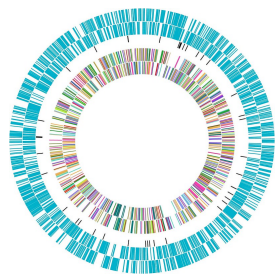


Robert John Elshire



The Elshire Group Limited

Website: <https://www.elshiregroup.co.nz>

About

I tinker, joyfully.

Current Position

Director, The Elshire Group Limited

Positions Held

2013 - 2015	Senior Scientist, Genetic Analysis, Forage Improvement Group. AgResearch Ltd.
2007 - 2013	Sequencing Technology Lead, 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 Champaign Urbana

Education

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

Award

2014	People's Choice, New Zealand Open Source Award
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Community Service

Leading

2017 - 2022	President, Genomics for Aotearoa New Zealand
2021	Councillor, New Zealand Association of Scientists
2016 - 2018	Councillor, New Zealand Open Source Society

2015 - Present Founder and Sponsor, Palmerston North Bioinformatics Meeting
2014 - 2019 Founder and Leader, Biospectra-by-Sequencing Project

Contributing

2016 Participant, International Science Workshop. MBIE
2014, 2016 Programme Committee Member, eResearch Conference
2015 Participant, eResearch Refresh Workshop. MBIE
2015 Participant, Breeding Days Workshop. MBIE
2015 Reviewer, Nature Methods
2013 - 2015 Participant, eResearch 2020 Workshops

Affiliations

2019 - Present Member, New Zealand Association of Scientists
2019 - Present Member, Maize Genetics Cooperation
2019 - Present Member, Software in the Public Interest
2019 - Present Associate Member, Lawyers for Climate Action New Zealand Inc.
2018 - Present Associate Member, Aotearoa Tech Union
2017 - Present Member, Genomics for Aotearoa New Zealand
2003 - Present Associate Member, Free Software Foundation

Talks & Workshops

Invited

2022 “Building Genomics Research Capability for More Efficient Crop Improvement” presented at the 1st International Symposium on Plant Genomics and Bioinformatics. Pan-Latin America Zoom Conference, Lima, Peru

“Better Bioinformatics, Better Biology” presented at University of Auckland. Auckland, New Zealand

2019 “Pub Genomics Talk” presented at 2019 Pint of Science. Palmerston North, New Zealand

2018 “Agri-Tech Innovation Ecosystem Workshop” presented at the Centre for Entrepreneurial Agri-Technology. Australian National University

“Collaboration, Capabilities, and Impact in NZ eResearch: Bridging the Gap” [Plenary] presented at eResearch 2016 Conference. Queenstown, New Zealand

2016 “Genetic Technologies & the Evolution of Corn” presented at the Summer Internship for Indigenous Peoples in Genomics – Aotearoa. Dunedin, New Zealand

“Democratising Genetic Analysis and Breeding with Genotyping-by-Sequencing” [Keynote] presented at the Australian Genomics Technologies Association Conference. Hunter Valley, Australia

- 2015 “Building an NZ Platform for Genetic Analysis – Genotyping-by-Sequencing and Beyond” presented at the Bioprotection CORE. Lincoln, New Zealand
- “Markers and Measurements to the Planter: Collecting, Integrating, and Applying Big Data in Plant Breeding” [*Keynote*] presented at the 15th Australasian Plant Breeding Conference. Melbourne, Australia
- “Applications of High Throughput Sequencing-based Technologies for Agricultural Genomics” [*Keynote*] presented at the Illumina Science Summit. Penang, Malaysia
- 2014 “Bioinformatics Workshop for Ecological and Evolutionary Research – GBS Workshop” organized and presented at Deakin University. Geelong, Australia
- “Genotyping-by-Sequencing: Principles and Practice” presented at the Molecular Markers in Horticulture Symposium. Riva del Garda, Italy
- 2013 “Genotyping-by-Sequencing (GBS): A Brief Overview and Applications” presented at QMB 2013. Queenstown, New Zealand
- “Genotyping-by-Sequencing (GBS): Overview and Applications” presented at the Upstate New York Illumina User Group Meeting. Ithaca, New York
- 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, Florida
- 2011 “Educational Workshop on Genotyping-by-Sequencing (GBS)” presented at the Northeast Regional Life Sciences Core Directors Meeting. Ithaca, New York
- 2010 “Reduced Representation Sequencing for Rapidly Genotyping Highly Diverse Species” presented at AgResearch Limited. Palmerston North, New Zealand
- Uninvited
- 2022 “#NZResearchRethink A Community Approach” presented at the New Zealand Association of Scientists Conference. Wellington, New Zealand
- 2019 “Bioinformatics Cloud Computing Workshop Series” organiser and instructor. Palmerston North, New Zealand
- 2018 “Non-Model Genomics Workshop” organiser and moderator by Genomics for Aotearoa New Zealand. Wellington, New Zealand
- “Sharing Improvements in Genotyping-by-Sequencing” presented at the MapNet conference. Palmerston North, New Zealand
- 2017 “Bioinformatic Computational Science Workshop” organiser and presenter. Palmerston North, New Zealand
- “Genomics Innovation: Shifting the Paradigm” presented at the Plant Biology Seminar. Palmerston North, New Zealand

- 2015 “Biospectra-by-Sequencing Workshop” organized and chaired at eResearch 2015. Queenstown, New Zealand
- “Genomics for Production and Security in a Biological Economy – GBS Community Workshop” organized and presented at the MapNet Conference. Invermay, New Zealand
- “Enabling Very Complex Experiments: Genomics for Production and Security in a Biological Economy” presented at the eResearch 2014 Conference. Hamilton, New Zealand
- “Genomics for Production and Security in a Biological Economy” presented at Plant and Food Research. Palmerston North, New Zealand
- “Genomics for Production and Security in a Biological Economy” presented at the Plant Biology Seminar. Palmerston North, New Zealand
- “Genomics for Production and Security in a Biological Economy” presented at SCION. Rotorua, New Zealand
- 2014 “GBS Training Workshop” organized and presented with international speakers to 30+ New Zealand researchers. Palmerston North, New Zealand
- 2013 “Genotyping-by-Sequencing (GBS): A brief overview and applications” presented at the MapNet Conference. Lincoln, New Zealand

Publications

- 2016 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
- 2015 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

- 2014
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
- 2013
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, Kaeppler 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.
- 2012
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, Kaeppler 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.
- 2011
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.
- 2010
Zeid M, Yu JK, Goldowitz I, Denton ME, Costich DE, Jayasuriya CT, Saha M, Elshire RJ, Benschler 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.
- 2009
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.

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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. *PLoSGenet* 3(6): e101.