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Education

University of Minnesota	St. Paul, MN	Ph.D., 1999	Major: Plant Breeding. Minor: Sustainable Agriculture.
University of Maine	Orono, ME	M.S., 1995	Plant Sciences.
Haverford College	Haverford, PA	B.A., 1991	Biology.

Employment

Plant Research Geneticist USDA-ARS, Feb. 2007 – Present.
Small grains quantitative geneticist. Develop methods using DNA markers to increase the efficiency of small grains improvement and facilitate the use of those methods in public small grains breeding programs.

Adjunct Professor Cornell University, Jan. 2015 – Present.
Adjunct Associate Professor Cornell University, Jan. 2008 – 2015.
Associate Professor with tenure Iowa State University, Jul. 2006 – Feb. 2007.
Assistant Professor Iowa State University, Oct. 2000 – Jul. 2006.
Small grains breeding and quantitative genetics.

NSF-NATO Postdoctoral Fellow, Centre for Biometry, Wageningen University and Research Centre, The Netherlands. Sept. 1999 – Aug. 2000.

Teaching

Cornell Univ. 2018 – 2020. Quantitative Genetics for Plant and Animal Breeding.
Cornell Univ. 2016. Selection Theory.
Cornell Univ. 2009 – 2015. QTL Analysis: Mapping Genotype to Phenotype in Practice.
Summer Institute in Statistical Genetics. 2008 – 2010. Plant and Animal Association Mapping.
Iowa State Univ. 2000 – 2006. Population and Quantitative Genetics for Breeding
Iowa State Univ. 2005 – 2007. Graduate Prog. in Sustainable Agriculture Colloquium

Students Advised

Master's Degree (5): Donghong Pei (2004), Murli Gogula (2004), Jin Long (2005), Alona Chernyshova (2006), Fred Iutzi (2007)

Ph.D Degree (14): Lucia Gutierrez (2008), Shengqiang Zhong (2008), Mark Newell (2010), Franco Asoro (2010), Nicolas Heslot (2014), Uche Okeke (2017), Ugochukwu Ikeogu (2018), Alfred Ozimati (2018), Roberto Lozano (2019), Ariel Chan (2019), Moshood Bakare (current), Leah Nandudu (current), Chinedozie Amaefula (current), Seren Villwock (current)

Academic Honors

Organization for Economic Cooperation and Development Cooperative Research Fellow, 2007
Young Crop Scientist Award, The Crop Science Society of America, 2006.
Raymond and Mary Baker Agronomic Excellence Award, Iowa State University Department of Agronomy, 2005.
National Science Foundation–North Atlantic Treaty Organization Postdoctoral Research Fellowship, 1999-2000.
Doctoral Dissertation Fellowship, 1998. Univ. of Minnesota.
President's International Intern Fellowship, 1997. Univ. of Minnesota.

National Science Foundation Graduate Research Fellowship, 1993-1996.
Lambert Fellowship in Agronomy, 1995. Univ. of Minnesota.
Graduated Magna Cum Laude with honors in Biology, 1991. Haverford College.
Elected Phi Beta Kappa, 1989. Haverford College.

Leadership, Professional and Institutional Service

2017-	Associate Editor, G3: Genes, Genomes, Genetics
2013-2020	Technical Editor, *Crop Science*
2009-2012	Associate Editor, *Crop Science*
2012-2016	Associate Editor, *The Plant Genome*
2005-2008	Associate Editor, *Theoretical and Applied Genetics*
2019	Member, USDA NIFA Food & Agriculture Cyberinformatics & Tools Review Panel
2011	Member, USDA / DOE Plant Feedstock Genomics for Bioenergy Review Panel
2008-2011	Crop Science Society of America Young Crop Scientist Award Committee
2006-2007	Iowa State University Representative USDA-CSREES SCC-80: The Plant Breeding Coordinating Committee
2004	Panel Member, USDA NRI Plant Genome Program Grant Review Panel
2002-2006	Multi-state Research Committee NCR-204: The Interface of Molecular and Quantitative Genetics in Plant and Animal Breeding.

Major grants received, current $ Total ($ to Jannink, where applicable)

2018-2022	Next Generation Cassava Breeding. Bill & Melinda Gates Foundation and UK Department for International Development. $35,000,000 (1,205,257)
2018-2021	Integrated Seaweed Hatchery and Selective Breeding Technologies for Scalable Offshore Seaweed Farming. ARPA-E. $2,800,000 ($546,291)
2017-2021	Validation, characterization and deployment of QTL for grain yield components in wheat. USDA-NIFA-AFRI. $10,000,000 ($422,222)
2017-2021	Transcriptomics and metabolomics to identify drivers of seed composition in oat. USDA-NIFA-AFRI. $980,000

Publications

1. Lozano, R., G.T. Booth, B.Y. Omar, B. Li, E.S. Buckler, D. Pino del Carpio, and **J.-L. Jannink**. 2021. RNA polymerase mapping in plants identifies intergenic regulatory elements enriched in causal variants. G3. doi: 10.1093/g3journal/jkab273.
2. de Sousa, K., J. van Etten, J. Poland, C. Fadda, **J.-L. Jannink**, Y.G. Kidane, B.F. Lakew, D.K. Mengistu, M.E. Pè, S.O. Solberg, M. Dell'Acqua. 2021. Data-driven decentralized breeding increases prediction accuracy in a challenging crop production environment. Commun Biol 4(1): 944.
3. Wolfe, M.D., A.W. Chan, P. Kulakow, I. Rabbi, and **J.-L. Jannink**. 2021. Genomic mating in outbred species: predicting cross usefulness with additive and total genetic covariance matrices. bioRxiv: 2021.01.05.425443. doi: 10.1101/2021.01.05.425443.

4. Alfred, O.A., W. Esuma, T. Alicai, **J.-L. Jannink**, C. Egesi, et al. 2021. Outlook of Cassava Brown Streak Disease Assessment: Perspectives of Breeders' and Pathologists' Screening Methods. Front. Plant Sci. 12: 1248.
5. Wolfe, M.D., **J.-L. Jannink**, M.B. Kantar, and N. Santantonio. 2021. Multi-species genomics-enabled selection for improving agroecosystems across space and time. Front. Plant Sci. 12. doi: 10.3389/fpls.2021.665349.
6. Hu, H., M. Campbell, T.H. Yeats, X. Zheng, D. Runcie, et al. 2021. Multi-omics prediction of oat agronomic and seed nutritional traits across environments and in distantly related populations.
7. Jordan, K.W., P.J. Bradbury, Z.R. Miller, M. Nyine, F. He, et al. 2021. Development of the Wheat Practical Haplotype Graph Database as a Resource for Genotyping Data Storage and Genotype Imputation. bioRxiv: 2021.06.10.447944. doi: 10.1101/2021.06.10.447944.
8. Umanzor, S., Y. Li, D. Bailey, S. Augyte, M. Huang, et al. 2021. Comparative analysis of morphometric traits of farmed sugar kelp and skinny kelp, Saccharina spp., strains from the Northwest Atlantic. J. World Aquac. Soc. (jwas.12783). doi: 10.1111/jwas.12783.
9. Campbell, M., H. Hu, T. Yeats, L. Brzozowski, M. Caffe-Treml, …, and **J.-L. Jannink**. 2021. Improving genomic prediction for seed quality traits in oat (*Avena sativa* L.) using trait-specific relationship matrices. Front. Genet. 12: 437.
10. Campbell, M.T., H. Hu, T.H. Yeats, M. Caffe-Treml, L. Gutiérrez, K.P. Smith, M.E. Sorrells, M.A. Gore, and **J.-L. Jannink**. 2021. Translating insights from the seed metabolome into improved prediction for lipid-composition traits in oat (*Avena sativa* L.). Genetics. doi: 10.1093/genetics/iyaa043.
11. Mao, X., S. Augyte, M. Huang, M.P. Hare, D. Bailey, … , and **J.-L. Jannink** 2020. Population Genetics of Sugar Kelp Throughout the Northeastern United States Using Genome-Wide Markers. Frontiers in Marine Science 7: 694.
12. Yonis, B.O., D. Pino del Carpio, M. Wolfe, **J.-L. Jannink**, P. Kulakow, et al. 2020. Improving root characterisation for genomic prediction in cassava. Sci. Rep. 10(1): 8003.
13. Pinho Morais, P.P., D. Akdemir, L.R. Braatz de Andrade, **J.-L. Jannink**, R. Fritsche-Neto, et al. 2020. Using public databases for genomic prediction of tropical maize lines. Plant Breed. 139(4): 697–707.
14. Veenstra, L.D., J. Poland, **J.-L. Jannink**, and M.E. Sorrells. 2020. Recurrent genomic selection for wheat grain fructans. Crop Sci. 60(3): 1499–1512.
15. Somo, M., H. Kulembeka, K. Mtunda, E. Mrema, K. Salum, … , and **J.-L. Jannink** 2020. Genomic prediction and quantitative trait locus discovery in a cassava training population constructed from multiple breeding stages. Crop Sci. 60(2): 896–913.
16. Rabbi, I.Y., S.I. Kayondo, G. Bauchet, M. Yusuf, C.I. Aghogho, K. Ogunpaimo, R. Uwugiaren, I.A. Smith, P. Peteti, A. Agbona, E. Parkes, L. Ezenwaka; M. Wolfe, **J.-L. Jannink**, C. Egesi, P. Kulakow 2020. Genome-wide association analysis reveals new insights into the genetic architecture of defensive, agro-morphological and quality-related traits in cassava. Plant Mol. Biol. doi: 10.1007/s11103-020-01038-3.
17. Hu, H., J.J. Gutierrez-Gonzalez, X. Liu, T.H. Yeats, D.F. Garvin, O.A. Hoekenga, M.E. Sorrells, M.A. Gore, and **J.-L. Jannink**. 2020. Heritable temporal gene expression patterns correlate with metabolomic seed content in developing hexaploid oat seed. Plant Biotechnology Journal 18:1211–1222
18. Chan, A.W., A.L. Williams, and **J.-L. Jannink**. 2019. Sexual dimorphism and the effect of wild introgressions on recombination in Manihot esculenta. BioRxiv 794339.

19. Wolfe, M.D., G.J. Bauchet, A.W. Chan, R. Lozano, P. Ramu, C.N. Egesi, R. Kawuki, P. Kulakow, I.Y. Rabbi, and **J.-L. Jannink**. 2019. Historical introgressions from a wild relative of modern cassava improved important traits and may be under balancing selection. Genetics 213:1237-1253
20. Ikeogu, U.N., D. Akdemir, M.D. Wolfe, U.G. Okeke, C. Amaefula, **J.-L. Jannink**, and C.N. Egesi 2019. Genetic Correlation, Genome-Wide Association and Genomic Prediction of Portable NIRS Predicted Carotenoids in Cassava Roots. Frontiers in Plant Science 10:1570
21. Kaya, H.B., D. Akdemir, R. Lozano, O. Cetin, H.S. Kaya, M. Sahin, J.L. Smith, B. Tanyolac, and **J.-L. Jannink**. 2019. Genome wide association study of 5 agronomic traits in olive (Olea europaea L.). Scientific Reports 9:1-14
22. Somo, M., and **J.-L. Jannink**. 2020. Incorporating selfing to purge deleterious alleles in a cassava genomic selection program. BioRxiv 2020.04.04.025841
23. Blake, V.C., M.R. Woodhouse, G.R. Lazo, S.G. Odell, C.P. Wight, **Jannink, J.-L.**, et al. 2019. GrainGenes: centralized small grain resources and digital platform for geneticists and breeders. Database 2019. doi: 10.1093/database/baz065.
24. Carlson, M.O., G. Montilla-Bascon, O.A. Hoekenga, N.A. Tinker, J. Poland, **Jannink, J.-L.**, et al. 2019. Multivariate Genome-Wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (Avena sativa L.). G3 9(9): 2963–2975.
25. Fritsche-Neto, R., T.L.P.O. de Souza, H.S. Pereira, L.C. de Faria, L.C. Melo, **Jannink, J.-L.**, et al. 2019. Association mapping in common bean revealed regions associated with Anthracnose and Angular Leaf Spot resistance. Sci. Agric. 76(4): 321–327.
26. Ozimati, A., R. Kawuki, W. Esuma, S. I. Kayondo, A. Pariyo, M. Wolfe, and **J.-L. Jannink**. 2019. Genetic Variation and Trait Correlations in an East African Cassava Breeding Population for Genomic Selection. Crop Sci. 59:460-473. doi:10.2135/cropsci2018.01.0060
27. Sun, J., J.A. Poland, S. Mondal, J. Crossa, P. Juliana, **Jannink, J.-L.**, et al. 2019. High-throughput phenotyping platforms enhance genomic selection for wheat grain yield across populations and cycles in early stage. Theor. Appl. Genet. 132(6): 1705–1720.
28. Santantonio, N., **J.-L. Jannink**, and M. Sorrells. 2019a. Homeologous Epistasis in Wheat: The Search for an Immortal Hybrid. Genetics 211(3): 1105–1122.
29. Santantonio, N., **J.-L. Jannink**, and M. Sorrells. 2019b. Prediction of Subgenome Additive and Interaction Effects in Allohexaploid Wheat. G3 9(3): 685–698.
30. Santantonio, N., **J.-L. Jannink**, and M. Sorrells. 2019c. A Low Resolution Epistasis Mapping Approach To Identify Chromosome Arm Interactions in Allohexaploid Wheat. G3 9(3): 675–684.
31. Veenstra, L.D., N. Santantonio, **J.-L. Jannink**, and M.E. Sorrells. 2019. Influence of Genotype and Environment on Wheat Grain Fructan Content. Crop Sci. 59: 190–198.
32. Wang, D.R., C.R. Guadagno, X. Mao, D.S. Mackay, J.R. Pleban, **Jannink, J.-L.**, et al. 2019. A framework for genomics-informed ecophysiological modeling in plants. J. Exp. Bot. 70(9): 2561–2574.
33. Chan, A.W., A.L. Williams, and **J.-L. Jannink**. 2018. A statistical framework for detecting mislabeled and contaminated samples using shallow-depth sequence data. BMC Bioinformatics 19(1): 478.
34. Clohessy, J.W., D. Pauli, K.M. Kreher, E.S. Buckler V., P.R. Armstrong, **Jannink, J.-L.**, et al. 2018. A Low-Cost Automated System for High-Throughput Phenotyping of Single Oat Seeds. The Plant Phenome Journal 1. doi: 10.2135/tppj2018.07.0005.

35. Ozimati, A., R. Kawuki, W. Esuma, I.S. Kayondo, M. Wolfe, **Jannink, J.-L.**, et al. 2018. Training Population Optimization for Prediction of Cassava Brown Streak Disease Resistance in West African Clones. G3. doi: 10.1534/g3.118.200710.
36. Elias, A.A., I. Rabbi, P. Kulakow, and **J.-L. Jannink**. 2018. Improving genomic prediction in cassava field experiments using spatial analysis. G3: Genes, Genomes, Genetics: g3–300323.
37. Elias, A.A., I. Rabbi, P. Kulakow, and **J.-L. Jannink**. 2018. Improving genomic prediction in cassava field experiments by accounting for inter-plot competition. G3: Genes, Genomes, Genetics: g3–300354.
38. Ezenwaka, L., P. Del Carpio Dunia, **J.-L. Jannink**, I. Rabbi, E. Danquah, I. Asante, A. Danquah, E. Blay, and C. Egesi. 2018. Genome-Wide Association Study of Resistance to Cassava Green Mite Pest and Related Traits in Cassava. Crop Sci. doi:10.2135/cropsci2018.01.0024
39. Fristche-Neto, R., D. Akdemir, and **J.-L. Jannink**. 2018. Accuracy of genomic selection to predict maize single-crosses obtained through different mating designs. Theor. Appl. Genet. 131(5): 1153–1162.
40. Ikeogu, U.N., F. Davrieux, D. Dufour, H. Ceballos, C.N. Egesi, and **J.-L. Jannink**. 2017. Rapid analyses of dry matter content and carotenoids in fresh cassava roots using a portable visible and near infrared spectrometer (Vis/NIRS). PLoS One 12(12): e0188918.
41. Kayondo, S.I., D.P. Del Carpio, R. Lozano, A. Ozimati, M. Wolfe, Y. Baguma, V. Gracen, S. Offei, M. Ferguson, R. Kawuki, and **J.-L. Jannink**. 2018. Genome-wide association mapping and genomic prediction for CBSD resistance in Manihot esculenta. Sci. Rep. 8(1): 1549.
42. Ly, D., S. Huet, A. Gauffreteau, R. Rincent, G. Touzy, A. Mini, **J.-L. Jannink**, F. Cormier, E. Paux, S. Lafarge, and Others. 2018. Whole-genome prediction of reaction norms to environmental stress in bread wheat (Triticum aestivum L.) by genomic random regression. Field Crops Res. 216: 32–41.
43. Rosas, J.E., S. Martínez, P. Blanco, F. Pérez de Vida, V. Bonnecarrère, G. Mosquera, M. Cruz, S. Garaycochea, E. Monteverde, S. McCouch, S. Germán, **J.-L. Jannink**, and L. Gutiérrez. 2018. Resistance to Multiple Temperate and Tropical Stem and Sheath Diseases of Rice. Plant Genome 11(1). doi: 10.3835/plantgenome2017.03.0029.
44. Yabe, S., H. Iwata, and **J.-L. Jannink**. 2018. Impact of Mislabeling on Genomic Selection in Cassava Breeding. Crop Sci. 58(4): 1470–1480.
45. Okeke, U.G., D. Akdemir, I. Rabbi, P. Kulakow, and **J.-L. Jannink**. 2017. Regional Heritability Mapping Provides Insights into Dry Matter Content in African White and Yellow Cassava Populations. Plant Genome.
46. Okeke, U.G., D. Akdemir, I. Rabbi, P. Kulakow, and **J.-L. Jannink**. 2017. Accuracies of univariate and multivariate genomic prediction models in African cassava. Genet. Sel. Evol. 49(1): 88.
47. Akdemir, D., **J.-L. Jannink**, and J. Isidro-Sánchez. 2017. Locally epistatic models for genome-wide prediction and association by importance sampling. Genet. Sel. Evol. 49(1): 74
48. Wolfe, M.D., D.P. Del Carpio, O. Alabi, L.C. Ezenwaka, U.N. Ikeogu, I.S. Kayondo, R. Lozano, U.G. Okeke, A.A. Ozimati, E. Williams, C. Egesi, R.S. Kawuki, P. Kulakow, I.Y. Rabbi, and **J.-L. Jannink**. 2017. Prospects for Genomic Selection in Cassava Breeding. Plant Genome http://dx.doi.org/10.3835/plantgenome2017.03.0015.

49. Sun, J., J.E. Rutkoski, J.A. Poland, J. Crossa, **J.-L. Jannink**, and M.E. Sorrells. 2017. Multitrait, Random Regression, or Simple Repeatability Model in High-Throughput Phenotyping Data Improve Genomic Prediction for Wheat Grain Yield. Plant Genome 10(2) http://dx.doi.org/10.3835/plantgenome2016.11.0111.
50. Veenstra, L.D., **J.-L. Jannink**, and M.E. Sorrells. 2017. Wheat Fructans: A Potential Breeding Target for Nutritionally Improved, Climate-Resilient Varieties. Crop Sci. 57:1624-1640
51. Yabe, S., H. Iwata, and **J.-L. Jannink**. 2017. A Simple Package to Script and Simulate Breeding Schemes: The Breeding Scheme Language. Crop Sci. 57:1347-1354
52. Jafarzadeh, J., D. Bonnett, **J.-L. Jannink**, D. Akdemir, S. Dreisigacker, and M.E. Sorrells. 2016. Breeding Value of Primary Synthetic Wheat Genotypes for Grain Yield. PLoS One 11(9): e0162860
53. Wolfe, M.D., P. Kulakow, I.Y. Rabbi, and **J.-L. Jannink**. 2016. Marker-Based Estimates Reveal Significant Non-additive Effects in Clonally Propagated Cassava (Manihot esculenta): Implications for the Prediction of Total Genetic Value and the Selection of Varieties. Genes|Genomes|Genetics 6:3497-3506
54. Chan, A.W., M.T. Hamblin, and **J.-L. Jannink**. 2016. Evaluating Imputation Algorithms for Low-Depth Genotyping-By-Sequencing (GBS) Data. PLoS One 11(8): e0160733
55. Blake, V.C., C. Birkett, D.E. Matthews, D.L. Hane, P. Bradbury, and **J.-L. Jannink**. 2016. The Triticeae Toolbox: Combining Phenotype and Genotype Data to Advance Small-Grains Breeding. Plant Genome 9. doi:10.3835/plantgenome2014.12.0099
56. Esvelt Klos, K., Y.-F. Huang, W.A. Bekele, D.E. Obert, E. Babiker, A.D. Beattie, Å. Bjørnstad, J.M. Bonman, M.L. Carson, S. Chao, B.N. Gnanesh, I. Griffiths, S.A. Harrison, C.J. Howarth, G. Hu, A. Ibrahim, E. Islamovic, E.W. Jackson, **J.-L. Jannink**, F.L. Kolb, M.S. McMullen, J. Mitchell Fetch, J.P. Murphy, H.W. Ohm, H.W. Rines, B.G. Rossnagel, J.A. Schlueter, M.E. Sorrells, C.P. Wight, W. Yan, and N.A. Tinker. 2016. Population Genomics Related to Adaptation in Elite Oat Germplasm. Plant Genome 9. doi:10.3835/plantgenome2015.10.0103
57. Wolfe, M.D., I.Y. Rabbi, C. Egesi, M. Hamblin, R. Kawuki, P. Kulakow, R. Lozano, D.P.D. Carpio, P. Ramu, and **J.-L. Jannink**. 2016. Genome-Wide Association and Prediction Reveals Genetic Architecture of Cassava Mosaic Disease Resistance and Prospects for Rapid Genetic Improvement. Plant Genome 9. doi:10.3835/plantgenome2015.11.0118
58. Spindel, J.E., H. Begum, D. Akdemir, B. Collard, E. Redoña, **J.-L. Jannink**, and S. McCouch. 2016. Genome-wide prediction models that incorporate de novo GWAS are a powerful new tool for tropical rice improvement. Heredity 116: 395–408
59. Roorkiwal, M., A. Rathore, R.R. Das, M.K. Singh, A. Jain, S. Srinivasan, P.M. Gaur, B. Chellapilla, S. Tripathi, Y. Li, J.M. Hickey, A. Lorenz, T. Sutton, J. Crossa, **J.-L. Jannink**, and R.K. Varshney. 2016. Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. Front. Plant Sci. 7: 1666
60. de Leon, N., **J.-L. Jannink**, J.W. Edwards, and S.M. Kaeppler. 2016. Introduction to a Special Issue on Genotype by Environment Interaction. Crop Sci. 56: 2081–2089.
61. Rosas, J.E., S. Martínez, V. Bonnecarrère, F. Pérez de Vida, P. Blanco, M. Malosetti, **J.-L. Jannink**, and L. Gutiérrez. 2016. Comparison of Phenotyping Methods for Resistance to Stem Rot and Aggregated Sheath Spot in Rice. Crop Sci. 56: 1619–1627

62. Ashraf, B., V. Edriss, D. Akdemir, E. Autrique, D. Bonnett, J. Crossa, L. Janss, R. Singh, and **J.-L. Jannink**. 2016. Genomic prediction using phenotypes from pedigreed lines with no marker data. Crop Sci. 56: 957-964
63. Heslot, N., and **J.-L. Jannink**. 2015. An alternative covariance estimator to investigate genetic heterogeneity in populations. Genet. Sel. Evol. 47: 93.
64. Lozano, R., M.T. Hamblin, S. Prochnik, and **J.-L. Jannink**. 2015. Identification and distribution of the NBS-LRR gene family in the Cassava genome. BMC Genomics 16:360.
65. Rutkoski, J., R.P. Singh, J. Huerta-Espino, S. Bhavani, J. Poland, **J.-L. Jannink**, and M.E. Sorrells. 2015. Efficient Use of Historical Data for Genomic Selection: A Case Study of Stem Rust Resistance in Wheat. Plant Genome 8(1)
66. Rutkoski, J., R.P. Singh, J. Huerta-Espino, S. Bhavani, J. Poland, **J.-L. Jannink**, and M.E. Sorrells. 2015. Genetic Gain from Phenotypic and Genomic Selection for Quantitative Resistance to Stem Rust of Wheat. Plant Genome 8(2)
67. Heslot, N., **J.-L. Jannink**, and M.E. Sorrells, 2015. Perspectives for genomic selection applications and research in plants. Crop Sci. 55:1-12
68. Akdemir, D., and **J.-L. Jannink** 2015. Locally Epistatic Genomic Relationship Matrices for Genomic Association and Prediction. Genetics 199: 857–871.
69. Akdemir, D., J.I. Sanchez, and **J.-L. Jannink**, 2015. Optimization of genomic selection training populations with a genetic algorithm. Genet. Sel. Evol. 47:38.
70. Lopez-Cruz, M., Crossa, J., Bonnett, D., Dreisigacker, S., Poland, J., **Jannink, J.-L.**, Singh, R. P., Autrique, E., de los Campos, G. 2015. Increased Prediction Accuracy in Wheat Breeding Trials Using a Marker × Environment Interaction Genomic Selection Model. Genes|Genomes|Genetics 5: 569–582
71. Spindel, J., Begum, H., Akdemir, D., Virk, P., Collard, B., Redoña, E., Atlin, G., **Jannink, J.-L.**, McCouch, S.R. 2015. Genomic Selection and Association Mapping in Rice (Oryza sativa): Effect of Trait Genetic Architecture, Training Population Composition, Marker Number and Statistical Model on Accuracy of Rice Genomic Selection in Elite, Tropical Rice Breeding Lines. PLoS Genetics 11:e1004982
72. Zhang, X., Pérez-Rodríguez, P., Semagn, K., Beyene, Y., Babu, R., López-Cruz, M.A., San Vicente, F., Olsen, M., Buckler, E.; **Jannink, J.-L**., 2015. Genomic prediction in biparental tropical maize populations in water-stressed and well-watered environments using low-density and GBS SNPs. Heredity 114:291–299.
73. Isidro, J., **J.-L. Jannink**, D. Akdemir, J. Poland, N. Heslot, and M.E. Sorrells 2015. Training set optimization under population structure in genomic selection. Theor. Appl. Genet. 128:145-158
74. Tecle, Isaak Y., Edwards, J.D. Menda, N., Egesi, C., Rabbi, I. Y., Kulakow, P., Kawuki, R., **Jannink, J.-L.**, Mueller, L.A. 2014. solGS: a web-based tool for genomic selection. BMC bioinformatics 15:398
75. Sallam, A.H., J. Endelman, **J.-L. Jannink**, and K.P. Smith., 2014. Assessing Genomic Selection Prediction Accuracy in a Dynamic Barley Breeding. The Plant Genome 8:1
76. Jessica E. Rutkoski, Jesse A. Poland, Ravi P. Singh, Julio Huerta-Espino, Sridhar Bhavani, Hugues Barbier, Matthew N. Rouse, **J.-L. Jannink**, Mark E. Sorrells. 2014. Genomic selection for quantitative adult plant stem rust resistance in wheat. The Plant Genome 7:

77. Endelman, J.B., G.N. Atlin, Y. Beyene, K. Semagn, X. Zhang, M.E. Sorrells, and **J.-L. Jannink**. 2014. Optimal design of preliminary yield trials with genome-wide markers. Crop Sci. 54:48-59
78. Rabbi, I. Y., Hamblin M.T., Gedil M., Kulakow P.A., Ferguson M., Ikpan A.S., Ly D., & **Jannink, J.-L.**, 2014. Genetic Mapping using Genotyping-by-sequencing in the Clonally-propagated Cassava. Crop Sci. 54:1384-1396.
79. Akdemir, D., and **J.-L. Jannink**. 2014. Ensemble Learning with Trees and Rules: Supervised, Semi-supervised, Unsupervised. Intelligent Data Analysis. 18 (2014) 857–872.
80. Rabbi, I. Y., Hamblin, M. T., Kumar, P. L., Gedil, M. A., Ikpan, A. S., **Jannink, J.-L.**, & Kulakow, P. A., 2013. High-resolution mapping of resistance to cassava mosaic geminiviruses in cassava using genotyping-by-sequencing and its implications for breeding. Virus Research. 186:87-96.
81. Crossa, J., Y. Beyene, K. Semagn, P. Pérez, J. M. Hickey, C. Chen, G. de los Campos, J. Burgueño, V. S. Windhausen, E. Buckler, **J.-L. Jannink**, M. A. Lopez Cruz, R. Babu. 2013. Genomic Prediction in Maize Breeding Populations with Genotyping-by-Sequencing. G3: Genes|Genomes|Genetics 3(11): 1903-1926
82. Heslot, N., D. Akdemir, M.E. Sorrells, and **J.-L. Jannink**. 2013. Integrating environmental covariates and crop modeling into the genomic selection framework to predict genotype by environment interactions. Theor. Appl. Genet. 127:463-480
83. Heslot, N., J. Rutkoski, J. Poland, **J.-L. Jannink**, M.E. Sorrells. 2013. Impact of marker ascertainment bias on genomic selection accuracy and estimates of genetic diversity PloS One 8 (9), e74612
84. Newell M.A., H.J. Kim, F.G. Asoro, A. Moran Lauter, P.J. White, M.P. Scott, and **J.-L. Jannink**. 2013. Micro-enzymatic evaluation of oat (*Avena sativa* L.) beta-glucan for high-throughput phenotyping. Cereal Chemistry 91:183-188.
85. Dawson, J.C., J.B. Endelman, N. Heslot, J. Crossa, J. Poland, S. Dreisigacker, Y. Manès, M.E. Sorrells, **J.-L. Jannink**. 2013. The use of unbalanced historical data for genomic selection in an international wheat breeding program. Field Crops Res. 154:12-22
86. Asoro, F., M. Newell, W. Beavis, P. Scott, N. Tinker, and **J.-L. Jannink**. 2013. Comparison of Genomic, Marker-Assisted, and Pedigree-BLUP Selection Methods to Increase β-Glucan Concentration in Elite Oat Germplasm. Crop Sci. 53: 1894-1906
87. Newell, M., D. Cook, H. Hofmann, and **J.-L. Jannink**. 2013. An Algorithm for Deciding the Number of Clusters and Validating using Simulated Data with Application to Exploring Crop Population Structure. The Annals of Applied Statistics. 7:1898-1916
88. Ly, D., M. Hamblin, I. Rabbi, G. Melaku, M. Bakare, H.G. Gauch, R. Okechukwu, A.G.O. Dixon, P. Kulakow, and **J.-L. Jannink**. 2013. Relatedness and Genotype × Environment Interaction Affect Prediction Accuracies in Genomic Selection: A Study in Cassava. Crop Science 53(4): 1312–1325.
89. Rutkoski, J.E., J. Poland, **J.-L. Jannink**, and M.E. Sorrells. 2013. Imputation of unordered markers and the impact on genomic selection accuracy. G3: Genes|Genomes|Genetics 3(3): 427–39.
90. Riedelsheimer, C., J.B. Endelman, M. Stange, M.E. Sorrells, **J.-L. Jannink**, and A.E. Melchinger. 2013. Genomic Predictability of Interconnected Bi-parental Maize Populations. Genetics 194(2): 493–503.

91. Heslot, N., **J.-L. Jannink**, and M.E. Sorrells. 2013. Using genomic prediction to characterize environments and optimize prediction accuracy in applied breeding data. Crop Sci. 53: 921-933
92. Asoro, F.G., M.A. Newell, M.P. Scott, W.D. Beavis, and **J.-L. Jannink**. 2013. Genomewide Association Study for Beta-glucan Concentration in North American Elite Oat. Crop Sci. 53: 542-553
93. Oliver, R.E., N.A. Tinker, G.R. Lazo, S. Chao, E.N. Jellen, M.L. Carson, H.W. Rines, D.E. Obert, J.D. Lutz, I. Shackelford, A.B. Korol, C.P. Wight, K.M. Gardner, J. Hattori, A.D. Beattie, Å. Bjørnstad, J.M. Bonman, **J.-L. Jannink**, M.E. Sorrells, G.L. Brown-Guedira, J.W. Mitchell Fetch, S.A. Harrison, C.J. Howarth, A. Ibrahim, F.L. Kolb, M.S. McMullen, J.P. Murphy, H.W. Ohm, B.G. Rossnagel, W. Yan, K.J. Miclaus, J. Hiller, P.J. Maughan, R.R. Redman Hulse, J.M. Anderson, E. Islamovic, and E.W. Jackson. 2013. SNP discovery and chromosome anchoring provide the first physically-anchored hexaploid oat map and reveal synteny with model species. PloS one 8(3): e58068.
94. Jia, Y., and **J.-L. Jannink**. 2012. Multiple Trait Genomic Selection Methods Increase Genetic Value Prediction Accuracy. Genetics 192(4): 1513–1522.
95. Windhausen, V.S., G.N. Atlin, J.M. Hickey, J. Crossa, **J.-L. Jannink**, M.E. Sorrells, B. Raman, J.E. Cairns, A. Tarekegne, K. Semagn, Y. Beyene, P. Grudloyma, F. Technow, C. Riedelsheimer, and A.E. Melchinger. 2012. Effectiveness of Genomic Prediction of Maize Hybrid Performance in Different Breeding Populations and Environments. G3: Genes|Genomes|Genetics 2:1427–1436.
96. Endelman, J.B., and **J.-L. Jannink**. 2012. Shrinkage Estimation of the Realized Relationship Matrix. G3: Genes|Genomes|Genetics 2(11): 1405–1413.
97. Poland, J., J. Endelman, J. Dawson, J. Rutkoski, S. Wu, Y. Manes, S. Dreisigacker, J. Crossa, H. Sánchez-Villeda, M. Sorrells, and **J.-L. Jannink**. 2012. Genomic Selection in Wheat Breeding using Genotyping-by-Sequencing. The Plant Genome Journal 5(3): 103–113.
98. Newell, M.A., F.G. Asoro, M.P. Scott, P.J. White, W.D. Beavis, and **J.-L. Jannink**. 2012. Genome-wide association study for oat (*Avena sativa* L.) beta-glucan concentration using germplasm of worldwide origin. Theor. Appl. Genet. 125:1687-1696.
99. Blake, V.C., J.G. Kling, P.M. Hayes, **J.-L. Jannink**, S.R. Jillella, D.E. Matthews, S. Chao, T.J. Close, G.J. Muehlbauer, K.P. Smith, R.P. Wise, and J.A. Dickerson. 2012. The Hordeum Toolbox - The Barley CAP Genotype and Phenotype Resource. The Plant Genome 5:81–91.
100. Lorenz, A.J., K.P. Smith, and **J.-L. Jannink**. 2012. Potential and Optimization of Genomic Selection for Fusarium Head Blight Resistance in Six-Row Barley. Crop Science 52: 1609–1621.
101. Poland, J.A., P.J. Brown, M.E. Sorrells, and **J.-L. Jannink**. 2012. Development of High-Density Genetic Maps for Barley and Wheat Using a Novel Two-Enzyme Genotyping-by-Sequencing Approach. PLoS ONE 7: e32253.
102. Rutkoski, J., J. Benson, Y. Jia, G. Brown-guedira, and **J.-L. Jannink**. 2012. Evaluation of Genomic Prediction Methods for Fusarium Head Blight Resistance in Wheat. The Plant Genome 5:51-61.
103. Heslot N., Yang H.-P., Sorrells M.E., and **Jannink J.-L.** 2011. Genomic Selection in Plant Breeding: A Comparison of Models. Crop Science 52:146-160.
104. Heffner E.L., **Jannink J.-L.**, Iwata H., Souza E., Sorrells M.E. 2011. Genomic Selection

Accuracy for Grain Quality Traits in Biparental Wheat Populations. Crop Science 51:2597-2606.

105. Asoro, F.G., Newell, M.A., W.D. Beavis, M.P. Scott, and **J.-L. Jannink**. 2011. Accuracy and training population design for genomic selection in elite North American oats. The Plant Genome 4:132-144.

106. Hamblin M.T. and **J.-L. Jannink**, 2011 Factors affecting the power of haplotype markers in association studies. The Plant Genome 4:145-153.

107. Iwata, H. and **J.-L. Jannink**, 2011. Accuracy of genomic selection in barley breeding programs: a simulation study based on the real SNP data. Crop Sci. 51:1915-1927.

108. Heffner, E.L., **J.-L. Jannink**, and M.E. Sorrells, 2011. Genomic selection accuracy using multi-family prediction models in a wheat breeding program. The Plant Genome, 4:65-75.

109. Hamblin M.T., Buckler E.S., and **J.-L. Jannink**, 2011. Population genetics of genomics-based crop improvement methods. Trends in Genet. 27:98-106

110. Newell, M.A., D. Cook, N.A. Tinker, **J.-L. Jannink**. 2010. Population structure and linkage disequilibrium in oat (*Avena sativa* L.): Implications for genome-wide association studies. Theor. Appl. Genet. 122:623-632.

111. Lorenz, A.J., M.T. Hamblin, and **J.-L. Jannink**. 2010. Performance of single nucleotide polymorphisms versus haplotypes for genome-wide association analysis in barley. PLoS ONE 5:e14079.

112. Bradbury, P.J., T. Parker, M.T. Hamblin, and **J.-L. Jannink**, 2010. Assessment of power and false discovery in genome-wide association studies using the BarleyCAP germplasm, Crop Sci. 51:52-59.

113. **Jannink, J.-L.** 2010. Dynamics of long-term genomic selection. Genet. Sel. Evol. 42:35.

114. **Jannink, J.-L.**, A.J. Lorenz, and H. Iwata. 2010. Genomic selection in plant breeding: from theory to practice. Brief. Funct. Genom. Proteom. 9:166-177.

115. Hamblin, M.T., Close, T.J., Bhat, P.R., Chao, S., Kling, J.G., Abraham, K.J., Blake, T., Brooks, W.S., Cooper, B., Griffey, C.A., Hayes, P.M., Hole, D.J., Horsley, R.D., Obert, D.E., Smith, K.P., Ullrich, S.E., Muehlbauer, G.J., and **Jannink, J.-L.** 2010. Population structure and linkage disequilibrium in US barley germplasm: implications for association mapping. Crop Sci. 50:556–566.

116. Iwata, H., and **J.-L. Jannink**. 2010. Marker genotype imputation in a low-marker-density panel with a high-marker-density reference panel: accuracy evaluation in barley breeding lines. Crop Sci. 50:1269–1278.

117. Heffner, E.L., A.J. Lorenz, **J.-L. Jannink**, and M.E. Sorrells. 2010. Plant Breeding with Genomic Selection: Gain per Unit Time and Cost. Crop Sci. 50:1681-1690.

118. Iwata, H., Ebana, K., Uga, Y., Hayashi, T., and **Jannink, J.-L.** 2010. Whole genome association mapping of grain shape variation among Oryza sativa L. germplasms based on elliptic Fourier analysis. Mol. Breed. 25:203-215.

119. Waugh, R., **J.-L. Jannink**, G.J. Muehlbauer, and L. Ramsay. 2009. The Emergence of Whole Genome Association Scans in Barley. Curr. Opin. Plant Biol. 12:218-222.

120. **Jannink, J.-L.**, H. Iwata, P.R. Bhat, S. Chao, P. Wenzl, and G.J. Muehlbauer. 2009. Marker imputation in barley association studies. The Plant Genome 2:11-22.

121. Zhong, S., J.C.M. Dekkers, R.L. Fernando, and J.-L. Jannink. 2009. Factors Affecting Accuracy from Genomic Selection in Populations Derived From Multiple Inbred Lines: A Barley Case Study. Genetics 182:355-364.

122. Tinker, N.A. and 23 co-authors (**J.-L. Jannink** in 9th position). 2009. New DArT markers for oat provide enhanced map coverage and global germplasm characterization. BMC Genomics 10:39.

123. Iwata, H., K. Ebana, S. Fukuoka, **J.-L. Jannink**, and T. Hayashi. 2009. Bayesian multilocus association mapping on ordinal and censored traits and its application to the analysis of genetic variation among Oryza sativa L. germplasms. Theor. Appl. Genet. 118:865-880.

124. Heffner, E.L., M.E. Sorrells, and **J.-L. Jannink**. 2009 Genomic Selection for Crop Improvement. Crop Sci. 49:1-12.

125. Boddhireddy, P., **J.-L. Jannink**, and J.C. Nelson. 2009. Selective Advance for Accelerated Development of Recombinant Inbred QTL Mapping Populations. Crop Sci. 49:1284-1294.

126. Gutiérrez, L., J.D. Nason, and **J.-L. Jannink**. 2009. Morphological Genetic Diversity of Worldwide Barley and Mega-Targets of Selection. Crop Sci. 49:483-497.

127. **Jannink, J.-L.**, L. Moreau, G. Charmet, and A. Charcosset. 2008. Overview of QTL detection in plants and tests for synergistic epistatic interactions. Genetica. 136:225-236.

128. Doehlert, D.C., **J.-L. Jannink**, and M.S. McMullen. 2008. Size distributions of different orders of kernels within the oat spikelet. Crop Sci. 48: 298-304.

129. Yao, N., P.J. White, **J.-L. Jannink**, and S. Alavi. 2008. Impact of Dry Solids and Bile Acid Concentrations on Bile Acid Binding Capacity of Extruded Oat Cereals. J. Agric. Food Chem. 56:8672-8679.

130. **Jannink, J.-L.** 2007. QTL x Genetic Background Interaction: Predicting Inbred Progeny Value. Euphytica 161:61-69.

131. Yao, N., **J.-L. Jannink**, and P.J. White. 2007. Molecular weight distribution of (1–3)(1–4)-β-Glucan affects pasting properties of flour from oat lines with high and typical amounts of β-glucan. Cereal Chem. 84:471-479.

132. Chernyshova A.A., P.J.White, M.P. Scott, and **J.-L. Jannink.** 2007. Selection for nutritional function and agronomic performance in oat. Crop Sci. 47:2330-2339.

133. Zhong, S., and **J.-L. Jannink**. 2007. Using quantitative trait locus results to discriminate among crosses based on their progeny mean and variance. Genetics 177: 567-576.

134. Jia, H., D. Nettleton, J.M. Peterson, G. Vazquez-Carrillo, **J.-L. Jannink**, and M.P. Scott. 2007. Comparison of Transcript Profiles in Wild-Type and o2 Maize Endosperm in Different Genetic Backgrounds. The Plant Genome, a Suppl. to Crop Sci. 47:S45-S59.

135. **Jannink**., **J.-L.** 2007. Identifying QTL by genetic background interaction in association studies. Genetics. 176:553-561.

136. Sayar, S., **J.-L. Jannink**, and P.J. White. 2007. Digestion Residues of Typical and High-β-Glucan Oat Flours Provide Substrates for in Vitro Fermentation. J. Agric. Food Chem. 55:5306-5311.

137. Blaser, B.C., L.R. Gibson, J.W. Singer, and **J.-L. Jannink**. 2006. Optimizing seeding rates for winter cereal grains and frost-seeded red clover intercrops. Agron J 98:1041-1049.

138. Sayar, S., **J.-L. Jannink**, and P.J. White. 2006. In Vitro Bile Acid Binding Activity within Flour Fractions from Oat Lines with Typical and High β-Glucan Amounts. J. Agric. Food Chem. 54:5142-5148.

139. Yao, N., **J.-L. Jannink**, S. Alavi, and P. J. White. 2006. Physical and Sensory Characteristics of Extruded Products Made from Two Oat Lines with Different β-Glucan Concentrations. Cereal Chem. 83:692-699.

140. Verhoeven, K.J.F., **J.-L. Jannink**, and L.M. McIntyre. 2006. Using mating designs to uncover QTL and the genetic architecture of complex traits. Heredity. 96:139-149.

141. Edwards, J.E. and **J.-L. Jannink**. 2006. Bayesian Modeling of Heterogeneous Error and Genotype by Environment Interaction Variances. Crop Sci. 46:820-833.

142. Long, J., J.B. Holland, G.P. Munkvold, and **J.-L. Jannink**. 2006. Responses to Selection for Partial Resistance to Crown Rust in Oat. Crop Sci. 46:1260-1265.

143. Doehlert, D.C., M.S. McMullen, **J.-L. Jannink**. 2006. Oat Grain/Groat Size Ratios: A Physical Basis for Test Weight. Cereal Chem. 83:114-118.

144. Sayar, S. **J.-L. Jannink** and P. J. White. 2005. In vitro bile acid binding of flours from oat lines varying in percentage and molecular weight distribution of *β*-glucan. J. Agric. Food Chem. 53:8797-8803.

145. **Jannink, J.-L.** and S. W. Gardner. 2005. Expanding the pool of PCR-based markers for oat. Crop Sci. 45:2383-2387.

146. Doehlert, D.C., M.S. McMullen, **J.-L. Jannink**. 2005. Kernel size variation in naked oats. Crop Sci. 46:1117-1123.

147. Schwarte, A.J., L.R. Gibson, D.L. Karlen, M. Liebman, and **J.-L. Jannink**. 2005. Planting Date Effects on Winter Triticale Grain Yield and Yield Components. Crop Sci. 46:1218-1224.

148. Schwarte, A.J., L.R. Gibson, D.L. Karlen, M. Liebman, and **J.-L. Jannink**. 2005. Planting Date Effects on Winter Triticale Dry Matter and Nitrogen Accumulation. Agron. J. 97:1333-1341.

149. **Jannink, J.-L.** 2005. Selective phenotyping to accurately map QTL. Crop Sci. 45:901-908.

150. Baenziger, P.S., L.R. Gibson, and **J.-L. Jannink**. 2005. Registration of 'NE426GT' Winter Triticale. Crop Sci 45:796.

151. **Jannink, J.-L.** and R.L. Fernando. 2004. On the Metropolis-Hastings acceptance probability to add or drop a QTL in MCMC-based Bayesian analyses. Genetics 166: 641-643.

152. Wu, X.-L., and **J.-L. Jannink**. 2004. Optimal sampling of a population to determine QTL location, variance, and allelic number. Theor Appl Genet 108:1434-1442.

153. Doehlert, D.C., M.S. McMullen, **J.-L. Jannink**, S. Panigrahi, H. Gu, and N.R. Riveland. 2004. Influence of oat kernel size and size distributions on test weight. Cereal Research Communications: 32:135-142.

154. Doehlert, D.C., M.S. McMullen, **J.-L. Jannink**, S. Panigrahi, H. Gu, and N.R. Riveland. 2004. Evaluation of oat kernel size uniformity. Crop Sci 44:1178-1186.

155. Doehlert, D.C., M.S. McMullen, **J.-L. Jannink**, S. Panigrahi, H. Gu, and N.R. Riveland. 2005. A Bimodal Model for Oat Kernel Size Distributions. Can J Plant Sci 85:317-326.

156. Colleoni-Sirghie, M., **J.-L. Jannink**, and P.J. White. 2004. Pasting and thermal properties of flours from oat lines with high and typical amounts of β-glucan. Cereal Chem. 81:686-692.
157. Colleoni-Sirghie, M., **J.-L. Jannink**, I.V. Kovalenko, J.L. Briggs, and P.J. White. 2004. Prediction of β-glucan concentration based on viscosity evaluations of raw oat-flours from high beta-glucan and traditional oat lines. Cereal Chem. 81:434-443.
158. **Jannink, J.-L.** 2003. Selection dynamics and limits under additive-by-additive epistatic gene action. Crop Sci. 43: 489-497.
159. **Jannink, J.-L.** and X.-L. Wu. 2003. Estimating allelic number and identity in state of QTL in interconnected families. Genet. Res. 81: 133-144.
160. Jansen, R.C., **J.-L. Jannink**, and W.D. Beavis. 2003. Mapping quantitative trait loci in plant breeding populations: use of parental haplotype sharing. Crop Sci. 43: 829-834.
161. **Jannink, J.-L.**, M.C.A.M. Bink, and R.C. Jansen. 2001. Using complex plant pedigrees to map valuable genes. Trends Plant Sci. 6:337-342.
162. **Jannink, J.-L.** and R.C. Jansen. 2001. Mapping epistatic QTL with one-dimensional genome searches. Genetics 157:445-454.
163. **Jannink, J.-L.**, N.R. Jordan, and J.H. Orf. 2001. Feasibility of selection for high weed suppressive ability in soybean: absence of tradeoffs between rapid initial growth and sustained later growth. Euphytica 120:291-300.
164. **Jannink, J.-L.**, J.H. Orf, N.R. Jordan, and R.G. Shaw. 2000. Index selection for weed suppressive ability in soybean. Crop Sci. 40:1087-1094.
165. Blumenthal, D. and **J.-L. Jannink**. 2000. A classification of collaborative management methodologies. Conservation Ecology 4:13 [online] http://www.consecol.org/vol4/iss2/art13
166. **Jannink, J.-L.** and T.E. Abadie. 1999. Inbreeding method effects on genetic mean, variance, and structure of recurrent selection populations. Crop Sci. 39:988-997.
167. Jordan, N.R. and **J.-L. Jannink**. 1997. Assessing the practical importance of weed evolution: A research agenda. Weed Res. 37:237-246.
168. **Jannink, J.-L.**, M. Liebman, L.C. Merrick. 1996. Biomass production and nitrogen accumulation in pea, oat, and vetch green manure mixtures. Agron. J. 88:231-240.

Extension publications:

Skrdla, R.K. and **J.-L. Jannink**. (Annually from 2000 – 2006). Iowa crop performance tests – Spring Oat and Barley, 2006. Iowa State University Cooperative Extension Service Pamphlet PM 1645.

Skrdla, R.K. and **J.-L. Jannink**. (Annually from 2000 – 2006). Iowa crop performance tests – Winter Wheat and Triticale, 2006. Iowa State University Cooperative Extension Service Pamphlet AG 6.

Jannink, J.-L. 1997. What motivates farmers to engage in Whole Farm Planning? The Whole Farm Planner 2(3):1-5.

Jannink, J.-L. and D. Romig. 1991. Domestication of Illinois bundleflower as a perennial grain legume. Land Institute Res. Rep. 7:11-15.

Book sections and non peer-reviewed publications:

Newell, M.A., and **J.-L. Jannink**. 2014. Genomic Selection in Plant Breeding, p. 117-130, In D. Fleury and R. Whitford, ed. Crop Breeding: Methods and Protocols. Humana Press, Springer

New York, Heidelberg, Dordrecht, London.

McCouch, S., R.A. Wing, M. Semon, R. Venuprasad, G. Atlin, M.E. Sorrells, **J.-L. Jannink**, M.C.S. Wopereis, D.E. Johnson, N. Ahmadi, E. Tollens, A. Jalloh. 2013. Making rice genomics work for Africa. p. 108-129 *In* Realizing Africa's rice promise. CABI.

Lorenz, A.J., S. Chao, F.G. Asoro, E.L. Heffner, T. Hayashi, H. Iwata, K.P. Smith, M.E. Sorrells, and **J.-L. Jannink**. 2011. Genomic Selection in Plant Breeding: Knowledge and Prospects. Adv. Agron. 110:77-123.

Jannink, J.-L. 2003. Book Review: Likelihood, Bayesian and MCMC methods in quantitative genetics by Daniel Sorensen and Daniel Gianola. Crop Science 43:1574-1575.

Jannink, J.-L., and J.B. Walsh. 2002. Association mapping in plant populations, p. 59-68, *In* M. S. Kang, ed. Quantitative Genetics, Genomics and Plant Breeding. CABI, Wallingford, UK.

Jannink, J.-L. and R.C. Jansen. 2000. The diallel mating design for mapping interacting QTL, p. 81-87, *In* A. Gallais, C. Dillmann and I. Goldringer, eds. Quantitative Genetics and Plant Breeding Methods: The Way Ahead. Proc. 11th Meeting of the EUCARPIA Section Biometrics in Plant Breeding. INRA, Paris.

Invited presentations:

Jannink, J.-L., 2017. Signal from sequence: Potential to aid prediction and purging. International Conference on Selection Theory and Breeding Methodology. Technical University of Munich, Freising, Germany.

Jannink, J.-L., 2017. Genomic prediction meets transcriptomics. Genomics-assisted breeding Workshop, Plant and Animal Genome XXV, San Diego, CA.

Jannink, J.-L., 2014. Genomic selection on novel variation. GS and GWAS Workshop, Plant and Animal Genome XXII, San Diego, CA.

Jannink, J.-L., 2013. Genome-wide selection tools in plant breeding. EMBRAPA Short course in Londrina, Parana, Brazil.

Jannink, J.-L., 2013. Long-term comes quickly: Genomic selection on novel variation. Gordon Research Conference on Quantitative Genetics and Genomics, Galveston, TX.

Jannink, J.-L., 2013. If allele mining gets difficult, try genomic selection. Allele Mining Workshop, Plant and Animal Genome XXI, San Diego, CA.

Jannink, J.-L., 2012. Accelerating plant breeding using genomic selection: Some results and theory. Molecular Mapping and Marker Assisted Selection International Conference, Vienna, Austria.

Jannink, J.-L., 2012 Putting big data to work: Prediction-enabled plant breeding. USDA-ARS Administrator's Council (Webinar).

Jannink, J.-L., 2012. Genomic selection theory and application to alfalfa. Joint North American Alfalfa, Clover, and Grass Improvement Conference, Ithaca, NY.

Jannink, J.-L., 2012. The future of plant breeding and your future: genomic selection as a case study. Univ. of Nebraska, Lincoln Plant Breeding and Genetics Symposium, Lincoln, NE.

Jannink, J.-L., Endelman, J., Akdemir, D., Jia, Y., Heslot, N., Rutkoski, J., & Sorrells, M. 2012. Some methodological developments in genomic selection. Genomics-Assisted Breeding Workshop, Plant and Animal Genome XX, San Diego, CA.

Jannink, J.-L., Mark A. Newell, Franco Asoro, Paul Scott. 2012. Genome-Wide Association Study in Oat for Increased beta-glucan Content. Oat Workshop, Plant and Animal Genome XX, San Diego, CA.

Jannink, J.-L., Asoro, F.G., Newell, M.A., Scott, M.P., Tinker, N. & Wight, C. 2011. Association studies on oat β-glucan content using historical uniform nursery data. Meetings of the American Society of Agronomy, San Antonio, TX.

Jannink, J.-L. 2011. Applying Genomic Selection To Crops In The Public Sector. Meetings of the American Society of Agronomy, San Antonio, TX.

Jannink, J.-L. 2011. Genomic selection for introgression and Multi-parent populations for GS. Workshop on Multi-parent Populations for Genetic Analysis. CIMMYT, Mexico City, Mexico.

Jannink, J.-L. 2011. Methods and breeding schemes applying genomic selection to crops in the public sector. Plant and Animal Genome XIX, San Diego, CA.

Jannink, J.-L. 2010. Population-specific research needs to launch genomic selection. 2nd Indian National Workshop on Marker Assisted Selection, ICRISAT, Hyderabad, India.

Jannink, J.-L. 2010. Contemplating the switch to genomic selection. UGA Institute of Plant Breeding, Genetics, and Genomics Annual Retreat, Athens, GA.

Jannink, J.-L. & Iwata, H. 2009. Genomic selection in plant breeding: Potential and pitfalls. Japanese National Agriculture and Food Research Organization International Symposium, Tsukuba, Japan.

Jannink, J.-L. 2009. Structure / LD studies, SNP tagging, & high density MAS. Barley Coordinated Agricultural Project Meeting, Plant and Animal Genome XVII, San Diego, CA.

Jannink, J.-L., Asoro, F., Tinker, N. Wight, C. & Killian A. 2009. Association analyses for β-glucan content in elite North American oat. Plant and Animal Genome XVII, San Diego, CA.

Rokhsar, D. & **Jannink, J.-L.** 2008. Data analysis tools for a cyberinfrastructure, including next generation sequencing data. iPlant Collaborative Grand Challenge Workshop: Mechanistic basis of plant adaptations. Oracle, AZ.

Jannink, J.-L. & Tinker, N. 2008. Association Mapping in Oat. XXVIII Reunião da Comissão Brasileira de Pesquisa de Aveia. Pelotas, RS, Brazil.

Jannink, J.-L. 2007. Modeling epistatic interactions between QTL in plant populations. Animal Genetics and Plant Breeding and Genetics Joint Conference, AgroParisTech University, Paris, France.

Jannink, J.-L. 2007. Design and analysis for QTL mapping in plant populations. Third International Conference on Quantitative Genetics, Zheijiang University, Hangzhou, China.

Jannink, J.-L. 2007. Barley CAP Genome Coverage: How well will QTL variation be captured by SNP variation? Barley Coordinated Agricultural Project Meeting, Plant and Animal Genome XV, San Diego, CA.

Jannink, J.-L. 2006. QTL x genetic background interaction in complex pedigrees: application to predicting progeny value. EUCARPIA XIII 2006 Section Biometrics in Plant Breeding, University of Zagreb, Zagreb, Croatia.

Jannink, J.-L. 2006. Use of breeding programs to detect and use QTL. 2006 American Oat Workers' Conference, Fargo, ND.

Jannink, J.-L. 2006. QTL x genetic background and other challenges in applying association analysis to MAS. INRA – UMR de Génétique Végétale, Ferme du Moulon, Gif sur Yvette, France.

Jannink, J.-L. 2006. MAS as a form of Index selection. Barley Coordinated Agricultural Project Meeting, Plant and Animal Genome XIV, San Diego, CA.

Jannink, J.-L. 2004. Can parsimonious modeling of QTL variance help detect QTL? Plant and Animal Genome XII, San Diego, CA.

Jannink, J.-L. 2002. QTL analysis of long-term selection response. Plant and Animal Genome X, San Diego, CA.

Jannink, J.-L. 2002. QTL mapping in pedigrees: methods, potential, practice. American Oat Workers Conference 2002.

Jannink, J.-L. 2001. Using interconnected populations to map QTL. North Central Regional Corn Breeding Meetings (NCR-167), Ames, IA.

Jannink, J.-L. 1999. Statistical inference using the asymptotic dispersion matrix of maximum likelihood estimates. Invited seminar, Centre for Biometry Wageningen, The Netherlands.

Jannink, J.-L. 1998. Breeding soybean for high weed suppressive ability. Invited seminar, Instituto Nacional de Investigacion Agropecuaria, Colonia, Uruguay.

Jannink, J.-L. 1998. Computer simulation in Plant Breeding. Invited seminar, Facultad de Agronomia, Univ. de Montevideo, Uruguay.

Jannink, J.-L. 1998. La agricultura sostentable en los Estados Unidos: El debate actual (Sustainable agriculture in the United States: Current discussions). Invited seminar, Facultad de Agronomia, Univ. de Montevideo, Uruguay.

Other presentations:

Lorenz, A. J., M. T. Hamblin, **J.-L. Jannink**, 2010. Plant and Animal Genome XVIII, San Diego, CA. (P326) Comparing Haplotypes And Single Markers For Association Mapping In Barley.

Jannink, J.-L., Asoro, F., Newell, M. Scott, M.P. 2009. Association genetics of beta-glucan metabolism to enhance oat germplasm for food and nutritional function. USDA-NRI Plant Biology Program Genes to Products Workshop. Bethesda, MD.

Iwata, H., **J.-L. Jannink**, 2009. Plant and Animal Genome XVII, San Diego, CA. (P258) A Simulation Study To Evaluate The Efficacy Of Genomic Selection In Barley Breeding Programs.

Iwata, H., **J.-L. Jannink**, 2009. Gordon Conference on Quantitative Genetics and Genomics, Galveston TX. Accuracy of genomic selection in barley breeding programs - a simulation study.

Zhou, Hao, **J.-L. Jannink**, B. J. Steffenson, 2009. Plant and Animal Genome XVII, San Diego, CA. (P263) Association Mapping Of Adult Plant Spot Blotch Resistance In Barley Breeding Germplasm From The USA

Sorrells, M. E., E. L. Heffner, **J.-L. Jannink**, 2009. Plant and Animal Genome XVII, San Diego, CA. (W232) Association Breeding Strategies For Improvement Of Self-Pollinated Crops

Tinker, N. A., A. Kilian, E. Jackson, S. Molnar, C. Wight, B. Rossnagel, G. Scoles, P. Eckstein, H. Rines, M. Carson, D. Stuthman, M. Sorrells, **J.-L. Jannink**, S. Tuvesson, A. Ceplitis, R. Jonsson, C. Howarth, T. Langdon, D. Obert, M. Bonman, H. Ohm, J. Anderson, Å. Bjørnstad, O. Olsson, M. Bräutigam, L. Federrizi, F. Kolb, 2008. Plant and Animal Genome XVI, San Diego, CA. (W329) DArT Marker Development And Applications In Oat

Gutierrez, L., **J.-L. Jannink**, J. Nason, 2007. ASA-CSSA-SSSA Annual Meetings, New Orleans, LA. Genetic Characterization of Barley Breeding Programs.

Cheema, M., L. R. Gibson, and **J.-L. Jannink**, 2007. ASA-CSSA-SSSA Annual Meetings, New Orleans, LA. Genotypic Response to Early and Late Planting in Winter Triticale.

Gutierrez, L., **J.-L. Jannink**, and J. Nason, 2006. ASA-CSSA-SSSA Annual Meetings, Indianapolis, IN. Diversity of Cultivated Barley and Wild Barley.

Jannink, J.-L., J.E. Edwards, and M. Carson. 2005. Designing Variety Blends to Increase Performance Stability. *In*. Agron. Abstr. ASA. Madison, WI.

Jellen, E. N., D. E. Jarvis, I. Loskutov, **J.-L. Jannink**, D. C. Ames, F. D. Raymond, P. J. Maughan, 2005. Plant and Animal Genome XIII, San Diego, CA. (P109) Molecular Variation In The Secondary And Distant Primary Oat Gene Pools (*Avena* spp.)

Chernyshova, A., P.J. White, S. Sayar, and **J.-L. Jannink**. 2004. Additive and Epistatic Components of Beta-Glucan Content Variance in Oat. *In.* Agron. Abstr. ASA. Madison, WI.

Long, J., J.B. Holland, G. Munkvold, and **J.-L. Jannink**. 2004. Response to Selection for Partial Resistance to Crown Rust in Oat. *In.* Agron. Abstr. ASA. Madison, WI.

Jannink, J.-L. 2004. Selective phenotyping to accurately map QTL. *In.* Agron. Abstr. ASA. Madison, WI.

Gardner, S.W. and **J.-L. Jannink**. 2003. DNA marker analysis of an oat high oil selection program. Agronomy Meetings, 2003.

Gutierrez, L., **J.-L. Jannink**, and J. Nason. 2003. Multivariate differentiation among populations for quantitative traits. Agronomy Meetings, 2003.

Iutzi, F., E.C. Brummer, and **J.-L. Jannink**. 2003. Light competition and yield trade-offs in intercrops of small grains and red clover. Agronomy Meetings, 2003.

Jannink, J.-L. and E.C. Brummer. 2003. Evalutating oat compatibility with alfalfa using small seed quantities. Agronomy Meetings, 2003.

Colleoni-Sirghie, M., Kovalenko, I.V., Briggs, J.L., **Jannink, J.-L.**, White, P.J. 2003. Targeting new high-β-glucan oat lines with enhanced health benefits by measuring pasting and rheological properties of raw oat flours. IFT Meeting 2003, Chicago, IL, USA.

Jannink, J.-L., and X.-L. Wu. 2003. Joint mapping of QTL in three interconnected barley populations. Plant and Animal Genome XI, San Diego, CA. http://www.intl-pag.org/

Wu, X.-L., and **J.-L. Jannink**. 2003. Optimal sampling of line-cross populations to determine QTL location, variance, and allelic number. Plant and Animal Genome XI, San Diego, CA. http://www.intl-pag.org/

Gogula, M.K.R. and **J.-L. Jannink**. 2002. Recurrent Selection for Stable Groat Percentage in Oat using BLUP. Agronomy Meetings, 2002

Jannink, J.-L. 2001. QTL mapping in populations derived from related inbreds. Plant and Animal Genome IX Conference, San Diego, CA. http://www.intl-pag.org/

Jannink, J.-L. and R.C. Jansen. 2000. The diallel mating design for mapping interacting QTL. Eucarpia Section Biometrics, Paris.

Jannink, J.-L., J.H. Orf, N. Jordan, and R.G. Shaw. 1999. Index selection for weed suppressive ability in soybean. Agron. Abstr. 1999:69.

Jannink, J.-L., N. Jordan, and J.H. Orf. 1999. Phenology and soil resource availability affect soybean competition with weeds. Ecological Soc. Amer. 1999 Meeting Abstracts p. 264.

Jannink, J.-L., N. Jordan, and J.H. Orf. 1997. Crop weed suppressive ability at locations differing in soil fertility. Bull. Ecological Soc. Amer., Supplement 78(4):263.

Jannink, J.-L., M. Liebman, and L.C. Merrick. 1994. Pea genotype effects on competition for light in a pea, oat, and vetch green manure mixture. Agron. Abstr. 1994:155.

Jannink, J.-L., M. Liebman, L.C. Merrick, E.A. Dyck, and S.A. Corson. 1994. Potential of hairy vetch (*Vicia villosa* Roth) as a winter annual green manure in Maine. Agron. Abstr. 1994:511.