# Simon Renny-Byfield

### PERSONAL DETAILS

Address Department of Plant Sciences

Robbins Hall

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# **ACADEMIC QUALIFICATIONS**

#### Ph.D. Plant Evolutionary Genomics

2008-2012

Queen Mary University of London, UK Supervisors: Professor Andrew R. Leitch

Thesis Title: Evolution of repetitive DNA in angiosperms: Examples from Nicotiana

#### B.Sc Genetics First Class Honors

2005-2008

Queen Mary University of London, UK

# PROFESSIONAL EXPERIENCE

Post-Doctoral Research

University of California, Davis

Supervisor: Dr. Jeffrey Ross-Ibarra

2014-present

Post-Doctoral Research

Iowa State University

Supervisor: Prof. Jonathan F. Wendel

2012-2014

# **PUBLICATIONS**

- [1] Buggs, R. J., Renny-Byfield, S., Chester, M., Jordan-Thaden, I. E., Viccini, L. F., Chamala, S., Leitch, A. R., Schnable, P. S., Barbazuk, W. B., Soltis, P. S., and Soltis, D. E. (2012). Next-generation sequencing and genome evolution in allopolyploids. *American Journal of Botany*, 99:372–382.
- [2] Gong, L., Grover, C. E., Masonbrink, R., **Renny-Byfield, S.**, Gallagher, J. P., and Wendel, J. (2015). A cluster of recently inserted transposable elements associated with sirnas in gossypium raimondii. *The Plant Genome*, in press.
- [3] Kelly, L. J., Leitch, A. R., Fay, M. F., Renny-Byfield, S., Pellicer, J., Macas, J., and Leitch, I. J. (2012). Why size really matters when sequencing plant genomes. *Plant Ecology and Diversity*, 5(4):415–425.
- [4] Kelly, L. J., **Renny-Byfield, S.**, Pellicer, J., Macas, J., Novk, P., Neumann, P., Lysak, M. A., Day, P. D., Berger, M., Fay, M. F., Nichols, R. A., Leitch, A. R., and Leitch, I. J. (2015). Analysis of the giant genomes of *Fritillaria* (liliaceae) indicates that a lack of *DNA* removal characterizes extreme expansions in genome size. *New Phytologist*, pages n/a-n/a.
- [5] Koukalova, B., Moraes, A. P., Renny-Byfield, S., Matyasek, R., Leitch, A. R., and Kovarik, A. (2010). Fall and rise of satellite repeats in allopolyploids of *Nicotiana* over c. 5 million years. *New Phytologist*, 186(1):148–160.
- [6] Kovarik, A., Renny-Byfield, S., and Leitch, A. R. (2011). Evolutionary implications of genome and karyotype restructuring in Nicotiana tabacum L., pages 209–224. Springer, New York.

- [7] Masonbrink, R. E., Gallagher, J. P., Jareczek, J. J., **Renny-Byfield, S.**, Grover, C. E., Gong, L., and Wendel, J. F. (2014). Cenh3 evolution in diploids and polyploids of three angiosperm genera. *BMC plant biology*, 14(1):383.
- [8] Matyasek, R., **Renny-Byfield, S.**<sup>†</sup>, Fulnecek, J., Macas, J., Grandbastien, M.-A., Nichols, R., Leitch, A., and Kovarik, A. (2012). Next generation sequencing analysis reveals a relationship between rDNA unit diversity and locus number in *Nicotiana* diploids. *BMC Genomics*, 13:722.
- [9] **Renny-Byfield, S.**, Ainouche, M., Leitch, I. J., Lim, K. Y., Le Comber, S. C., and Leitch, A. R. (2010). Flow cytometry and GISH reveal mixed ploidy populations and *Spartina* nonaploids with genomes of *S. alterniflora* and *S. maritima* origin. *Annals of Botany*, 105(4):527–533.
- [10] Renny-Byfield, S., Chester, M., Kovak, A., Le Comber, S. C., Grandbastien, M.-A., Deloger, M., Nichols, R. A., Macas, J., Novk, P., W. Chase, M., and R. Leitch, A. (2011). Next generation sequencing reveals genome downsizing in allotetraploid *Nicotiana tabacum*, predominantly through the elimination of paternally derived repetitive DNAs. *Molecular Biology and Evolution*, 28(10):2843–2854.
- [11] Renny-Byfield, S., Gallagher, J. P., Grover, C. E., Szadkowski, E., Page, J. T., Udall, J. A., Wang, X., Paterson, A. H., and Wendel, J. F. (2014). Ancient gene duplicates in *Gossypium* (cotton) exhibit near-complete expression divergence. *Genome Biology and Evolution*, 6(3):559–571.
- [12] **Renny-Byfield, S.**, Gong, L., Gallagher, J. P., and Wendel, J. F. (2015). Persistence of subgenomes in paleopolyploid cotton after 60 my of evolution. *Molecular Biology and Evolution*, 32(4):1063–1071.
- [13] Renny-Byfield, S., Kovarik, A., Chester, M., Nichols, R. A., Macas, J., Novak, P., and Leitch, A. R. (2012). Independent, rapid and targeted loss of a highly repetitive DNA sequence derived from the paternal genome donor in natural and synthetic *Nicotiana tabacum. PLoS One*, 7(5):e36963.
- [14] Renny-Byfield, S., Kovarik, A., Kelly, L. J., Macas, J., Novak, P., Chase, M. W., Nichols, R. A., Pancholi, M. R., Grandbastien, M.-A., and Leitch, A. R. (2013). Diploidization and genome size change in allopolyploids is associated with differential dynamics of low- and high-copy sequences. *The Plant Journal*, 74(5):829–839.
- [15] **Renny-Byfield, S.** and Wendel, J. (2014). Doubling down on genomes: Polyploidy and crop plants. *American Journal of Botany*, 101(10):1–15.

# **TEACHING**

Teaching Assistant Queen Mary University of London

Chromosomal and Population Genomics 2008-2012

Teaching Assistant Queen Mary University of London

Undergraduate Thesis Advisor 2008-2012

Guest Lecturer Queen Mary University of London

MSc Research Seminar 2012

#### AWARDS AND GRANTS

**PhD Fellowship** Natural Environment Research Council via Queen Mary University of London £18,000 per annum stipend and consumables 2008-2012

<sup>†</sup> joint first author

Extra Consumables

£4000

2008-2012

**Bevan Prize** 

Queen Mary University of London

Outstanding Academic achievement in Genetics

Irene Manton Prize

Best Ph.D in Botany

2014

Linnean Society of London

Queen Mary University of London

# CODING AND HIGH PERFORMANCE COMPUTING

Perl Advanced  $\mathbf{R}$ Advanced Proficient Bash **High Performance Computing Proficient** 

# **PEER REVIEW**

Heredity **BMC Genomics** PLOS One Botanical Journal of the Linnean Society BMC Plant Biology

# REFERENCES

New Phytologist

#### Dr. Jeffrey Ross-Ibarra

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#### Prof. Jonathan F. Wendel

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#### Prof. Andrew R. Leitch

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