

Genome sequence and genetic diversity of European as

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Citation Report

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Emerging Genomics of Angiosperm Trees. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 85-99. | 0.3 | 0 |
| 2 | Silvicultural strategies for <i>Fraxinus excelsior</i> in response to dieback caused by <i>Hymenoscyphus fraxineus</i> . <i>Forestry</i> , 2017, 90, 455-472. | 1.2 | 51 |
| 3 | The evolutionary significance of polyploidy. <i>Nature Reviews Genetics</i> , 2017, 18, 411-424. | 7.7 | 1,288 |
| 4 | Long-read sequencing uncovers the adaptive topography of a carnivorous plant genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4435-E4441. | 3.3 | 95 |
| 5 | Genome of wild olive and the evolution of oil biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9413-E9422. | 3.3 | 233 |
| 6 | Genome skimming and plastid microsatellite profiling of alder trees (<i>Alnus</i> spp., Betulaceae): phylogenetic and phylogeographical prospects. <i>Tree Genetics and Genomes</i> , 2017, 13, 1. | 0.6 | 17 |
| 7 | Extensive gene tree discordance and hemiplasy shaped the genomes of North American columnar cacti. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12003-12008. | 3.3 | 90 |
| 8 | Exploring public perceptions of solutions to tree diseases in the UK: Implications for policy-makers. <i>Environmental Science and Policy</i> , 2017, 76, 70-77. | 2.4 | 14 |
| 9 | Analysis of DNA profiles of ash (<i>Fraxinus excelsior</i> L.) to provide evidence of illegal logging. <i>Wood Science and Technology</i> , 2017, 51, 1377-1387. | 1.4 | 12 |
| 10 | A first assessment of <i>Fraxinus excelsior</i> (common ash) susceptibility to <i>Hymenoscyphus fraxineus</i> (ash) Tj ETQq1 1 0,784314,rgBT /Over | 1.6 | 18 |
| 11 | Ash leaf metabolomes reveal differences between trees tolerant and susceptible to ash dieback disease. <i>Scientific Data</i> , 2017, 4, 170190. | 2.4 | 13 |
| 12 | Genome-wide analysis of SSR and ILP markers in trees: diversity profiling, alternate distribution, and applications in duplication. <i>Scientific Reports</i> , 2017, 7, 17902. | 1.6 | 20 |
| 13 | Ash dieback epidemic in Europe: How can molecular technologies help?. <i>PLoS Pathogens</i> , 2017, 13, e1006381. | 2.1 | 5 |
| 14 | The use of ascospores of the dieback fungus <i>Hymenoscyphus fraxineus</i> for infection assays reveals a significant period of biotrophic interaction in penetrated ash cells. <i>Plant Pathology</i> , 2018, 67, 1354-1361. | 1.2 | 30 |
| 15 | Branching out: a new era of investigating physiological processes in forest trees using genomic tools. <i>Tree Physiology</i> , 2018, 38, 303-310. | 1.4 | 5 |
| 16 | The ash dieback invasion of Europe was founded by two genetically divergent individuals. <i>Nature Ecology and Evolution</i> , 2018, 2, 1000-1008. | 3.4 | 82 |
| 17 | Genomewide identification and development of microsatellite markers for <i>Marssonina brunnea</i> and their applications in two populations. <i>Forest Pathology</i> , 2018, 48, e12433. | 0.5 | 3 |
| 18 | Mitigating pest and pathogen impacts using resistant trees: a framework and overview to inform development and deployment in Europe and North America. <i>Forestry</i> , 2018, 91, 1-16. | 1.2 | 25 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Prospects on the evolutionary mitogenomics of plants: A case study on the olive family (Oleaceae). <i>Molecular Ecology Resources</i> , 2018, 18, 407-423. | 2.2 | 49 |
| 20 | Validation of an updated Associative Transcriptomics platform for the polyploid crop species <i>Brassica napus</i> by dissection of the genetic architecture of erucic acid and tocopherol isoform variation in seeds. <i>Plant Journal</i> , 2018, 93, 181-192. | 2.8 | 75 |
| 21 | Genetic analysis of inherited reduced susceptibility of <i>Fraxinus excelsior</i> L. seedlings in Austria to ash dieback. <i>Forestry</i> , 2018, 91, 514-525. | 1.2 | 8 |
| 22 | Advanced spectroscopy-based phenotyping offers a potential solution to the ash dieback epidemic. <i>Scientific Reports</i> , 2018, 8, 17448. | 1.6 | 20 |
| 23 | Epigenetics in Forest Trees. <i>Advances in Botanical Research</i> , 2018, 88, 387-453. | 0.5 | 37 |
| 24 | Transcriptomic characterization elucidates a signaling network that controls antler growth. <i>Genome</i> , 2018, 61, 829-841. | 0.9 | 5 |
| 25 | The Endophytic Mycobiome of European Ash and Sycamore Maple Leaves – Geographic Patterns, Host Specificity and Influence of Ash Dieback. <i>Frontiers in Microbiology</i> , 2018, 9, 2345. | 1.5 | 48 |
| 26 | Proteome of olive non-glandular trichomes reveals protective protein network against (a)biotic challenge. <i>Journal of Plant Physiology</i> , 2018, 231, 210-218. | 1.6 | 17 |
| 27 | A Metabolomic and HPLC-MS/MS Analysis of the Foliar Phenolics, Flavonoids and Coumarins of the <i>Fraxinus</i> Species Resistant and Susceptible to Emerald Ash Borer. <i>Molecules</i> , 2018, 23, 2734. | 1.7 | 22 |
| 28 | Tripal Developer Toolkit. Database: the Journal of Biological Databases and Curation, 2018, 2018, . | 1.4 | 3 |
| 29 | Survival of European Ash Seedlings Treated with Phosphite after Infection with the <i>Hymenoscyphus fraxineus</i> and <i>Phytophthora</i> Species. <i>Forests</i> , 2018, 9, 442. | 0.9 | 11 |
| 30 | Genetic engineering of trees: progress and new horizons. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2018, 54, 341-376. | 0.9 | 47 |
| 31 | High-quality assembly of the reference genome for scarlet sage, <i>Salvia splendens</i> , an economically important ornamental plant. <i>GigaScience</i> , 2018, 7, . | 3.3 | 49 |
| 32 | Leveraging multiple transcriptome assembly methods for improved gene structure annotation. <i>GigaScience</i> , 2018, 7, . | 3.3 | 122 |
| 33 | Plant phylogenomics based on genome-partitioning strategies: Progress and prospects. <i>Plant Diversity</i> , 2018, 40, 158-164. | 1.8 | 36 |
| 34 | Phylogenomics of the olive tree (<i>Olea europaea</i>) reveals the relative contribution of ancient allo- and autopolyploidization events. <i>BMC Biology</i> , 2018, 16, 15. | 1.7 | 30 |
| 35 | Genome-wide epigenetic variation among ash trees differing in susceptibility to a fungal disease. <i>BMC Genomics</i> , 2018, 19, 502. | 1.2 | 14 |
| 36 | The post-politics of plant biosecurity: The British Government's response to ash dieback in 2012. <i>Transactions of the Institute of British Geographers</i> , 2019, 44, 195-208. | 1.8 | 8 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | Convergent horizontal gene transfer and cross-talk of mobile nucleic acids in parasitic plants. <i>Nature Plants</i> , 2019, 5, 991-1001. | 4.7 | 72 |
| 39 | Antifungal Potency and Modes of Action of a Novel Olive Tree Defensin Against Closely Related Ascomycete Fungal Pathogens. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1649-1664. | 1.4 | 17 |
| 40 | Dealing with dieback: forest manager attitudes towards developing resistant ash trees in the United Kingdom. <i>Forestry</i> , 2019, 92, 554-567. | 1.2 | 12 |
| 41 | Responding to ash dieback (<i>Hymenoscyphus fraxineus</i>) in the UK: woodland composition and replacement tree species. <i>Forestry</i> , 2019, 92, 108-119. | 1.2 | 19 |
| 42 | Dating Whole Genome Duplication in <i>Ceratopteris thalictroides</i> and Potential Adaptive Values of Retained Gene Duplicates. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1926. | 1.8 | 11 |
| 43 | De novo origination of MIRNAs through generation of short inverted repeats in target genes. <i>RNA Biology</i> , 2019, 16, 846-859. | 1.5 | 14 |
| 44 | Phylogenomics using low-depth whole genome sequencing: A case study with the olive tribe. <i>Molecular Ecology Resources</i> , 2019, 19, 877-892. | 2.2 | 48 |
| 45 | Genomic basis of European ash tree resistance to ash dieback fungus. <i>Nature Ecology and Evolution</i> , 2019, 3, 1686-1696. | 3.4 | 50 |
| 46 | Exome resequencing and GWAS for growth, ecophysiology, and chemical and metabolomic composition of wood of <i>Populus trichocarpa</i> . <i>BMC Genomics</i> , 2019, 20, 875. | 1.2 | 19 |
| 47 | The use of tissue culture and in-vitro approaches for the study of tree diseases. <i>Plant Cell, Tissue and Organ Culture</i> , 2019, 136, 415-430. | 1.2 | 12 |
| 48 | The first genetic linkage map for <i>Fraxinus pennsylvanica</i> and syntenic relationships with four related species. <i>Plant Molecular Biology</i> , 2019, 99, 251-264. | 2.0 | 9 |
| 49 | Saving the world's ash forests calls for international cooperation now. <i>Nature Ecology and Evolution</i> , 2019, 3, 141-144. | 3.4 | 13 |
| 50 | Pests and diseases of trees in Africa: A growing continental emergency. <i>Plants People Planet</i> , 2020, 2, 14-28. | 1.6 | 39 |
| 51 | The viability of a breeding programme for ash in the British Isles in the face of ash dieback. <i>Plants People Planet</i> , 2020, 2, 29-40. | 1.6 | 15 |
| 52 | Complex associations between cross-kingdom microbial endophytes and host genotype in ash dieback disease dynamics. <i>Journal of Ecology</i> , 2020, 108, 291-309. | 1.9 | 37 |
| 53 | Transcriptional responses in developing lesions of European common ash (<i>Fraxinus excelsior</i>) reveal genes responding to infection by <i>Hymenoscyphus fraxineus</i> . <i>BMC Plant Biology</i> , 2020, 20, 455. | 1.6 | 1 |
| 54 | Asterid Phylogenomics/Phylotranscriptomics Uncover Morphological Evolutionary Histories and Support Phylogenetic Placement for Numerous Whole-Genome Duplications. <i>Molecular Biology and Evolution</i> , 2020, 37, 3188-3210. | 3.5 | 82 |
| 55 | Pest survey card on <i>Agrilus planipennis</i> . <i>EFSA Supporting Publications</i> , 2020, 17, 1945E. | 0.3 | 4 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 56 | Diversity of secoiridoid glycosides in leaves of UK and Danish ash provide new insight for ash dieback management. <i>Scientific Reports</i> , 2020, 10, 19566. | 1.6 | 4 |
| 57 | Accurate Genomic Predictions for Chronic Wasting Disease in U.S. White-Tailed Deer. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1433-1441. | 0.8 | 17 |
| 58 | Genome sequencing and population genomics modeling provide insights into the local adaptation of weeping forsythia. <i>Horticulture Research</i> , 2020, 7, 130. | 2.9 | 33 |
| 59 | Resolving the Phylogeny of the Olive Family (Oleaceae): Confronting Information from Organellar and Nuclear Genomes. <i>Genes</i> , 2020, 11, 1508. | 1.0 | 25 |
| 60 | Marker-Trait Associations for Tolerance to Ash Dieback in Common Ash (<i>Fraxinus excelsior</i> L.). <i>Forests</i> , 2020, 11, 1083. | 0.9 | 5 |
| 61 | Transposon activation is a major driver in the genome evolution of cultivated olive trees (<i>Olea</i>). <i>Journal of Experimental Botany</i> , 2020, 71, 6074-6083. | 1.6 | 54 |
| 62 | Synteny-Guided Resolution of Gene Trees Clarifies the Functional Impact of Whole-Genome Duplications. <i>Molecular Biology and Evolution</i> , 2020, 37, 3324-3337. | 3.5 | 28 |
| 63 | Candidate metabolites for ash dieback tolerance in <i>Fraxinus excelsior</i> . <i>Journal of Experimental Botany</i> , 2020, 71, 6074-6083. | 2.4 | 13 |
| 64 | Resistance of European ash (<i>Fraxinus excelsior</i>) saplings to larval feeding by the emerald ash borer (<i>Agrilus planipennis</i>). <i>Plants People Planet</i> , 2020, 2, 41-46. | 1.6 | 9 |
| 65 | Identifying <i>Fraxinus excelsior</i> tolerant to ash dieback: Visual field monitoring versus a molecular marker. <i>Forest Pathology</i> , 2020, 50, e12572. | 0.5 | 9 |
| 66 | Draft genome sequence of <i>Kocuria indica</i> DP-K7, a methyl red degrading actinobacterium. <i>3 Biotech</i> , 2020, 10, 175. | 1.1 | 9 |
| 67 | The genome of a cave plant, <i>Primulina huaijiensis</i> , provides insights into adaptation to limestone karst habitats. <i>New Phytologist</i> , 2020, 227, 1249-1263. | 3.5 | 32 |
| 68 | Ash dieback risks an extinction cascade. <i>Biological Conservation</i> , 2020, 244, 108516. | 1.9 | 48 |
| 69 | Mass spectrometry-based forest tree metabolomics. <i>Mass Spectrometry Reviews</i> , 2021, 40, 126-157. | 2.8 | 25 |
| 70 | Olive tree genetics, genomics, and transcriptomics for the olive oil quality improvement. , 2021, , 27-49. | | 2 |
| 71 | The population genomics of adaptive loss of function. <i>Heredity</i> , 2021, 126, 383-395. | 1.2 | 33 |
| 72 | Spread and Severity of Ash Dieback in Switzerland – Tree Characteristics and Landscape Features Explain Varying Mortality Probability. <i>Frontiers in Forests and Global Change</i> , 2021, 4, . | 1.0 | 8 |
| 74 | Research advances in and prospects of ornamental plant genomics. <i>Horticulture Research</i> , 2021, 8, 65. | 2.9 | 38 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 75 | Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537. | 2.0 | 21 |
| 77 | MicroRNAs in Woody Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 686831. | 1.7 | 11 |
| 78 | Chromosome-scale assembly and evolution of the tetraploid <i>Salvia splendens</i> (Lamiaceae) genome. <i>Horticulture Research</i> , 2021, 8, 177. | 2.9 | 27 |
| 79 | A high-quality genome assembly of <i>Jasminum sambac</i> provides insight into floral trait formation and Oleaceae genome evolution. <i>Molecular Ecology Resources</i> , 2022, 22, 724-739. | 2.2 | 18 |
| 80 | Uses and benefits of digital sequence information from plant genetic resources: Lessons learnt from botanical collections. <i>Plants People Planet</i> , 2022, 4, 33-43. | 1.6 | 10 |
| 81 | Olive-Tree Genome Sequencing: Towards a Better Understanding of Oil Biosynthesis. , 2021, , 75-87. | | 1 |
| 82 | Convergent molecular evolution among ash species resistant to the emerald ash borer. <i>Nature Ecology and Evolution</i> , 2020, 4, 1116-1128. | 3.4 | 26 |
| 83 | Building an octaploid genome and transcriptome of the medicinal plant <i>Pogostemon cablin</i> from Lamiales. <i>Scientific Data</i> , 2018, 5, 180274. | 2.4 | 17 |
| 87 | Demographically idiosyncratic responses to climate change and rapid Pleistocene diversification of the walnut genus <i>Juglans</i> (Juglandaceae) revealed by whole-genome sequences. <i>New Phytologist</i> , 2018, 217, 1726-1736. | 3.5 | 98 |
| 88 | Many, but not all, lineage-specific genes can be explained by homology detection failure. <i>PLoS Biology</i> , 2020, 18, e3000862. | 2.6 | 113 |
| 95 | Identification and Characterization of LEA Genes in Ash Tree (<i>Fraxinus excelsior</i>) Genome. <i>Journal of Forestry Faculty of Kastamonu University</i> , 0, , 299-309. | 0.1 | 0 |
| 99 | Transformation of European Ash (<i>Fraxinus excelsior</i> L.) Callus as a Starting Point for Understanding the Molecular Basis of Ash Dieback. <i>Plants</i> , 2021, 10, 2524. | 1.6 | 2 |
| 100 | A high-quality reference genome for <i>Fraxinus pennsylvanica</i> for ash species restoration and research. <i>Molecular Ecology Resources</i> , 2022, 22, 1284-1302. | 2.2 | 12 |
| 101 | Extraction and isolation of lignin from ash tree (<i>Fraxinus excelsior</i>) with protic ionic liquids (PILs). <i>Chemosphere</i> , 2022, 290, 133297. | 4.2 | 18 |
| 102 | In vitro and in silico analysis of Brilliant Black degradation by <i>Actinobacteria</i> and a <i>Paraburkholderia</i> sp.. <i>Genomics</i> , 2022, 114, 110266. | 1.3 | 4 |
| 103 | Host-Pathogen Interactions in Leaf Petioles of Common Ash and Manchurian Ash Infected with <i>Hymenoscyphus fraxineus</i> . <i>Microorganisms</i> , 2022, 10, 375. | 1.6 | 2 |
| 104 | European-wide forest monitoring substantiate the necessity for a joint conservation strategy to rescue European ash species (<i>Fraxinus</i> spp.). <i>Scientific Reports</i> , 2022, 12, 4764. | 1.6 | 10 |
| 105 | Molecular sexual determinants in <i>Pistacia</i> genus by KASP assay. <i>Molecular Biology Reports</i> , 2022, 49, 5473-5482. | 1.0 | 7 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 106 | Can Forest Trees Cope with Climate Change?â€”Effects of DNA Methylation on Gene Expression and Adaptation to Environmental Change. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13524. | 1.8 | 7 |
| 116 | Phylogenomic approaches untangle early divergences and complex diversifications of the olive plant family. <i>BMC Biology</i> , 2022, 20, 92. | 1.7 | 30 |
| 117 | Evolution of coastal forests based on a full set of mangrove genomes. <i>Nature Ecology and Evolution</i> , 2022, 6, 738-749. | 3.4 | 41 |
| 119 | Genomic Survey and Microsatellite Marker Investigation of Patagonian Moray Cod (<i>Muraenolepis</i>) Tj ETQq1 1 0.784314 rgBT ₁ /Overlode | 1.0 | 1 |
| 120 | The rooting ability of in vitro shoot cultures established from a UK collection of the common ash (<i>Fraxinus excelsior</i> L.) and their ex vitro survival. <i>Annals of Forest Science</i> , 2022, 79, . | 0.8 | 1 |
| 121 | Lilac (<i>Syringa oblata</i>) genome provides insights into its evolution and molecular mechanism of petal color change. <i>Communications Biology</i> , 2022, 5, . | 2.0 | 13 |
| 122 | Introductory Chapter: Factors That Affect Biodiversity and Species Richness of Ecosystems - A Review. , 0, , . | | 0 |
| 124 | The sage genome provides insight into the evolutionary dynamics of diterpene biosynthesis gene cluster in plants. <i>Cell Reports</i> , 2022, 40, 111236. | 2.9 | 26 |
| 125 | Novel RNA viruses from the native range of <i>Hymenoscyphus fraxineus</i> , the causal fungal agent of ash dieback. <i>Virus Research</i> , 2022, 320, 198901. | 1.1 | 8 |
| 126 | Characterisation of nuclear microsatellite markers for <i>Fraxinus excelsior</i> L. and their transferability to six related species. <i>Silvae Genetica</i> , 2022, 71, 65-71. | 0.4 | 0 |
| 127 | Current status and trends in forest genomics. <i>Forestry Research</i> , 2022, 2, 0-0. | 0.5 | 12 |
| 128 | Characterising the molecular diversity of ash (<i>Fraxinus excelsior</i> L.) at its western marginal range in Europe â€” phylogeographic insights and implications for conservation in Ireland. <i>Tree Genetics and Genomes</i> , 2022, 18, . | 0.6 | 1 |
| 129 | The updated weeping forsythia genome reveals the genomic basis for the evolution and the forsythidin and forsythoside A biosynthesis. <i>Horticultural Plant Journal</i> , 2023, 9, 1149-1161. | 2.3 | 3 |
| 130 | Whole-Genome Survey and Microsatellite Marker Detection of Antarctic Crocodile Icefish, <i>Chionobathyscus dewitti</i> . <i>Animals</i> , 2022, 12, 2598. | 1.0 | 0 |
| 131 | The genome of single-petal jasmine (<i>Jasminum sambac</i>) provides insights into heat stress tolerance and aroma compound biosynthesis. <i>Frontiers in Plant Science</i> , 0, 13, . | 1.7 | 2 |
| 132 | Genome-Wide SNP Markers Accelerate Perennial Forest Tree Breeding Rate for Disease Resistance through Marker-Assisted and Genome-Wide Selection. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12315. | 1.8 | 5 |
| 133 | A novel genome sequence of <i>Jasminum sambac</i> helps uncover the molecular mechanism underlying the accumulation of jasmonates. <i>Journal of Experimental Botany</i> , 2023, 74, 1275-1290. | 2.4 | 4 |
| 134 | <i>Syringa oblata</i> genome provides new insights into molecular mechanism of flower color differences among individuals and biosynthesis of its flower volatiles. <i>Frontiers in Plant Science</i> , 0, 13, . | 1.7 | 0 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 136 | The Jasmine (<i>Jasminum sambac</i>) Genome Provides Insight into the Biosynthesis of Flower Fragrances and Jasmonates. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 127-149. | 3.0 | 5 |
| 137 | Complex scaffold remodeling in plant triterpene biosynthesis. <i>Science</i> , 2023, 379, 361-368. | 6.0 | 31 |
| 138 | The chromosome-level genome of double-petal phenotype jasmine provides insights into the biosynthesis of floral scent. <i>Horticultural Plant Journal</i> , 2024, 10, 259-272. | 2.3 | 1 |
| 139 | Taxonomically Restricted Genes in <i>Bacillus</i> may Form Clusters of Homologs and Can be Traced to a Large Reservoir of Noncoding Sequences. <i>Genome Biology and Evolution</i> , 2023, 15, . | 1.1 | 4 |
| 140 | How genomics can help biodiversity conservation. <i>Trends in Genetics</i> , 2023, 39, 545-559. | 2.9 | 55 |
| 141 | Computational identification and systematic classification of cytochrome P450 genes in <i>Pogostemon cablin</i> provide insights into flavonoids biosynthesis. <i>Acta Physiologiae Plantarum</i> , 2023, 45, . | 1.0 | 1 |
| 144 | Integrative analysis of green ash phloem transcripts and proteins during an emerald ash borer infestation. <i>BMC Plant Biology</i> , 2023, 23, . | 1.6 | 1 |
| 161 | Olive Genome Structure, Evolution and Domestication. , 2023, , 121-130. | | 0 |