Simon Renny-Byfield

PERSONAL DETAILS

Address	Department of Plant Sciences Robbins Hall University of California, Davis California, USA, 95616
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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.**[†], 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.

[†] joint first author

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

Extra Consumables Queen Mary University of London
£4000
2008-2012

Bevan Prize Queen Mary University of London
Outstanding Academic achievement in Genetics
2008

Irene Manton Prize Linnean Society of London
Best Ph.D in Botany
2014

CODING AND HIGH PERFORMANCE COMPUTING

Perl	Advanced
R	Advanced
Bash	Proficient
High Performance Computing	Proficient

PEER REVIEW

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

REFERENCES

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