

Charles Chen

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Ph.D. Quantitative Genetics, University of British Columbia
Vancouver, BC Canada, November 2009

Employment History

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|-----------------------------------|------------------------------------|---------------|
| • Assistant Professor | Oklahoma State University | 2015- current |
| • Scientist | Genetic Resource Program
CIMMYT | 2013-2014 |
| • Postdoctoral Research Associate | Cornell University | 2009-2012 |
| • Statistical Analyst | Gramene Database | 2009-2012 |

Selected List of Peer-reviewed Publications

1. Zhang N., Y. Gibson, N. Lepak, P. Li, L. Dedow, **C. Chen**, Y.-S. So, T. Bruntnell, M. Stitt and E. Buckler. 2015. Genome-wide association study of carbon and nitrogen metabolism in the maize nested association mapping population. bioRxiv doi:<http://dx.doi.org/10.1101/010785>
2. Willcox, M., J. A. Burgueno Ferreira, E. Rodriguez Chanona, A. Guadarrama, D. Jeffer, E. Buckler, S. Hearn and **C. Chen**. 2015. Mining alleles from the CIMMYT maize germplasm bank for tar spot disease complex resistance. Current Opinion of Plant Biology (in prep).
3. Raghavan, C., **C. Chen**, J. Ulat, V. Bartolome and H. Liang. 2015. Brown spot disease in rice- can we move from association to marker development? Molecular Breeding (submitting)
4. Gamal El-Dien, O., B. Ratcliffe, J. Klápště, **C. Chen**, I. Poth and Y.A. El-Kassaby. 2015. Genomic prediction accuracy of growth and wood quality attributes of Interior Spruce in space using genotyping-by-sequencing. BMC Genomics (accepted)
5. Ratcliffe, B., O. Gamal El-Dien, J. Klápště, I. Poth, **C. Chen**, B. Jaquish and Y.A. El-Kassaby. 2015. A comparison of genomic selection models across time in Interior Spruce (*Picea engelmannii* x *glauca*) using high density SNP imputation methods. Heredity (accepted)
6. Gamal El-Dien, O., B. Ratcliffe, J. Klápště, I. Porth, **C. Chen**, Y.A. El-Kassaby. 2015. Implementation of the realized genomic relationship matrix to open-pollinated family testing: additive and non-additive genetic effects in interior spruce. New Phytologist (in review)
7. Sandip, M., **C. Chen** and R. Varshney. 2015. Identification of candidate genes from a "QTL-hotspot" region for drought tolerance in chickpea using high density bin mapping and whole genome re-sequencing. (submitting)
8. Huang, C.L., C.W. Ho, Y.-C. Chiang, Y. Shigemoto, T.-W. Hsu, C.-C. Hwang, X.-J. Ge, **C. Chen**, T.-H. Wu, C.-H. Chou, H.-J. Huang, T. Gojobori, N. Osaka and T.-Y. Chiang. 2014. Adaptive divergence with gene flow in incipient speciation of *Miscanthus floridulus/sinensis* complex (Poaceae). The Plant Journal doi:10.1111/tpj.12676

9. **Chen, C.** and K. Ritland. 2013. Lineage specific mapping of quantitative trait loci. *Heredity* 2013:1-8, doi:10.1038/hdy.2013.24
10. **Chen, C.**, S. E. Mitchell, R. J. Elshire, E. S. Buckler and Y. A. El-Kassaby. 2013. Mining conifer's mega-genome using rapid and efficient multiplexed high-throughput genotyping-by-sequencing (GBS) SNP discovery platform. *Tree Genetics and Genomics*, doi:10.1007/s11295-013-0657-1
11. Lipka, A., M. Gore, M. Megallanes-Lundback, A. Mesberg, H. Lin, T. Tiede, **C. Chen**, C. Robin Buell, E. Buckler, T. Rocheford and D. DellaPenna. 2013. Genome-wide association study and pathway-level analysis of Tocochromanol levels in maize grain. *G3* 7: 1287-1299
12. Spindel, J., M. Wright, **C. Chen**, J. Cobb, J. Gage, S. Harrington, N. Ahmadi and S. McCouch. 2013. Bridging the genotyping gap: using genotyping by sequencing (GBS) to add high-density SNP markers and new value to traditional bi-parental mapping and breeding populations. *Theoretically and Applied Genetics* 126:2699-2716 doi:10.1007/s00122-013-2166-x.
13. Crossa, J., B. S. Kassa, P. Perez, J. Hickey, **C. Chen**, G. de los Campos, J. Burgueno, V. S. Windhausen, E. Buckler, J.-L. Jannick, M. A. Lopez Cruz and R. Babu. 2013. Genomic prediction in maize breeding population with genotyping-by-sequencing. *G3*, doi:10.1534/g3.113.008227
14. **Chen C.**, G. DeClerck, F. Tien, J. C. Stein, S. McCouch and E. Buckler. 2012. *PICARA*, a probabilistic inference on functional implications of *a priori* candidate and its application on genome-wide associations of flowering time variations in maize. *PLoS ONE* 7(11): e46596. doi:10.1371.
15. Hung, H-Y., L. M. Shannon, F. Tian, P. J. Bradbury, **C. Chen**, S. A. Flint-Garcia, M. D. McMullen, D. Ware, E. S. Buckler, J. F. Doebley and J. B. Holland. 2012. The genetic basis of day length adaptation underlying the post-domestication spread of maize. *Proc. Natl. Acad. Sci. USA* 109(28): E1913-E1921
16. **Chen, C.**, G. DeClerck, T. Casstevens, K. Youens-Clark, J. Zhang, D. Ware, P. Jaiswal, S. R. McCouch and E. Buckler. 2010. The Gramene genetic diversity module: a resource for genotype-phenotype association analysis in grass species. *Nature Precedings* doi:10.1011/npre.2010.4645.1
17. Youens-Clark, K., E. Buckler, T. Casstevens, **C. Chen**, G. DeClerck, P. Derwent, P. Dharmawardhana, P. Jaiswal, P. Kersey, A.-S. Karthikeyan, J. Lu, S. R. McCouch, L. Ren, W. Spooner, J. C. Stein, J. Thomason, S. Wei and D. Ware. 2010. Gramene database in 2010, updates and extensions. *Nucleic Acid Research*. D1085-D1904
18. Zhang, N., Y. Gibson, A. Gur, **C. Chen**, N. Lepak, M. Hohne, Z. Zhang, D. Kroon, H. Tschoep, M. Stitt and E. Buckler. 2010. Fine QTL mapping of carbon and nitrogen metabolism enzyme activities and seedling biomass in the intermated maize IBM mapping population. *Plant Physiology* 154:1753-1765

19. **Chen, C.**, C. Liewlaksaneeyanawin, T. Funda, A. Kenaway, C. H. Newton and Y. El-Kassaby. 2008. Development and characterization of microsatellite loci in western larch (*Larix occidentalis* Nutt.). *Molecular Ecology Resources* 9:843-845
20. Funda, T., **C. Chen**, C. Liewlaksaneeyanawin, A. Kenaway and Y. El-Kassaby. 2008. Pedigree and mating system analyses in a western larch (*Larix occidentalis* Nutt.) experimental population. *Annals Forest Sciences* 65: 705

Selected List of Non-peer-reviewed Publications

- **PICARA**: analytical pipeline for *a priori* candidate gene identification from GWAS association (<http://sourceforge.net/projects/picarapvalue/>) 2012
- **LDimpute**: imputation algorithm on genotyping-by-sequencing (GBS) SNP using parallel computing on HPC environment (<http://sourceforge.net/projects/ldimpute/>) 2013
- **kNN-Fam**: family-based k-nearest neighbor imputation for un-referenced and semi-reference SNPs calling algorithm, (in code review) 2015
- Hearne, Sarah; **Chen, Charles**; Buckler, Ed; Mitchell, Sharon, 2014, "Unimputed GbS derived SNPs for maize landrace accessions represented in the SeeD-maize GWAS panel", <http://hdl.handle.net/11529/10034> International Maize and Wheat Improvement Center [Distributor] V1 [Version]
- Hearne, Sarah; Buckler, Ed; **Chen, Charles**; Mitchell, Sharon; Swarts, Kelly; Li, Huihui; Romero, Alberto, 2014, "Imputed GbS derived SNPs for maize landrace accessions represented in the SeeD-maize GWAS panel: Imputation using FILLIN", <http://hdl.handle.net/11529/10036> International Maize and Wheat Improvement Center [Distributor] V1 [Version]
- Hearne, Sarah; Buckler, Ed; **Chen, Charles**; Mitchell, Sharon; Swarts, Kelly; Li, Huihui; Romero, Alberto, 2014, "Imputed GbS derived SNPs for maize landrace accessions represented in the SeeD-maize GWAS panel: Imputation using Beagle v4", <http://hdl.handle.net/11529/10036> International Maize and Wheat Improvement Center [Distributor] V1 [Version]

Teaching Activities

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| • Introduction to Bioinformatics | Oklahoma State Univ. | Fall 2015 |
| • Genome Database (PB4060) | Cornell University | 2009-2011 |
| • Population and Conversation Genetics (CONS330) | Univ. of British Columbia | 2005-2006 |