

Robert J. Elshire

Professional Positions

2015-	Director, The Elshire Group Ltd.
2013-2015	Senior Scientist – Genetic Analysis, Forage Improvement Group, AgResearch Ltd.
2007-2013	Sequencing Technology Lead, Buckler Laboratory, Institute for Genomic Diversity, Cornell University
2006-2007	Laboratory Technician, Scanlon Laboratory, Cornell University
2001-2003	Director, Illinois Genetic Marker Center, University of Illinois at Urbana-Champaign

Education

2003-2005	Cornell University	Graduate Programme (Non-matriculating) in Plant Breeding and Genetics
1999-2001	University of Illinois	MSc in Natural Resources and Environmental Sciences
1997-1999	University of Illinois	BSc in General Biology

Community Participation

President of **Genomics for Aotearoa New Zealand**, 2017 (ongoing)
Participant in the **International Science Workshop**, *Ministry of Business, Innovation and Employment*, December 2016
Founder and leader of the **Biospectra-By-Sequencing Project**, 2014 (ongoing)
Founder and sponsor of the **Palmerston North Bioinformatics Meeting**, 2015 (ongoing)
Member of the **MapNet Community Steering Committee**, 2015 (ongoing)
Councilor of the **New Zealand Open Source Society**, 2016 (ongoing)
Participant in the **eResearch Refresh Workshop**, *Ministry of Business, Innovation and Employment*, October 2015
Participant in the **Breeding Days Workshop**, *Ministry of Business, Innovation and Employment*, May 2015
Participant in many **eResearch 2020 Workshops**, 2013- 2015
Reviewer for **Nature Methods**, 2015
Programme Committee member **eResearch 2014 & 2016 Conferences**

Award

Recipient of the **New Zealand Open Source Award**, People's Choice category, 2014

Publications

Galla, SJ., Buckley TR, **Elshire R**, Hale ML, Knapp M, McCallum J, Moraga R, Santure AW, Wilcox P, and Steeves TE. (2016) Building Strong Relationships between Conservation Genetics and Primary Industry Leads to Mutually Beneficial Genomic Advances. *Molecular Ecology* doi:10.1111/mec.13837.

Lu F, Romay MC, Glaubitz JC, Bradbury PJ, **Elshire RJ**, Wang T, Li Y, Li Y, Semagn K, Zhang X, Hernandez AG, Mikel MA, Soifer I, Barad O, Buckler ES. (2015) High-resolution genetic mapping of maize pan-genome sequence anchors. *Nature Communications* doi:10.1038/ncomms7914.

Takuno S, Ralph P, Swarts KL, **Elshire RJ**, Glaubitz JC, Buckler ES, Hufford MB, Ross-Ibarra J. (2015) Independent molecular basis of convergent highland adaptation in maize. *Genetics* doi: 10.1534/genetics.115.178327

Rodgers-Melnick E, Bradbury P, **Elshire R**, Glaubitz J, Acharya C, Mitchell S, Li C, Li Y, Buckler E. (2015) Recombination in diverse maize is stable, predictable, and associated with genetic load. *PNAS* 112 (12) 3823-3828

Swarts K, Li H, Romero Navarro A, An D, Romay M, Hearne S, Acharya C, Glaubitz J, Mitchell S, **Elshire R**, Buckler E, Bradbury P. (2014) Novel Methods to Optimize Genotypic Imputation for Low-Coverage, Next-Generation Sequence Data in Crop Plants. *The Plant Genome* 7(3) doi:10.3835/plantgenome2014.05.0023

Glaubitz JC, Casstevens TM, Lu F, Harriman J, **Elshire RJ**, Sun Q, Buckler ES. (2014). TASSEL-GBS: A high capacity genotyping by sequencing analysis pipeline. *PLoS ONE*9(2): e90346. doi:10.1371/journal.pone.0090346

Romay MC, Millard M, Glaubitz JC, Peiffer JA, Swarts KL, Casstevens TM, **Elshire RJ**, Acharya CB, Mitchell SE, Flint-Garcia S, McMullen MD, Holland JB, Buckler ES, Gardner C. (2013) Comprehensive genotyping of the US national maize inbred seed bank: genetic structure, diversity, and genome-wide association studies of a global treasure. *Genome Biology* 14:R55

Chen C, Mitchell S, **Elshire R**, Buckler E, El-Kassaby Y. (2013) Mining Conifers' Mega-Genome Using Rapid and Efficient Multiplexed High-throughput Genotyping-by-Sequencing (GBS) SNP Discovery Platform. *Tree Genetics and Genomes* doi:10.1007/s11295-013-0657-1

Lu F, Lipka AE, **Elshire RJ**, Glaubitz JC, Cherney JH, Casler MD, Buckler ES, Costich DE. (2013) Switchgrass genomic diversity, ploidy and evolution: novel insights from a network-based SNP discovery protocol. *PLoS Genetics*9(1):e1003215.

Hufford MB, Xun X, van Heerwaarden J, Pyhäjärvi T, Chia JM, Cartwright RA, **Elshire RJ**, Glaubitz JC, Guill KE, Kaeppeler SM, Lai J, Morrell PL, Shannon LM, Song C, Springer NM, Swanson-Wagner RA, Tiffin P, Wang J, Zhang G, Doebley J, McMullen MD, Ware D, Buckler ES, Yang S, Ross-Ibarra J. (2012) Comparative population genomics of maize domestication and improvement. *Nature Genetics* doi:10.1038/ng.2309.

Chia JM, Song C, Bradbury PJ, Costich D, de Leon N, Doebley J, **Elshire RJ**, Gaut B, Geller L, Glaubitz JC, Gore M, Guill KE, Holland J, Hufford MB, Lai J, Li M, Liu X, Lu Y, McCombie R, Nelson R, Poland J, Prasanna BM, Pyhäjärvi T, Rong T, Sekhon RS, Sun Q, Tenaillon MI, Tian F, Wang J, Xu X, Zhang Z, Kaeppeler SM, Ross-Ibarra J, McMullen MD, Buckler ES, Zhang G, Xu Y, Ware D. (2012) Maize HapMap2 identifies extant variation from a genome in flux. *Nature Genetics* doi:10.1038/ng.2313.

Elshire RJ, Glaubitz JC, Sun Q, Poland JA, Kawamoto K, Buckler ES, Mitchell SE. (2011) A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *PLoS ONE* 6(5): e19379.

Zeid M, Yu JK, Goldowitz I, Denton ME, Costich DE, Jayasuriya CT, Saha M, **Elshire RJ**, Benscher D, Breseghello F, Munkvold J, Varshney RK, Belay G, Sorrells ME. (2010) Cross-amplification of EST-derived markers among 16 grass species. *Field Crops Research* Vol. 118 No. 1:28-35.

Gore MA, Chia J, **Elshire RJ**, Sun Q, Ersoz ES, Hurwitz BL, Peiffer JA, McMullen MD, Grills GS, Ross-Ibarra J, Ware DH, Buckler ES. (2009) A First-Generation Haplotype Map of Maize. *Science* 326, 1115.

Brooks L, Strable J, Zhang X, Ohtsu K, Zhou R, Sarkar A, Hargreaves S, **Elshire RJ**, Eudy D, Pawlowska T, Ware D, Janick-Buckner D, Buckner B, Timmermans MCP, Schnable PS, Nettleton D, and Scanlon MJ. (2009) Microdissection of Shoot Meristem Functional Domains. *PLoS Genet* 5(5): e1000476.

Zhang X, Madi S, Borsuk L, Nettleton D, **Elshire RJ**, Buckner B, Janick-Buckner D, Beck J, Timmermans M, Schnable PS, Scanlon MJ. (2007) Laser Microdissection of Narrow Sheath Mutant Maize Uncovers Novel Gene Expression in the Shoot Apical Meristem. *PLoS Genet* 3(6): e101.

Talks and Workshops

Sharing Improvements in Genotyping-by-Sequencing: presented at the *MapNet* conference, Palmerston North, NZ November 2017.

Bioinformatic Computational Science Workshop: organiser and presenter, Palmerston North, NZ, November 2017.

Collaboration, Capabilities, and Impact in NZ eResearch: Bridging the Gap (Keynote Plenary): presented at the *eResearch 2016 Conference*, Queenstown, NZ, February 2016.

Genetic Technologies & the Evolution of Corn: presented at the *Summer Internship for Indigenous Peoples in Genomics – Aotearoa*, Otago University, Dunedin, NZ, January 2016.

Genomics Innovation: Shifting the Paradigm: presented at the *Plant Biology Seminar*, Palmerston North, NZ, October 2015.

Democratising Genetic Analysis and Breeding with Genotyping-By-Sequencing: presented at Australian National University, Canberra, AU, October 2015.

Democratising Genetic Analysis and Breeding with Genotyping-By-Sequencing (Keynote): presented at the *Australian Genomic Technologies Association Conference*, Hunter Valley, AU, October 2015.

Building an NZ Platform for Genetic Analysis – Genotyping-by-Sequencing and Beyond: presented at the *Bioprotection CORE*, Lincoln, NZ, April 2015.

Biospectra-by-Sequencing Workshop: organized and chaired at *eResearch 2015*, Queenstown, NZ, March 2015.

Markers and Measurements to the Planter: Collecting, Integrating and Applying Big Data in PlantBreeding(Keynote): presented at *15th Australasian Plant Breeding Conference*, Melbourne, AU, October 2014.

Genomics for Production and Security in a Biological Economy -- GBS Community Workshop: organized and presented at the *MapNet Conference*, Invermay, NZ, October 2014.

Enabling Very Complex Experiments: Genomics for Production and Security in a Biological Economy: presented at the *eResearch 2014 Conference*, Hamilton, NZ, July 2014.

Genomics for Production and Security in a Biological Economy: presented at *Plant and Food Research*, Palmerston North, NZ, July 2014.

Genomics for Production and Security in a Biological Economy: presented at the *Plant Biology Seminar*, Palmerston North, NZ, June 2014.

Genomics for Production and Security in a Biological Economy: presented at *SCION*, Rotorua, NZ, May 2014.

Applications of High Throughput Sequencing-based Technologies for Agricultural Genomics (Keynote): presented at the *Illumina Science Summit*, Penang, Malaysia, April 2014.

GBS Training Workshop: organized and presented, Palmerston North, NZ, February 2014.

Bioinformatics Workshop for Ecological and Evolutionary Research -- GBS Workshop: organized and presented, Deakin University, Geelong, AU, February 2014.

Genotyping-by-Sequencing (GBS): A brief overview and applications: presented at the *MapNet Conference*, Lincoln, NZ, October 2013.

Genotyping-by-Sequencing: principles and practice: presented at the *Molecular Markers in Horticulture Symposium*, Riva del Garda, Italy, September 2013.

Genotyping-by-Sequencing (GBS): A brief overview and applications: presented at *QMB 2013*, Queenstown, NZ, August 2013.

Genotyping-by-Sequencing (GBS): Overview and Applications: presented at the *Upstate New York Illumina User Group Meeting*, Ithaca, NY, May 2012.

Genotyping on High Throughput Sequencers: Preparation and Analysis of Reduced Representation Genomic Libraries: co-presented with Eric Johnson at the *Association of Biomolecular Resource Facilities Annual Conference*, Orlando, FL, March 2012.

Genotyping-by-Sequencing: Webinar with Mary Cornett of IDEX, January 2012.

Educational Workshop on Genotyping-by-Sequencing (GBS): presented at the *Northeast Regional Life Sciences Core Directors Meeting*, Ithaca, NY, November 2011.

Reduced Representation Sequencing for Rapidly Genotyping Highly Diverse Species: presented at *AgResearch*, Palmerston North, New Zealand, December 2010.