WON CHEOL **YIM** Ph. D.

Plant Genomics Lab
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CURRENT POSITION

07/2018 – present **Assistant Professor,** Department of Biochemistry & Molecular Biology, University of Nevada, Reno

PROFESSIONAL PREPARATION

02/2018 – 06/2018 **Research scientist**, Department of Biochemistry & Molecular Biology, University of Nevada, Reno, Supervisor: John C. Cushman

01/2013 – 01/2018 **Postdoctoral research associate**, Department of Biochemistry & Molecular Biology, University of Nevada, Reno, Supervisor: John C. Cushman

09/2012 – 01/2013 **Postdoctoral research associate**, Plant Biotechnology, Dongguk University, Seoul, Korea Rep., Supervisor: Byung-moo Lee

03/2008 – 08/2012 **Doctor of Philosophy**, Plant Biotechnology, Dongguk University, Seoul, Korea Rep., Advisor: Byung-moo Lee

03/2006 – 02/2008 **Master of Science**, Plant Biotechnology, Dongguk University, Seoul, Korea Rep., Advisor: Byung-moo Lee

03/1999 – 02/2006 **Bachelor of Science**, Plant Biotechnology, Dongguk University, Seoul, Korea Rep., Advisor: Byung-moo Lee

AWARDED PROPOSAL

2019 *Kalanchoe* and *Brassica* genome assembly (**PI**: Won C. Yim, Funding agency: Google), Location of Project: University of Nevada, Reno, **Total Award Amount: $10,000**

2019 Development of waxy sorghum breeding lines for diverse food, feed, and fermentation applications (PI: Melinda K. Yerka, Funding agency: United States Department of Agriculture, **Co-PI**), Location of Project: University of Nevada, Reno, **Total Award Amount: $1,012,408**

2018 Dissecting the Transcriptional Networks Underlying Plant Wound Suberin Biosynthesis Lands (PI: Dylan K Kosma, Funding agency: United States National Science Foundation, **Co-PI**), Location of Project: University of Nevada, Reno, **Total Award Amount: $1,371,210**

2018 *Opuntia Ficus-Indica*: A Highly Water-Use Efficient And Productive Biomass Feedstock For Semi-Arid Lands, **Co-PI** (PI: John C. Cushman, Funding agency: United States Department of Agriculture, **Co-PI**), Location of Project: University of Nevada, Reno, **Total Award Amount: $1,012,408**

2018 *Opuntia Ficus-Indica* and *Brassica carinata* genome assembly (**PI**: Won C. Yim, Funding agency: Google), Location of Project: University of Nevada, Reno, **Total Award Amount: $10,000**

2018 Construct Chromosome-level assembly in Kalanchoe tetraploid genome (**PI**: Won C. Yim, Funding agency: UNR Genomics Center), Location of Project: University of Nevada, Reno, **Total Award Amount: $2,000**

2016 Ice plant gene atlas resource development: *Mesembryanthemum crystallinum* L., a facultative crassulacean acid metabolism (CAM) model for improved water-use efficiency of bioenergy feedstocks using CAM bioengineering. **Proposal (WIP) ID**: 502939, **Co-PI** (PI: John C. Cushman, Funding agency: Joint Genome Institute) ***405 RNA-Seq samples valued at $68,529***

2015 The Extreme Science and Engineering Discovery Environment (XSEDE) Computational Resources: Characterization of Genomes from Crassulacean acid metabolism (CAM) Plants, **Collaborator** (PI: John C. Cushman, Funding agency: XSEDE) ***519,508 SUs valued at $25,975***

2014 The Extreme Science and Engineering Discovery Environment (XSEDE) Computational Reso urces*:* Characterization of Genomes from Crassulacean acid metabolism (CAM) Plants, **Collaborator** (PI: John C. Cushman, Funding agency: XSEDE) ***50,974 SUs valued at $2,548***

CURRENT RESEARCH PROJECT

01/2019 – 01/2023 **Development of waxy sorghum breeding lines for diverse food, feed, and fermentation applications** (PI: Melinda K. Yerka, Funding agency: United States Department of Agriculture, **Co-PI**)

01/2018 – 01/2023 ***Opuntia Ficus-Indica*: A Highly Water-Use Efficient And Productive Biomass Feedstock For Semi-Arid Lands** (PI: John C. Cushman, Funding agency: United States Department of Agriculture, **Co-PI**)

01/2018 – 01/2021 **Dissecting the Transcriptional Networks Underlying Plant Wound Suberin Biosynthesis Lands** (PI: Dylan K Kosma, Funding agency: United States National Science Foundation, **Co-PI**)

PENDING RESEARCH PROJECT

07/2019 – 01/2024 **Assessing evolution in the Brassicaceae: Relationships between the four-dimensional genome, regulatory landscape, and phenotypic diversity** (PI: Won C. Yim, Funding agency: National Science Foundation)

PAST RESEARCH PROJECTS

01/2013 – 01/2018	**Engineering CAM Photosynthetic Machinery into Bioenergy Crops for Biofuels Production in Marginal Environments** (PI: John C. Cushman, United States: US Department of Energy)
08/2011 – 09/2011	**Effective Traceless Immobilization of Proteins Using NPU-Intein Mediated Protein Trans-splicing** (PI: Young-eun Kwon, Funding agency: Ministry of Education, Science and Technology, Korea Rep.)
05/2011 – 01/2013	**Genome resequencing and a large-scale analysis of agronomically important genes using mutant populations in rice** (PI: Byung-moo Lee, Funding agency: Rural Development Administration, Korea Rep.)
03/2011 – 12/2012	**Identification of yield and quality variation under high temperature in crop** (PI: Byung-moo Lee, Funding agent: Rural Development Administration, Korea Rep.)
11/2009 – 12/2009	**Gene marker set for identification of exposure to 17-β estradiol, microarray chip and method of determination using thereof** (PI: Young-eun Kwon, Funding agency: Ministry of Environment, Korea Rep.)
03/2008 – 03/2009	**A close look at plant responses to abiotic stresses through their gene networks.** (PI: Byung-moo Lee, Funding agency: Dongguk University, Korea Rep.)
03/2008 – 12/2011	**Gene Network and Genotype Modeling for Crop Improvement** (PI: Cheol Seong Jang, Funding agency: Rural Development Administration, Korea Rep.)
01/2007 – 12/2007	**Analysis of transcriptome and proteome of soybean responded to ozone or UV-B stress**. (PI: Byung-moo Lee, Funding agency: Rural Development Administration, Korea Rep.)
01/2007 – 12/2010	**Employment of rye chromatins in development of high quality and stress tolerance wheat cultivars**. (PI: Byung-moo Lee, Funding agency: Rural Development Administration, Korea Rep.)

PUBLICATIONS

1. Amin et al., (2019) Crassulacean Acid Metabolism Abiotic Stress-Responsive Transcription Factors: A Potential Genetic Engineering Approach for Improving Crop Tolerance to Abiotic Stress. **Frontier in Plant Science** *Accepted*

2. Lim et al., (2019) Laying the foundation for crassulacean acid metabolism (CAM) Biodesign: Expression of the C4 metabolism cycle genes of CAM in Arabidopsis. **Frontier in Plant Science** *Accepted*

3. Wone BWM, **Yim WC**, Schutz H, Meek TH, Garland Jr T. (2018) Mitochondrial haplotypes are not associated with mice selectively bred for high voluntary wheel running. **Mitochondrion** doi:10.1016/j.mito.2018.04.002

4. Lim SD, **Yim WC**, Liu D, Hu R, Yang X, Cushman JC. (2018) A *Vitis vinifera* basic helix-loop-helix transcription factor enhances plant cell size, vegetative biomass, and reproductive yield. **Plant Biotechnology Journal** doi:10.1111/pbi.12898

5. Polle J, Barry K, Cushman JC, Schmutz J, Tran D, Hathwaik L, Yim WC, Jenkins J, McKie-Krisberg Z, Prochnik S, Lindquist S, Dockter R, Adam C, Molina H, Bunkenborg J, Jin ES, Buchheim M, J Magnuson. (2017) The Draft Nuclear Genome of the Halophilic and Beta-Carotene Accumulating Green Alga Dunaliella salina Strain CCAP19/18. **Genome Announcements** doi:10.1128/genomeA.01105-17

6. Song K, Yim WC, Lee B-M. (2017) Expression of Heat Shock Proteins by Heat Stress in Soybean **Plant Breeding and Biotechnology** doi:10.9787/PBB.2017.5.4.344

7. Yang X, Hu R. Yin H, Jenkins J, Shu S, Tang H, Liu D, Weighill DA, **Yim WC**, Ha J, Heyduk K, Goodstein D, Gou HB, Moseley R, Fitzek E, Jawdy S, Zhang Z, Xie M, Hartwell J, Grimwood J, Abraham P, Mewalal R, Beltrán J, Boxall S, Denver L, Palla K, Albion R, Garcia T, Mayer J, Lim SD, Wai CM, Peluso P, VanBuren R, De Paoli H, Borland A, Guo H, Chen JG, Muchero W, Yin Y, Jacobson D, Tschaplinski T, Hettich R, Ming R, Winter K, Leebens-Mack K, Smith JAC, Cushman JC, Schmutz J, Tuskan G. (2017) The *Kalanchoë* genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism**.** Accepted**. Nature Communications** doi:10.1038/s41467-017-01491-7

8. Yerramsetty PK, Agar EM, **Yim WC**, Cushman JC, Berry JO. (2017) An rbcL mRNA binding protein is associated with C3 to C4 evolution and light-induced production of Rubisco in *Flaveria.* **Journal of Experimental Botany** 10.1093/jxb/erx264

9. Wai CM, Van Buren R, Zhang J, Huang L, Miao W, Edger PP, **Yim WC**, Priest H, Meyers BC, Mockler TC, Smith, JAC, Cushman JC, Ming R. (2017) Temporal and spatial dynamics of CAM photosynthesis in pineapple. **The Plant Journal** 10.1111/tpj.13630

10. **Yim WC** & Cushman JC (2017) Divide and Conquer BLAST: using grid engines to accelerate BLAST and other sequence analysis tools. **PeerJ** 10.7717/peerj.3486

11. Yobi A, Schlauch KA, Tillett RL, **Yim WC**, Espinoza C, Wone BWM, Cushman JC, Oliver MJ (2017) Sporobolus stapfianus: Insights into desiccation tolerance in the resurrection grasses from linking transcriptomics to metabolomics. **BMC Plant Biology** 17: 67

12. Chiang C-P, **Yim WC**, Sun Y-H, Ohnishi M, Mimura T, Cushman JC, Yen HE (2016) Identification of Ice Plant (*Mesembryanthemum crystallinum L.*) MicroRNAs Using RNA-Seq and Their Putative Roles in High Salinity Responses in Seedlings**. Frontier in Plant Science** 10.3389/fpls.2016.01143

13. Ming R, Van Buren R, Wai CM, Tang H, Schatz MC, Bowers, JE, Lyons E, Wang M-L, Chen J, Biggers E, Zhang J, Huang L, Zhang L, Miao W, Zhang J, Ye Z, Miao C, Lin Z, Wang H, Zhou H**, Yim WC**, Priest HD, Zheng C, Woodhouse M, Edger PP, Guyot R, Guo H-B, Guo H, Zheng G, Singh R, Sharma A, Min X, Zheng Y, Lee H, Gurtowski J, Sedlazeck F, Harkess A, McKain MR, Liao Z, Fang J, Liu J, Zhang X, Zhang Q, Hu W, Yuan Q, Wang K, Chen L-Y, Shirley N, Lin Y-R, Liu L-Y, Hernandez AG, Wright CL, Bulone V, Tuskan GA, Heath K, Zee F, Moore PH, Sunkar R, Leebens-Mack JH, Mockler T, Bennetzen JL, Freeling M, Sankoff D, Paterson AH, Zhu X, Yang X, Smith, JAC, Cushman JC, Paull RE, Yu, Q. (2015) The pineapple genome and the evolution of CAM photosynthesis**. Nature Genetics** 47: 1435–1442

14. Yang X, Cushman JC, Borland AM, Edwards EJ, Wullschleger SD, Tuskan GA, Owen NA, Griffiths H, Smith JAC, De Paoli HC, Weston DJ, Cottingham R, Hartwell J, Davis SC, Silvera K, Ming R, Schlauch KA, Abraham P, Stewart JR, Guo H-B, Albion RA, Ha J, Lim SD, Wone BWM, **Yim WC**, Garcia T, Mayer JA, Petereit J, Nair SS, Casey E, Hettich RL, Ceusters J, Ranjan P, Palla KJ, Yin H, Reyes-García C, Andrade JL, Freschi L, Beltran JD, Dever LV, Boxall SF, Waller J, Davies J, Bupphada P, Kadu N, Winter K, Sage RF,

Aguilar CN, Schmutz J, Jenkins J, Holtum, JAC. (2015) A roadmap for research on crassulacean acid metabolism to enhance sustainable food and bioenergy production in a hotter, drier world. **New Phytologist**. 207: 491–504.

15. Song K, Kim JH, Yoon GY, Kim HC, Shin S, **Yim WC**, Kim K-H, Lee B-M (2015) Distribution of Genetic Variants in Korean Soybeans. **The Korean Journal of Crop Science** 60: 224–230

16. Moon J-C, **Yim WC**, Lim SD, Song K, Lee B-M (2014) Differentially expressed genes and *in silico* analysis in response to ozone (O3) stress of soybean leaves**. Australian Journal of Crop Science** 8(2):276-283

17. Song K, **Yim WC**, Jung G-H, Kim SL, Kwon Y-U, Lee B-M (2013) Relationship of Transformation Efficiency and Metabolites Induced in Korean Soybean Cotyledons Treated with Sonication. **Korean Journal of Crop Science** 58: 119–127

18. Moon J-C, Lim SD, **Yim WC**, Song K, Lee B-M (2013) Characterization of Expressed Genes Under Ozone Stress in Soybean. **Plant Breeding and Biotechnology** 1: 270–276

19. **Yim WC**, Yu Y, Song K, Jang CS, Lee B-M (2013) PLANEX: the plant co-expression database**. BMC Plant Biology** 13: 83

20. Moon J-C, **Yim WC**, Lee J-E, Kwon Y-U, Song K, Lee B-M (2012) Transcriptome analysis in response to UV-B stress in soybean [*Glycine max* (L.) Merr.]. **Australian Journal of Crop Science** 6(9)

21. Kim DS, Lee KJ, **Yim WC**, Kim J-B, Ha B-K, Kim SH, Kang S-Y (2012**)** Transcriptional network analysis of the tryptophan-accumulating rice mutant during grain filling. **Molecular Genetics and Genomics** 287: 699–709

22. **Yim WC**, Lee B-M, Kwon Y (2012**)** Cross-experimental analysis of microarray gene expression datasets for in silico risk assessment of TiO2 nano-particles. **Molecular Cell Toxicology** 8: 229–239

23. **Yim WC**, Min K, Jung D, Lee B-M, Kwon Y (2011**)** Cross experimental analysis of microarray gene expression data from volatile organic compounds treated targets**. Molecular Cell Toxicology** 7: 233–241

24. Wang HW, Kwon HJ, **Yim WC**, Lim SD, Moon J-C, Lee B-M, Seo YW, Kim W, Jang CS (2010) Expressional diversity of wheat nsLTP genes: evidence of subfunctionalization via cis-regulatory divergence. **Genetica** 138: 843–852

25. **Yim WC**, Keum C, Kim S, Cho Y, Lee B-M, Kwon Y (2010a) Identification of novel 17B-estradiol (E2) target genes using cross-experiment gene expression datasets. **Toxicology Environment Health** Sci 2: 25–38

26. **Yim WC**, Keum C, Kim S, Jang CS, Lee B-M (2010b) Identification of the Housekeeping Genes Using Cross Experiments via *in silico* Analysis**. Korean Journal of Crop Science**

27. Lim SD, **Yim WC**, Moon J-C, Kim DS, Lee B-M, Jang CS (2010) A gene family encoding RING finger proteins in rice: their expansion, expression diversity, and co-expressed genes. **Plant Molecular Biology** 72: 369–380

28. **Yim WC**, Kim DS, Moon J-C, Jang CS, Lee B-M (2009a) A Genome-wide Approach for Functional Analysis Using Rice Mutant. **Korean Journal of Crop Science** 54(3): 332-338

29. **Yim WC**, Lee B-M, Jang CS (2009b) Expression diversity and evolutionary dynamics of rice duplicate genes. **Molecular Genetics and Genomics** 281: 483–493

30. Jang CS, **Yim WC**, Moon J-C, Jung JH, Lee TG, Lim SD, Cho SH, Lee KK, Kim W, Seo YW, et al (2008) Evolution of non-specific lipid transfer protein (nsLTP) genes in the *Poaceae* family: their duplication and diversity. **Mol Genet Genomics** 279: 481–497

31. Jang CS, Jung JH, **Yim WC**, Lee B-M, Kim YWS and W (2007) Divergence of Genes Encoding Non-specific Lipid Transfer Proteins in the *Poaceae* Family. **Molecules and Cells** 24: 215–223

32. **Yim WC**, Jang CS (2007) Discovery of gene regulatory networks via *in silico* analysis and their application in abiotic stress responses. **Korean Journal of Breeding Science** 39(4) : 464-472

33. **Yim WC**, Kang MS, Kwon Y-U, Jang CS, Seo YW, Lim SD, Kim K-H, Moon J-C, Lee S-K, Lee B-M (2007) Evaluation of genetic diversity among Korean wheat using RAPD and ISSR analysis**. Korean Journal of Breeding Science** 39: 309–315

MANUSCRIPTS IN PREPARATION

1. **Yim WC**, Bilgi BG, Albion RL, Tillett RL, Schlauch KA, Seaver SMD, Cushman JC, **High quality de novo assembly of the common ice plant (*Mesembryanthemum crystallinum* L.) transcriptome – a functional genomics resource for crassulacean acid metabolism (CAM) and halophytism.** *In preparation. Target journal: The plant journal*

2. **Yim WC** *et al.,* **High Quality *De Novo* Genome Assemblies of the Common Ice Plant (*Mesembryanthemum crystallinum* L.) - a Functional Genomics Resource for Crassulacean Acid Metabolism (CAM) and Halophytism.** *In preparation*. *Target journal: Nature*

3. VanBuren et al., **Sexual recombination and selection during domestication of clonally propagated pineapple.** *Under review : Nature*

PATENTS

1. Lim SD, **Yim WC**, Cushman JC (2017) Engineering Crassulacean Acid Metabolism (CAM) Pathways in Plants. US Patent #62276438

2. Kwon YE, Lee BM, **Yim WC** (2010) Gene marker set for identification of exposure to 17-β estradiol, microarray chip and method of determination using thereof. Korea Patent #1020100079936

TRAININGS

2012 **Distinguished Ph.D. Student Award**, Dongguk University, Seoul, Korea Rep.

2010 **Plant bioinformatics course,** EMBL-EBI, Hinxton, Cambridge, U.K.

2010 **Transcriptomics and related tools,** EBI - School of Biological Science, University of Cambridge, U.K.

2008 **Distinguished Paper Award & Scholarship,** Dongguk University, Seoul, Korea Rep. $1,751

2008 **University Scholarship**, Dongguk University, Seoul, Korea Rep. $5,078

2007 **Best Oral Presentation Award**, The Korean Society of Breeding Science, Korea Rep.

2007 **University Chancellor's Scholarship**, Dongguk University, Seoul, Korea Rep. $3,935

2006 **University Scholarship**, Dongguk University, Seoul, Korea Rep.

TEACHINGS EXPERIENCES

Fall 2018	**Part-time Instructor in Molecular Genetics BCH 705** (Genomes) University of Nevada, Reno
Spring 2017	**Part-time Instructor in Functional Genomics BCH 706** (Third Generation DNA Sequencing) University of Nevada, Reno
Fall 2016	**Part-time Instructor in Plant Molecular Biology & Biotechnology BCH718** (Genome structure and organization) University of Nevada, Reno
09/2012 – 12/2012	**Instructor** (Molecular biology lab course) Dongguk University, Seoul, Korea Rep.
09/2009 – 02/2010	**Instructor** (Molecular biology lab course) Dongguk University, Seoul, Korea Rep.
03/2008 – 01/2013	**Undergraduate and graduate research mentor**, Dongguk University, Seoul, Korea Rep.
03/2006 – 09/2009	**Research Assistant** Dongguk University, Seoul, Korea Rep.

SYNERGISTIC ACTIVITIES

1) Faculty Membership of the American Society of Plant Biology (ASPB)
2) Guest Editor for Journal Genes (2018-2019)
3) President of student association, College of Life science and resource, Dongguk University, Seoul, Korea Rep. (2004-2005)
4) Korean military service (2001-2003)
5) Open source contribution (https://github.com/ascendo)

PROFESSIONAL BIOINFORMATIC SKILL

1) Proficiency in Perl, Python and R language
2) *De novo* genome assembly (Canu, Falcon, Supernova)
3) *De novo* transcriptome assembly (ABySS, SOAPdenovo-Trans, Trinity)
4) Gene annotation (PASA, MAKER, FGENESH, AUGUSTUS)
5) Functional genomics analysis (Gene Ontology, Co-Expression, Reactome & KEGG pathway)
6) Development of custom bioinformatics tools (DCBLAST), software (Chloroplast genome assembler) and web databases (PLANEX)
7) Solid experience of HPC and supercomputing environments.

INVITED CONFERENCE TALKS

1. **Yim WC** (2018) The complete de novo assembly of the Ice plant (*Mesembryanthemum crystallinum* L.) genome University of Idaho, Moscow, Idaho, USA, Feb 6, 2018
2. **Yim WC** (2017) The complete de novo assembly of the Ice plant (*Mesembryanthemum crystallinum* L.) genome University of Nevada-Reno, Reno, Nevada, USA, Dec 21, 2017
3. **Yim WC** (2017) Modern Molecular Diagnostic Methods for Medical Laboratory Sciences and Forensics. Michigan Technological University, Houghton, Michigan, USA, Nov 30, 2017
4. **Yim WC** (2017) Empowering Genome Research with Bioinformatics-Enabled Systems Biology. Michigan Technological University, Houghton, Michigan, USA, Nov 29, 2017
5. **Yim WC** (2017) Transcriptome Analysis & Beyond: Advanced Approaches for Transcriptome Analysis in Diploid and Polyploid Plant Species**.** Plant and Animal Genome XXV Conference, San Diego, California, USA, Jan 14-18, 2017.
6. **Yim WC** (2015) Transcriptome and Genome Assemblies of the Common Ice Plant, a Halophytic, Facultative Plant and Animal Genome XXIII Conference, San Diego, California, USA, Jan 10-14, 2015.
7. **Yim WC** (2014) Transcriptome sequencing and RNA-seq mRNA expression profiling in the facultative CAM model species *Mesembryanthemum crystallinum*. 34th New Phytologist Symposium, Tahoe City, CA, USA, July 15–18, 2014.

ABSTRACTS AND POSTER PRESENTATIONS

1. **Yim WC,** Lim SD, Ha J, Wone BWM, Albion RL, Yin H, Yang X, Cushman JC. Genome Sequencing of the Common Ice Plant (*Mesembryanthemum crystallinum* L.) . 25th Plant and Animal Genome Conference, San Diego, California, USA, Jan 14-18, 2017

2. **Yim WC,** Lim SD, Mayer JA ,Cushman JC. Transcriptome Analysis & Beyond: Advanced Approaches for Transcriptome Analysis in Diploid and Polyploid Plant Species. 25th Plant and Animal Genome Conference, San Diego, California, USA, Jan 14-18, 2017.

3. Garcia TM, Wone BWM, Ha J, Lim SD, **Yim WC**, Schlauch KA, Cushman JC. Characterization of the Transcriptional Regulation of Crassulacean Acid Metabolism (CAM) in *Kalanchoe fedtschenkoi* Mesophyll Tissue. 25th Plant and Animal Genome Conference, San Diego, California, USA, Jan 14-18, 2017.

4. Lim SD, **Yim WC**, Cushman JC. CAM Biodesign: Engineering Crassulacean Acid Metabolism into C_3 Plant to Improve Water-Use Efficiency. 25th Plant and Animal Genome Conference, San Diego, California, USA, Jan 14-18, 2017.

5. Mayer JA, **Yim WC**, Wone BWM, Paterson AH, Cushman JC. Generating a robust genome and transcriptome of the high output Crassulacean acid metabolism species *Opuntia ficus-indica***.** . 25th Plant and Animal Genome Conference, San Diego, California, USA, Jan 14-18, 2017.

6. **Yim WC**, Lim SD, Ha J, Wone BWM, Albion RL, Yin H, Yang X, Cushman JC. High quality de novo genome assembly of the common ice plant (*Mesembryanthemum crystallinum*) - a functional genomics

resources for crassulacean acid metabolism (CAM) and halophytism. 24th Plant and Animal Genome Conference, San Diego, California, USA, Jan 9-13, 2016.

7. Yang X, Cushman JC, Hu R, Jenkins J, Schmutz J, Tuskan GA, Yin H, Shu S, Rokhsar D, Goodstein D, Hellsten U, Borland AM, Ming R, Van Buren R, Wai CM, Tang H, Abraham P, Guo H-B, Guo H, Albion RL, Garcia T, Ha JM, Lim SD, Mayer JA, **Yim WC**, Wone BWM, Jacobson DA, Weighill DA, Harwell J, Li X, Yin Y, Leebens-Mack J, Smith A, Winter K. Comparative Evolution of Crassulacean Acid Metabolism (CAM). 24th Plant and Animal Genome Conference, San Diego, California, USA, Jan 9-13, 2016.

8. Ha J, Lim SD, **Yim WC**, Hartwell J, Yang X, Cushman JC. Crassulacean acid metabolism (CAM) Ppc promoter and transcription factor analysis in *Kalanchoe* species. 24th Plant and Animal Genome Conference, San Diego, California, USA, Jan 9-13, 2016.

9. Garcia TM, Wone BWM, **Yim WC**, Lim SD, Ha J, Schlauch KS, Cushman JC. Characterization of the transcriptional regulation of crassulacean acid metabolism in *Kalanchoe laxiflora* mesophyll tissue. 24th Plant and Animal Genome Conference, San Diego, California, USA, Jan 9-13, 2016.

10. Mayer JA, **Yim WC**, Wone BWM, Paterson AH, Cushman JC. Generating a robust genome and transcriptome of the high-output crassulacean acid metabolism (CAM) species *Opuntia ficus-indica*. 24th Plant and Animal Genome Conference, San Diego, California, USA, Jan 9-13, 2016.

11. Lim SD, **Yim WC**, Cushman JC. Engineering tissue succulence to improve water-use efficiency of bioenergy feedstocks. 2016 Genomic Science Annual Contractor-Grantee Meeting. Tyson's Corner, VA, USA, March 7-9, 2016.

12. Yang X, Cushman JC, Hu R, Jenkins J, Schmutz J, Tuskan GA, Yin H, Shu S, Rokhsar D, Goodstein D, Hellsten U, Borland AM, Ming R, Van Buren R, Wai CM, Tang H, Abraham P, Guo H-B, Guo H, Albion RL, Garcia T, Ha JM, Lim SD, Mayer JA, Wone BWM, **Yim WC**, Jacobson DA, Weighill DA, Harwell J, Li X, Yin Y. The Kalanchoe genome – An important model for systems biology and synthetic biology of crassulacean acid metabolism. 2016 Genomic Science Annual Contractor-Grantee Meeting. Tyson's Corner, VA, USA, March 7-9, 2016.

13. Cushman JC, Albion RL, Ha J, Lim SD, Wone BWM, Cheol **Yim WC**, Garcia T, Yerramsetty PK, Petereit J, Tillett RL, Schlauch KA, Borland AM, Leverett A, De Paoli HC, Hu R, Degao Liu D, Palla K, Moseley RC, Tschaplinski TJ, Weston DJ, Tuskan GA, Chen J, Hartwell J, Dever LV, Boxall SF, Waller J, Davies J, Bupphada P, Kadu N, Guo H, Guo H-B, Abraham P, Hettich R, and Yang X. Engineering Crassulacean Acid Metabolism (CAM) to Improve Water-use Efficiency of Bioenergy Feedstocks. 2016 Genomic Science Annual Contractor-Grantee Meeting. Tyson's Corner, VA, USA, March 7-9, 2016.

14. **Yim WC**, Lim SD, Wone BWM, Ha J, Albion RL, Yin H, Yang X, Cushman JC. High quality de novo genome sequencing of the common ice plant (*Mesembryanthemum crystallinum*) - a functional genomics resources for crassulacean acid metabolism (CAM) biodesign. 2016 Genomic Science Annual Contractor-Grantee Meeting. Tyson's Corner, VA, USA, March 7-9, 2016.

15. Abraham P, **Yim WC**, Bilgi BG, Albion RL, Wone BWM, Hettich RL, Cushman JC. Protein machinery underpinning the transition between C3 photosynthesis and crassulacean acid metabolism (CAM) in the common ice plant (*Mesembryanthemum crystallinum*). 2016 American Society of Plant Biologists Meeting. Austin, TX, USA, June 9-13, 2016.

16. Mayer JA, **Yim WC**, Albion RL, Shintani DK, Kosma DK, Cushman JC. Developing *Opuntia ficus-indica* as a platform for low-input biofuels production and a model for cuticular wax synthesis. 2016 American Society of Plant Biologists Meeting. Austin, TX, USA, June 9-13, 2016.

17. Garcia TM, Wone BWM, Ha J, Lim SD, **Yim WC**, Schlauch KA, Cushman JC. Characterization of the transcriptional regulation of crassulacean acid metabolism (CAM) in *Kalanchoe laxiflora* mesophyll tissue. Molecular Biosciences Graduate Student Retreat, August 21, 2015. Reno, NV.

18. Mayer JA, **Yim WC**, Albion RL, Shintani DK, Kosma DK, Cushman JC. Developing i as a platform for low-input biofuels production and a model for cuticular wax synthesis. Molecular Biosciences Graduate Student Retreat, August 21, 2015. Reno, NV.

19. Garcia TM, Wone BWM, Ha J, Lim SD, **Yim WC**, Schlauch KA, Cushman JC. Characterization of the transcriptional regulation of crassulacean acid metabolism (CAM) in *Kalanchoe laxiflora* mesophyll tissue. Nevada Agricultural Experiment Station, Ag Field Day, September 26, 2015. Reno, NV.

20. Mayer JA, **Yim WC**, Albion RL, Shintani DK, Kosma DK, Cushman JC. Developing i as a platform for low-input biofuels production and a model for cuticular wax synthesis. Nevada Agricultural Experiment Station, Ag Field Day, September 26, 2015. Reno, NV.

21. Mayer JA, Wone BWM, **Yim WC**, Albion RL, Shintani DK, Cushman JC. Metabolic engineering *of Opuntia ficus-indica* for use as a low-water use biofuel feedstock. National Biodiesel Conference, January 19-22, 2015. Fort Worth, TX.

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