University of Birmingham

Dr Lindsey Jane Leach BSc, PhD

Birmingham Fellow

School of Biosciences (/schools/biosciences/index.aspx)

Contact details

Telephone +44 (0)121 414 5883 (tel:+44 121 414 5883)

Email l.j.leach@bham.ac.uk (mailto:l.j.leach@bham.ac.uk)

School of Biosciences
University of Birmingham
Edgbaston
Birmingham
B15 2TT
UK

About

(/university/colleges/les/research-gallery/lindsey-leach.aspx) Dr Leach joined the University of Birmingham as a Birmingham Fellow in 2012 and is based in the Plant Genetics and Cell Biology group in the School of Biosciences. Her work involves using statistical genetics and bioinformatic approaches to dissecting the genetic architecture of quantitative trait variation.

Qualifications

PhD in Statistical Genetics 2008, University of Birmingham, supervisor Professor Z Luo.
BSc Hons Biological Sciences 2003, University of Birmingham.

Biography

Lindsey gained a PhD in Statistical Genetics at the University of Birmingham under the supervision of Professor Z Luo and Professor Michael J Kearsey. She then worked with Professor Nicholas Harberd as a Postdoctoral Researcher in the Department of Plant Sciences, University of Oxford and gained experience in next generation sequencing and bioinformatic analysis of polyploid plant genomes. Lindsey returned to Birmingham appointed as a Birmingham Fellow in the School of Biosciences in March 2012.

Teaching

Undergraduate teaching

- Lindsey teaches quantitative genetics and QTL mapping to 1st, 2nd and 3rd year Undergraduate genetics students.
- BIO154 - Genetics I.
- BIO265 – Genes and genomes from microorganisms to man.
- BIO348 – Genetic variation in humans.
- BIO398 - Plant Science in the 21st century.

Postgraduate supervision

Students interested in Dr Leach's research and the possibility of a PhD position are encouraged to contact Lindsey via email: **l.j.leach@bham.ac.uk (mailto:l.j.leach@bham.ac.uk)** .

For a list of possible PhD projects offered by Dr Leach: **www.findaphd.com/search/ProjectDetails.aspx?PJID=37210&LID=124 (http://www.findaphd.com/search/ProjectDetails.aspx?PJID=37210&LID=124)**

Research

My research interests lie in the dissection of complex trait phenotypes in human, plant and animal populations into their underlying genetic components. This central problem in statistical genetics consists of multiple interrelated parts, from genetic and epigenetic studies to identify genetic variants involved, transcriptomics to explore the genome-wide expression patterns, to the related fields of proteomics and metabolomics. Integrating knowledge from each level of information has the potential to build realistic understanding of the molecular networks underpinning complex trait variation.

Advances in next generation sequencing (NGS) technologies have enabled a high- throughput genome-wide approach to unravelling the genetic components of phenotypic variation at an unprecedented level of resolution. The rapid pace at which new sequencing technologies are emerging is generating a growing disparity between the rate of data generation and its full and biologically meaningful analysis. I am interested in keeping pace with these advances by developing novel methodological and analytical approaches to integrate NGS into theoretical and empirical studies of complex trait genetics.

I am also interested in the evolution of polyploid species that have multiple copies of the genome. The polyploid state creates sophisticated patterns of chromosome behaviour and thus inheritance, posing a major challenge to genetic analyses in these species. Yet, many of the world's most important food crops are polyploids, including bread wheat, cotton, potato and oil seed rape. Progress in this area is thus essential for meeting the challenge of global food security.

Recent projects include:

Homoeologous gene expression in the hexaploid bread wheat genome

This bioinformatics project uses Illumina “next generation sequencing” to dissect the architecture of gene expression in bread wheat (Triticum aestivum), one of the world’s major food crops. It has an enormous allohexaploid genome comprised of three homoeologous subgenomes (A, B and D), presenting a major challenge to reliably distinguish the contributions made by the 3 subgenomes to total gene expression. We use deep sequencing of wheat gene transcripts to characterise the fate of wheat genes following polyploidization and assess the detailed gene expression patterns for genes present on all 3 subgenomes.

Molecular evolution of duplicate genes

Taking advantage of rapidly accumulating 'omics' datasets, we have investigated the process and molecular mechanisms driving the divergent evolution of duplicate genes in the yeast protein-protein interaction network, the evolution of enzymatic genes in the yeast metabolic network, and the expression divergence between duplicate genes in the yeast genome.

Theory and methods for constructing genetic linkage maps in polyploid species

Construction of genetic linkage maps is usually the first milestone in launching a genome project for an organism. In the era of genomics, genetic linkage maps are now available or quickly becoming available in humans and in almost all important animal and plant species. In sharp contrast, the corresponding study in polyploid species is theoretically challenging and still in its infancy. Our research on this topic focuses on developing theory and statistical approaches for genetic map construction in autotetraploid species, an example of which is cultivated potato, currently the world's fourth most important food crop and thus important for future food security.

Other activities

- Member of the Genetics Society (2005-present).
- Higher Education Academy associate (2007-present).

Publications

Leach, L.J., Belfield, E., Jiang, C. et al. (2014). Patterns of homoeologous gene expression shown by RNA sequencing in hexaploid bread wheat. *BMC Genomics*. 15: 276.

Wang, L., Jiang, N., Wang, L., Fang, O., **Leach, L.J**., et al. 3' untranslated regions mediate transcriptional interference between convergent genes both locally and ectopically in S cerevisiae. *PLoS Genetics*. 10: e1004021.

Yang, S., Liu, Y., Jiang, N., Chen, J., **Leach, L.J.**, et al. (2014). Genome-wide eQTLs and heritability for gene expression traits in unrelated individuals. *BMC Genomics.* 15: 13.

Wu, X., Liu, T., Fang, O., **Leach, L.J.**, *et al*. (2013). miR-194 suppresses metastasis of non-small cell lung cancer through regulating expression of BMP1 and p27(kip1). *Oncogene*. doi:10.1038/onc.2013.108.

Mithani, A., Belfield, E., Brown, C., Jiang, C., **Leach, L.J.**, *et al.* (2013). HANDS: a tool for genome-wide discovery of subgenome-specific base identity in polyploids. *BMC Genomics.* 14: 653.

Jiang, N., Wang, M., Jia, T., **Leach, L.J.**, *et al*. (2011). A robust statistical method for association-based eQTL analysis. *PLoS One* 6(8): e231912. doi:10.1371/journal.pone.0023192.

Wang M., Jiang N., Jia T., **Leach L.J.**, Cockram J., Thomas B., Ramsay L., Waugh R. and Luo Z.W. (2011). Genome-wide association mapping of agronomic and morphologic traits in highly structured populations of barley cultivars. *Theor. Appl. Genet.* doi 10.1007/s00122-011-1697-2.

Leach, L.J., Wang, L. Kearsey, M.J. and Luo, Z.W. (2010). Multilocus tetrasomic linkage analysis using Hidden Markov chain model. *PNAS*. 107: 4270 – 4274.

Lu, C., Hu, X., Wang, G., **Leach, L.J.**, *et al*. (2010). Why do essential proteins tend to be clustered in the yeast interactome network? *Molecular Biosystems*. doi: 10.1039/b921069e.

Wang, M., Hu, X., Li, G., **Leach, L.J.**, Potokina, E., Duka, A., Waugh, R., Kearsey, M.J., Luo, Z. (2009). Robust detection and genotyping of single feature polymorphisms from gene expression data. *PLoS Computational Biology.* 5(3): e1000317.

Jiang, N., **Leach, L.J.**, *et al*. (2008). Methods for evaluating gene expression from Affymetrix microarray datasets. *BMC Bioinformatics.* 9:284.

Lu, C., Zhang, Z., **Leach, L.** *et al*. (2007). Impacts of yeast metabolic network structure on enzyme evolution. *Genome Biology*. 8:407.

Leach, L. J., Zhang, Z., Lu, C.Q., Kearsey, M. J. and Luo, Z. W. (2007). The role of *cis* regulatory motifs and genetical control of expression in the divergence of yeast duplicate genes. *Mol. Biol. Evol*. 24(11): 2556-2565.

Luo, Z.W., Zhang, Z., **Leach, L.** *et al.* (2006). Constructing genetic linkage maps under a tetrasomic model. *Genetics.* 172: 2635-2645.

Hu, X.H., Wang, M.H., Tan, T., Li, J.R., **Leach, L.** *et al*. (2006). Genetic dissection of ethanol tolerance in budding yeast *S. cerevisiae*. *Genetics.* 175:1479-1487.

Wu, X., Liu, T., Fang, O., **Leach, L J**., Hu. X., and Luo, Z. miR-194 suppresses metastasis of non-small cell lung cancer through regulating expression of BMP1 and p27(kip1). *Oncogene* . doi:10.1038/onc.2013.108.

© University of Birmingham 2015