

# Cathrine L McIntyre

## List of Publications by Year in descending order

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Version: 2024-02-01

105  
papers

7,618  
citations

36203

51  
h-index

54797

84  
g-index

108  
all docs

108  
docs citations

108  
times ranked

6142  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | Articulating the effect of food systems innovation on the Sustainable Development Goals. <i>Lancet Planetary Health</i> , The, 2021, 5, e50-e62.  | 5.1 | 135       |
| 2  | Genotypic variation for lodging tolerance in spring wheat: wider and deeper root plates, a feature of low lodging, high yielding germplasm. <i>Field Crops Research</i> , 2020, 258, 107942.  | 2.3 | 18        |
| 3  | Innovation can accelerate the transition towards a sustainable food system. <i>Nature Food</i> , 2020, 1, 266-272.  | 6.2 | 285       |
| 4  | Overexpression of <i>TaCML20</i> , a calmodulin-like gene, enhances water soluble carbohydrate accumulation and yield in wheat. <i>Physiologia Plantarum</i> , 2019, 165, 790-799.  | 2.6 | 17        |
| 5  | Heat shock factor C2a serves as a proactive mechanism for heat protection in developing grains in wheat via an ABA-mediated regulatory pathway. <i>Plant, Cell and Environment</i> , 2018, 41, 79-98.   | 2.8 | 102       |
| 6  | Overexpression of a predominantly root-expressed NAC transcription factor in wheat roots enhances root length, biomass and drought tolerance. <i>Plant Cell Reports</i> , 2018, 37, 225-237.  | 2.8 | 77        |
| 7  | Mapping QTLs associated with agronomic and physiological traits under terminal drought and heat stress conditions in wheat ( <i>Triticum aestivum</i> L.). <i>Genome</i> , 2017, 60, 26-45.   | 0.9 | 106       |
| 8  | A strong root-specific expression system for stable transgene expression in bread wheat. <i>Plant Cell Reports</i> , 2016, 35, 469-481.   | 2.8 | 14        |
| 9  | Drought-Up-Regulated TaNAC69-1 is a Transcriptional Repressor of <i>TaSHY2</i> and <i>TaAA7</i> , and Enhances Root Length and Biomass in Wheat. <i>Plant and Cell Physiology</i> , 2016, 57, 2076-2090.                                      | 1.5 | 44        |
| 10 | Abiotic stress upregulated TaZFP34 represses the expression of type-B response regulator and SHY2 genes and enhances root to shoot ratio in wheat. <i>Plant Science</i> , 2016, 252, 88-102.  | 1.7 | 41        |
| 11 | An Assessment of Heavy Ion Irradiation Mutagenesis for Reverse Genetics in Wheat ( <i>Triticum aestivum</i> ) Tj ETQq1 1,0784314,rgBT/Ove   | 1.1 | 23        |
| 12 | Characterisation of alleles of the sucrose phosphate synthase gene family in sugarcane and their association with sugar-related traits. <i>Molecular Breeding</i> , 2015, 35, 1.  | 1.0 | 12        |
| 13 | Brachypodium as an emerging model for cereal-pathogen interactions. <i>Annals of Botany</i> , 2015, 115, 717-731.   | 1.4 | 60        |
| 14 | TaHsfA6f is a transcriptional activator that regulates a suite of heat stress protection genes in wheat ( <i>Triticum aestivum</i> L.) including previously unknown Hsf targets. <i>Journal of Experimental Botany</i> , 2015, 66, 1025-1039. | 2.4 | 153       |
| 15 | More fertile florets and grains per spike can be achieved at higher temperature in wheat lines with high spike biomass and sugar content at booting. <i>Functional Plant Biology</i> , 2014, 41, 482.   | 1.1 | 64        |
| 16 | The heat shock factor family from <i>Triticum aestivum</i> in response to heat and other major abiotic stresses and their role in regulation of heat shock protein genes. <i>Journal of Experimental Botany</i> , 2014, 65, 539-557.          | 2.4 | 208       |
| 17 | Preferential retention of chromosome regions in derived synthetic wheat lines: a source of novel alleles for wheat improvement. <i>Crop and Pasture Science</i> , 2014, 65, 125.  | 0.7 | 8         |
| 18 | Major QTL for Fusarium crown rot resistance in a barley landrace. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2511-2520.   | 1.8 | 31        |

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|----|---|-----|-----------|
| 19 | QTL for yield and associated traits in the Seri/Babax population grown across several environments in Mexico, in the West Asia, North Africa, and South Asia regions. <i>Theoretical and Applied Genetics</i> , 2013, 126, 971-984.                     | 1.8 | 119       |
| 20 | Dissecting the molecular basis of the contribution of source strength to high fructan accumulation in wheat. <i>Plant Molecular Biology</i> , 2013, 81, 71-92.  | 2.0 | 26        |
| 21 | TaMYB13-1, a R2R3 MYB transcription factor, regulates the fructan synthetic pathway and contributes to enhanced fructan accumulation in bread wheat. <i>Journal of Experimental Botany</i> , 2013, 64, 3681-3696.                                       | 2.4 | 47        |
| 22 | A Novel and Major Quantitative Trait Locus for Fusarium Crown Rot Resistance in a Genotype of Wild Barley ( <i>Hordeum spontaneum</i> L.). <i>PLoS ONE</i> , 2013, 8, e58040.   | 1.1 | 42        |
| 23 | Characterization of a QTL affecting spike morphology on the long arm of chromosome 3H in barley ( <i>Hordeum vulgare</i> L.) based on near isogenic lines and a NIL-derived population. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1385-1392. | 1.8 | 38        |
| 24 | Assessment of the genetic diversity in a collection of <i>Erianthus arundinaceus</i> . <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 1483-1491.   | 0.8 | 16        |
| 25 | Genotypic variation in the accumulation of water soluble carbohydrates in wheat. <i>Functional Plant Biology</i> , 2012, 39, 560.   | 1.1 | 29        |
| 26 | Overexpression of TaNAC69 Leads to Enhanced Transcript Levels of Stress Up-Regulated Genes and Dehydration Tolerance in Bread Wheat. <i>Molecular Plant</i> , 2011, 4, 697-712.   | 3.9 | 233       |
| 27 | TaMYB13 is a transcriptional activator of fructosyltransferase genes involved in linked fructan synthesis in wheat. <i>Plant Journal</i> , 2011, 68, 857-870.   | 2.8 | 70        |
| 28 | TaNf-YB3 is involved in the regulation of photosynthesis genes in <i>Triticum aestivum</i> . <i>Functional and Integrative Genomics</i> , 2011, 11, 327-340.  | 1.4 | 74        |
| 29 | Linked gene networks involved in nitrogen and carbon metabolism and levels of water-soluble carbohydrate accumulation in wheat stems. <i>Functional and Integrative Genomics</i> , 2011, 11, 585-597.   | 1.4 | 20        |
| 30 | Molecular detection of genomic regions associated with grain yield and yield-related components in an elite bread wheat cross evaluated under irrigated and rainfed conditions. <i>Theoretical and Applied Genetics</i> , 2010, 120, 527-541.           | 1.8 | 151       |
| 31 | Heat and drought adaptive QTL in a wheat population designed to minimize confounding agronomic effects. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1001-1021.   | 1.8 | 484       |
| 32 | Construction of a high-density composite map and comparative mapping of segregation distortion regions in barley. <i>Molecular Genetics and Genomics</i> , 2010, 284, 319-331.  | 1.0 | 55        |
| 33 | TaNf-YC11, one of the light-upregulated NF-YC members in <i>Triticum aestivum</i> , is co-regulated with photosynthesis-related genes. <i>Functional and Integrative Genomics</i> , 2010, 10, 265-276.  | 1.4 | 38        |
| 34 | Molecular mapping of adult plant stripe rust resistance in wheat and identification of pyramided QTL genotypes. <i>Euphytica</i> , 2010, 176, 251-260.  | 0.6 | 112       |
| 35 | Members of the Dof transcription factor family in <i>Triticum aestivum</i> are associated with light-mediated gene regulation. <i>Functional and Integrative Genomics</i> , 2009, 9, 485-498.   | 1.4 | 99        |
| 36 | The Complex Genetic Structure of Sugarcane Limits Identification of Additional SNP-Defined Simplex Alleles in Microsatellite Loci. <i>Tropical Plant Biology</i> , 2009, 2, 133-142.  | 1.0 | 1         |

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|----|---|-----|-----------|
| 37 | Genetic control of wheat quality: interactions between chromosomal regions determining protein content and composition, dough rheology, and sponge and dough baking properties. <i>Theoretical and Applied Genetics</i> , 2009, 118, 1519-1537.     | 1.8 | 85        |
| 38 | Use of dry matter content as a rapid and low-cost estimate for ranking genotypic differences in water-soluble carbohydrate concentrations in the stem and leaf sheath of <i>Triticum aestivum</i> . <i>Crop and Pasture Science</i> , 2009, 60, 51. | 0.7 | 31        |
| 39 | Use of expression analysis to dissect alterations in carbohydrate metabolism in wheat leaves during drought stress. <i>Plant Molecular Biology</i> , 2008, 67, 197-214.   | 2.0 | 131       |
| 40 | Comparative genetics in sugarcane enables structured map enhancement and validation of marker-trait associations. <i>Molecular Breeding</i> , 2008, 21, 233-247.  | 1.0 | 32        |
| 41 | Identification of QTL for sugar-related traits in a sweet grain sorghum ( <i>Sorghum bicolor</i> L. Moench) recombinant inbred population. <i>Molecular Breeding</i> , 2008, 22, 367-384.   | 1.0 | 138       |
| 42 | QTL analysis of ergot resistance in sorghum. <i>Theoretical and Applied Genetics</i> , 2008, 117, 369-382.  | 1.8 | 46        |
| 43 | Multi-environment QTL mixed models for drought stress adaptation in wheat. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1077-1091.  | 1.8 | 160       |
| 44 | Genetic control of yield related stalk traits in sugarcane. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1191-1203.   | 1.8 | 82        |
| 45 | Molecular characterization of the waxy locus in sorghum. <i>Genome</i> , 2008, 51, 524-533.   | 0.9 | 46        |
| 46 | Molecular Dissection of Variation in Carbohydrate Metabolism Related to Water-Soluble Carbohydrate Accumulation in Stems of Wheat. <i>Plant Physiology</i> , 2008, 146, 323-324.  | 2.3 | 157       |
| 47 | Construction of a genetic linkage map for <i>Saccharum officinarum</i> incorporating both simplex and duplex markers to increase genome coverage. <i>Genome</i> , 2007, 50, 742-756.  | 0.9 | 52        |
| 48 | Genome-wide identification and expression analysis of the NF-Y family of transcription factors in <i>Triticum aestivum</i> . <i>Plant Molecular Biology</i> , 2007, 65, 77-92.  | 2.0 | 176       |
| 49 | An assessment of the genetic relationship between sweet and grain sorghums, within <i>Sorghum bicolor</i> ssp. <i>bicolor</i> (L.) Moench, using AFLP markers. <i>Euphytica</i> , 2007, 157, 161-176.   | 0.6 | 83        |
| 50 | Identification of common root-lesion nematode ( <i>Pratylenchus thornei</i> Sher et Allen) loci in bread wheat. <i>Genome</i> , 2006, 49, 1319-1323.  | 0.9 | 28        |
| 51 | Genetic Components of Variance and the Role of Pollen Traits in Sorghum Ergot Resistance. <i>Crop Science</i> , 2006, 46, 2387-2395.  | 0.8 | 15        |
| 52 | AFLP analysis of genetic diversity within <i>Saccharum officinarum</i> and comparison with sugarcane cultivars. <i>Australian Journal of Agricultural Research</i> , 2006, 57, 1167.  | 1.5 | 45        |
| 53 | TaNAC69 from the NAC superfamily of transcription factors is up-regulated by abiotic stresses in wheat and recognises two consensus DNA-binding sequences. <i>Functional Plant Biology</i> , 2006, 33, 43.  | 1.1 | 81        |
| 54 | Differential gene expression of wheat progeny with contrasting levels of transpiration efficiency. <i>Plant Molecular Biology</i> , 2006, 61, 863-881.  | 2.0 | 44        |

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|----|---|-----|-----------|
| 55 | The identification and characterisation of alleles of sucrose phosphate synthase gene family III in sugarcane. <i>Molecular Breeding</i> , 2006, 18, 39-50.   | 1.0 | 39        |
| 56 | Quantitative trait loci identified for sugar related traits in a sugarcane ( <i>Saccharum</i> spp.) cultivar— <i>Saccharum officinarum</i> population. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1306-1317.  | 1.8 | 85        |
| 57 | Characterisation of single nucleotide polymorphisms in sugarcane ESTs. <i>Theoretical and Applied Genetics</i> , 2006, 113, 331-343.  | 1.8 | 58        |
| 58 | Associations between DNA markers and resistance to diseases in sugarcane and effects of population substructure. <i>Theoretical and Applied Genetics</i> , 2006, 114, 155-164.  | 1.8 | 97        |
| 59 | Analysing diversity in sugarcane resistance gene analogues. <i>Australasian Plant Pathology</i> , 2006, 35, 631.  | 0.5 | 4         |
| 60 | Quantitative trait loci for root lesion nematode ( <i>Pratylenchus thornei</i> ) resistance in Middle-Eastern landraces and their potential for introgression into Australian bread wheat. <i>Australian Journal of Agricultural Research</i> , 2005, 56, 1059. | 1.5 | 34        |
| 61 | Relationships between hard-seededness and seed weight in mungbean ( <i>Vigna radiata</i> ) assessed by QTL analysis. <i>Plant Breeding</i> , 2005, 124, 292-298.  | 1.0 | 57        |
| 62 | Verification of the introgression of <i>Erianthus arundinaceus</i> germplasm into sugarcane using molecular markers. <i>Plant Breeding</i> , 2005, 124, 322-328.  | 1.0 | 66        |
| 63 | A combination of AFLP and SSR markers provides extensive map coverage and identification of homo(eo)logous linkage groups in a sugarcane cultivar. <i>Theoretical and Applied Genetics</i> , 2005, 110, 789-801.  | 1.8 | 174       |
| 64 | A "Chinese Spring" wheat ( <i>Triticum aestivum</i> L.) bacterial artificial chromosome library and its use in the isolation of SSR markers for targeted genome regions. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1489-1494.                        | 1.8 | 17        |
| 65 | Characterisation of genome regions incorporated from an important wild relative into Australian sugarcane. <i>Molecular Breeding</i> , 2005, 15, 367-381.   | 1.0 | 47        |
| 66 | Identification and Validation of Molecular Markers Associated with Pachymetra Root Rot and Brown Rust Resistance in Sugarcane Using Map- and Association-based Approaches. <i>Molecular Breeding</i> , 2005, 16, 151-161.                                       | 1.0 | 29        |
| 67 | Resistance gene analogues in sugarcane and sorghum and their association with quantitative trait loci for rust resistance. <i>Genome</i> , 2005, 48, 391-400.   | 0.9 | 66        |
| 68 | Genomics approaches for the identification of genes determining important traits in sugarcane. <i>Field Crops Research</i> , 2005, 92, 137-147.   | 2.3 | 70        |
| 69 | Identification of differentially expressed genes in wheat undergoing gradual water deficit stress using a subtractive hybridisation approach. <i>Plant Science</i> , 2005, 168, 661-670.  | 1.7 | 23        |
| 70 | A preliminary assessment of the genetic relationship between <i>Erianthus rockii</i> and the "Saccharum complex" using microsatellite (SSR) and AFLP markers. <i>Plant Science</i> , 2005, 169, 976-984.  | 1.7 | 54        |
| 71 | Identification of Differentially Expressed Transcripts from Maturing Stem of Sugarcane by in silico Analysis of Stem Expressed Sequence Tags and Gene Expression Profiling. <i>Plant Molecular Biology</i> , 2004, 54, 503-517.                                 | 2.0 | 110       |
| 72 | Homologues of the maize rust resistance gene Rp1-D are genetically associated with a major rust resistance QTL in sorghum. <i>Theoretical and Applied Genetics</i> , 2004, 109, 875-883.  | 1.8 | 29        |

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|----|--|-----|-----------|
| 73 | Markers associated with stalk number and suckering in sugarcane colocate with tillering and rhizomatousness QTLs in sorghum. <i>Genome</i> , 2004, 47, 988-993.  | 0.9 | 37        |
| 74 | Identification of a novel sugar transporter homologue strongly expressed in maturing stem vascular tissues of sugarcane by expressed sequence tag and microarray analysis. <i>Plant Molecular Biology</i> , 2003, 52, 371-386. | 2.0 | 126       |
| 75 | Prediction of hybrid performance in grain sorghum using RFLP markers. <i>Theoretical and Applied Genetics</i> , 2003, 106, 559-567.  | 1.8 | 109       |
| 76 | Identifications of two different mechanisms for sorghum midge resistance through QTL mapping. <i>Theoretical and Applied Genetics</i> , 2003, 107, 116-122.  | 1.8 | 67        |
| 77 | Identification of a major locus conferring resistance to powdery mildew ( <i>Erysiphe polygoni</i> DC) in mungbean ( <i>Vigna radiata</i> L. Wilczek) by QTL analysis. <i>Genome</i> , 2003, 46, 738-744.                      | 0.9 | 63        |
| 78 | Development of a mungbean ( <i>Vigna radiata</i> ) RFLP linkage map and its comparison with lablab ( <i>Lablab</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T Genetics, 2002, 105, 160-166.  | 1.8 | 97        |
| 79 | Microsatellite markers from sugarcane ( <i>Saccharum</i> spp.) ESTs cross transferable to erianthus and sorghum. <i>Plant Science</i> , 2001, 160, 1115-1123.  | 1.7 | 384       |
| 80 | Low level of selfing found in a sample of crosses in Australian sugarcane breeding programs. <i>Euphytica</i> , 2001, 117, 245-249.  | 0.6 | 28        |
| 81 | Molecular analyses suggest a need for a significant rearrangement of Rutaceae subfamilies and a minor reassessment of species relationships within Flindersia. <i>Plant Systematics and Evolution</i> , 2000, 223, 15-27.      | 0.3 | 57        |
| 82 | Identification of genomic regions associated with stay green in sorghum by testing RILs in multiple environments. <i>Theoretical and Applied Genetics</i> , 2000, 100, 1225-1232.  | 1.8 | 166       |
| 83 | Title is missing!. <i>Euphytica</i> , 1998, 102, 1-7.  | 0.6 | 43        |
| 84 | Identification of genomic regions for rust resistance in sorghum. <i>Euphytica</i> , 1998, 103, 287-292.   | 0.6 | 39        |
| 85 | Assessing genetic diversity in a sugarcane germplasm collection using an automated AFLP analysis. <i>Genetica</i> , 1998, 104, 143-153.  | 0.5 | 62        |
| 86 | Construction of a genetic map in a sorghum recombinant inbred line using probes from different sources and its comparison with other sorghum maps. <i>Australian Journal of Agricultural Research</i> , 1998, 49, 729.         | 1.5 | 43        |
| 87 | Isolation and characterisation of repeated DNA sequences from <i>Erianthus</i> spp. (Saccharinae:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T   | 0.9 | 1         |
| 88 | Using genomic slot blot hybridization to assess intergeneric <i>Saccharum</i> x <i>Erianthus</i> hybrids (Andropogoneae æ“ Saccharinae). <i>Genome</i> , 1997, 40, 428-432.  | 0.9 | 22        |
| 89 | Title is missing!. <i>Euphytica</i> , 1997, 93, 283-292.   | 0.6 | 52        |
| 90 | Strategies for the suppression of peroxidase gene expression in tobacco. I. Designing efficient ribozymes. <i>Transgenic Research</i> , 1996, 5, 257-262.  | 1.3 | 3         |

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|-----|--|-----|-----------|
| 91  | Strategies for the suppression of peroxidase gene expression in tobacco. II. In vivo suppression of peroxidase activity in transgenic tobacco using ribozyme and antisense constructs. <i>Transgenic Research</i> , 1996, 5, 263-270.                | 1.3 | 29        |
| 92  | Ribosomal DNA variations in <i>Erianthus</i> , a wild sugarcane relative (Andropogoneae-Saccharinae). <i>Theoretical and Applied Genetics</i> , 1996, 92, 733-743.   | 1.8 | 37        |
| 93  | Cloning and Sequence of a cDNA Encoding Phenylalanine Ammonia-Lyase from the Tropical Forage Legume <i>Stylosanthes humilis</i> . <i>Plant Physiology</i> , 1995, 108, 1301-1302.  | 2.3 | 12        |
| 94  | Differential Expression of Peroxidase Isogenes During the Early Stages of Infection of the Tropical Forage Legume <i>Stylosanthes humilis</i> by <i>Colletotrichum gloeosporioides</i> . <i>Molecular Plant-Microbe Interactions</i> , 1995, 8, 398. | 1.4 | 50        |
| 95  | Analysis of phylogenetic relationships in the Triticeae tribe using RFLPs. <i>Theoretical and Applied Genetics</i> , 1993, 86, 649-655.  | 1.8 | 58        |
| 96  | A strain-specific cyclin homolog in the fungal phytopathogen <i>Colletotrichum gloeosporioides</i> . <i>Gene</i> , 1993, 133, 141-145.   | 1.0 | 12        |
| 97  | An RFLP species-specific DNA sequence for the A genome of rice. <i>Genome</i> , 1993, 36, 445-448.   | 0.9 | 4         |
| 98  | Characterization of minisatellite sequences from <i>Oryza sativa</i> . <i>Genome</i> , 1993, 36, 978-983.  | 0.9 | 42        |
| 99  | Relationships between <i>Oryza</i> species (Poaceae) based on 5S DNA sequences. <i>Plant Systematics and Evolution</i> , 1992, 183, 249-264.   | 0.3 | 18        |
| 100 | Physical mapping of a low-copy DNA sequence in rye ( <i>Secale cereale</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 1899-1902.  | 3.3 | 87        |
| 101 | Evolution and systematic relationships in the Triticeae (Poaceae). <i>Plant Systematics and Evolution</i> , 1988, 160, 1-28.   | 0.3 | 27        |
| 102 | Amplification and dispersion of repeated DNA sequences in the Triticeae. <i>Plant Systematics and Evolution</i> , 1988, 160, 39-59.  | 0.3 | 86        |
| 103 | DNA sequence analyses of the ribosomal spacer regions in the Triticeae. <i>Plant Systematics and Evolution</i> , 1988, 160, 91-104.  | 0.3 | 23        |
| 104 | Frequent duplication and deletion events in the 5S RNA genes and the associated spacer regions of the Triticeae. <i>Plant Systematics and Evolution</i> , 1988, 160, 105-122.  | 0.3 | 133       |
| 105 | Variation at isozyme loci in Triticeae. <i>Plant Systematics and Evolution</i> , 1988, 160, 123-142.   | 0.3 | 58        |