/fpls.2022.926621>