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Total number of publications (WoS - Thomson Routers): 139
Total number of citations and h-index (WoS - Thomson Routers): 43
Five selected publications: Becher H, Ma L, Kelly LJ, Kovarik A, Leitch IJ, Leitch AR. 2014. Endogenous pararetrovirus sequences associated with 24 nt small RNAs at the centromeres of *Fritillaria imperialis* L. (Liliaceae), a species with a giant genome. *Plant Journal* 80: 823-833.; Dodsworth S, Chase MW, Kelly LJ, Leitch IJ, Macas J, Novak P, Piednoel M, Weiss-Schneeweiss H, Leitch AR. 2015. Genomic repeat abundances contain phylogenetic signal. *Systematic Biology* 64(1): 112-126.; Guignard G, Leitch I, Romila C, Nichols R, Knell R, MacDonald A, Trimmer M, Leitch A. 2016. Genome size and ploidy influence angiosperm species biomass under nitrogen and phosphorus limitation. *New Phytologist* 210: 1195–1206.; Leitch AR, Leitch IJ. 2012. Ecological and genetic factors linked to contrasting genome dynamics in seed plants. *New Phytologist* 194(3): 629-646.; Ma L, Hatlen A, Kelly LJ, Becher H, Wang W, Kovarik A, Leitch IJ, Leitch AR. 2015. Angiosperms are unique amongst land plants for the occurrence of key genes in the RNA-Directed DNA methylation (RdDM) pathway. *Genome Biology and Evolution* 7: 2648–2662. **Other papers:** Kelly LJ, Renny-Byfield S, Pellicer J, Macas J, Novák P, Neumann P, Lysák M, Day PD, Berger M, Fay MF, et al. 2015. Lack of DNA removal determines extreme expansions in genome size. *New Phytologist* 208: 596–607.; Leitch AR, Leitch IJ, Trimmer M, Guignard MS, Woodward G. 2014. Impact of genomic diversity in river ecosystems. *Trends in Plant Science* 19(0): 361-366.; McCarthy EW, Arnold SEJ, Chittka L, Le Comber SC, Verity R, Dodsworth S, Knapp S, Kelly LJ, Chase MW, Baldwin IT, et al. 2015. The effect of polyploidy and hybridization on the evolution of floral colour in *Nicotiana* (Solanaceae). *Annals of Botany* 115: 1117-1131.; Renny-Byfield S, Chester M, Kovařík A, Le Comber SC, Grandbastien M-A, Deloger M, Nichols RA, Macas J, Novák P, Chase MW, et al. 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.; Renny-Byfield S, Kovarik A, Kelly LJ, Macas J, Novak P, Chase MW, Nichols RA, Pancholi MR, Grandbastien MA, Leitch AR. 2013. Diploidization and genome size change in allopolyploids is associated with differential dynamics of low- and high-copy sequences. *Plant Journal* 74(5): 829-839. **Work experience:** 2003- Chair of Plant Genetics, School of Biological and Chemical Sciences, Queen Mary University of London, UK.; 2001-03 Reader in Evolutionary Genetics, School of Biological and Chemical Sciences, Queen Mary University of London, UK; 1998-01- Senior Lecturer, School of Biological and Chemical Sciences, Queen Mary University of London, UK; 1992-98 Lecturer, School of Biological and Chemical Sciences, Queen Mary University of London, UK; 1990-92 -Senior Scientific Officer, Department of Cell Biology, John Innes Institute, Norwich, UK; 1986-90 Higher Scientific Officer, Plant Breeding Institute, Cambridge, UK. **Education:** 1983-86 - PhD. Botany Department, University of Bristol, UK, Thesis "Studies on Living and Fossil Charophyte Oosporangia"; 1979-82 Honours degree in Botany. Botany Department, University of Bristol, UK. **Research and other project:** My research has focused for over 20 years on the evolution of plant genomes, particularly in the context of polyploidy, exploiting the power of Next Generation Sequencing (NGS) to study plant genome dynamics. I have pioneered applied NGS to study repeat DNA sequence divergence after polyploidy [4,5], and more recently to develop novel phylogenetic tree building methods [2]. I have applied my expertise to determine if there is selection against genome enlargement imposed by limiting availability of N and P in the environment. I have significant management experience, having coordinated UK and EU funded projects, including international genomics projects (e.g. INTAS project, mobility programme between Russia, Israel and the UK; Alliance project, involving mobility with France). I am project partner on a Marie Curie ITN network called INTERCROSSING and a project partner on NERC macronutrient cycles programme. **Teaching:** 1.I teach on programmes in Aquatic Ecology, Genetics, Biology, Psychology, Zoology, Genetics and Biochemistry; 2.My teaching is across a range of modules and amounts to 20% of my time (e.g. 1st year (level 4) Genetics (600 students annually), 2nd year (level 5) Evolutionary Genetics (100 students), 3rd year (level 6) Population and Chromosome Genetics (70 students); 3.I run residential ecology field trips to UK and overseas (Kruger National Park, South Africa); 4.I set up and organise MSc Plant and Fungal Diversity and Conservation http://www.qmul.ac.uk/postgraduate/taught/coursefinder/courses/138996.html. **Membership in science organizations and bodies:** 2003- Fellow of Linnean Society of London, UK; 2006- Honorary Research Associate at Royal Botanic Gardens, Kew.