CURRICULUM VITAE

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I. EDUCATION

2006 – 2011: Department of Electronics Engineering (uncompleted), Chungbuk National University, Cheongju, Korea.

2013 – 2015 (February): B.S., Department of Horticulture, Chungbuk National University, Cheongju, Korea.

2015 – 2020 (February): Combined M.S. and Ph.D., Department of Horticultural Science, Chungbuk National University, Cheongju, Korea.

II. POSITIONS HELD

2020 (February) – 2020 (October) : Post doctor, Department of Horticultural Science, Chungbuk National University, Cheongju, Korea.

2020 (October) – 2021 (Jun): Visiting scholar, Department of Horticulture science, University of Florida, Wimauma, Korea.

2021 (Jun) – Present : Postdoc research associates, Department of Horticulture science, University of Florida, Wimauma, Korea.

III. SPECIAL TRAINING

2015: Workshop on genome analysis for agricultural crops. 23-24. July.

2016: Workshop on genome analysis for agricultural crops. 23-24. Aug.

IV. ACADEMIC HONORS AND SCHOLARSHIPS

2017: Annual Spring Conference of the Korean Society for Horticultural Science Award, (May, 25)

2018: Annual Autumn Conference of the Korean Society for Horticultural Science Award, (Oct, 18)

2019: Annual Autumn Conference of the Korean Society for Horticultural Science Award, (Oct, 25)

V. SUPPLEMENTARY SKILLS

• Phylogenetic Computer Analysis: MEGA, Power Marker.

• Molecular Techniques: DNA extraction, PCR, electrophoresis, primer design, sequencing.

• Sequence Data Management: Clustal X, Bioedit, Geneious, Axiom Analysis Suites

• SNP calling, Sabre, SolexaQA++, samtools, GATK, BWA, VCFtools, Picard tools

• Genome annotation: GenSAS

• Linkage Mapping and QTL Software: JoinMap, MapQTL, MapChart

• Computer language: Python (learner), Scripting

• Scientific Illustration: Sigmaplot

• Statistical analysis: R language

• Genome analysis tools: Geneious Prime, CLC workbench

• Transcriptome analysis

VI. PUBLICATIONS

– Papers –

15. Chandra, S., Oh, Y., **Han, H.,** Salinas, N., Anciro, A., Whitaker, V. M., ... & Lee, S. (2021). Comparative transcriptome analysis to identify candidate genes for *FaRCg1* conferring resistance against *Colletotrichum gloeosporioides* in cultivated strawberry (*Fragaria× ananassa*). *Frontiers genetics*, 12.

14. Oh, S., Oh, Y., Kim, K., **Han, H.**, Kim, Y., Won, K., & Kim, D. (2020). Construction of high-resolution genetic linkage map in pear pseudo-BC 1 ((*Pyrus pyrifolia× P. communis*) × *P. pyrifolia*) using GBS-SNPs and SSRs. Hortic Environ Biotech, 61(4), 745-753.

13. Hwang K., Oh, S., Kim K., **Han H.**, Oh, Y., Lim H., Kim Y., Kim D. (2019). Genotyping-by-sequencing approaches using optimized two-enzyme combinations in Asian pears (*Pyrus* spp.). *Molecular Breeding, 39:161* (19, November)

12. Kim, K., Oh, Y., **Han, H.**, Oh, S., Lim, H., Chung, J. W., ... & Kim, D. (2019). Genetic relationships and population structure of pears (*Pyrus* spp.) assessed with genome-wide SNPs detected by genotyping-by-sequencing. *Horticulture, Environment, and Biotechnology*, 1-9. (10 October 2019) **[SCI]**

11. **Han, H.**, Oh, Y., Kim, K., Oh, S., Cho, S., Kim, Y. K., & Kim, D. (2019). Integrated genetic linkage maps for Korean pears (*Pyrus* hybrid) using GBS-based SNPs and SSRs. *Horticulture, Environment, and Biotechnology*, *60*(5), 779-786. (11 September 2019) **[SCI]**

10. Ha, W., Shin, H., Lim, H. K., Oh, Y., **Han, H.**, Kim, K., ... & Kim, D. (2019). Growth of One-Year-Old Pot-Cultivated'Fuji'/M. 9 Apple Trees under Different Concentrations of Nitrogen Fertilization. *Korean Journal of Plant Resources*, *32*(5), 499-508. **[SCI]**

9. Lim, H. K., Shin, H., Son, I. C., Oh, Y., Kim, K., **Han, H.**, ... & Kim, D. (2019). Defoliation and Fruit Coloration in 'Fuji'/M. 9 Apple Affected by Cu-EDTA and Fe-EDTA Foliar Spray. *Horticultural Science and Technology*, *37*(4), 448-454. **[SCI]**

8. Oh, S., Kim, K., **Han, H.**, Shin, H., Oh, Y., & Kim, D. (2017, June). Proline content and related gene expression in response to seasonal temperature variation in three Rosaceae fruit trees. In *VIII International Cherry Symposium 1235* (pp. 441-448).

7. Oh, S., Lee, M., Kim, K., **Han, H.**, Won, K., Kwack, Y. B., ... & Kim, D. (2019). Genetic diversity of kiwifruit (*Actinidia* spp.), including Korean native A. arguta, using single nucleotide polymorphisms derived from genotyping-by-sequencing. *Horticulture, Environment, and Biotechnology*, *60*(1), 105-114. **[SCI]**

6. Won, J., Shin, H., Oh, Y., Han, H., Kwon, Y., & Kim, D. (2018). Tree Growth and Fruit Characteristics of 'Nero' Black Chokeberry According to Different Cultivation Regions and Altitudes. *Korean Journal of Plant Resources*, *31*(2), 136-148.

5. Oh, S., Shin, H., Kim, K., Oh, Y., Won, J., **Han, H.**, & Kim, D. (2015, June). Relationship between cold hardiness and bud opening among peach cultivars during a constant experimental deacclimation. In *XIV EUCARPIA Symposium on Fruit Breeding and Genetics 1172* (pp. 371-374).

4. Kim, D., Oh, Y., Shin, H., Oh, S. I., **Han, H.**, Won, J., ... & Kim, Y. (2015, June). Development of high-throughput microsatellite markers for Korean pears using next generation sequencing. In *XIV EUCARPIA Symposium on Fruit Breeding and Genetics 1172* (pp. 279-282).

3. Won, J., Shin, H., Oh, Y., **Han, H.**, Kim, K., Oh, S., & Kim, D. (2017). Comparison of quality and cell enlargement of 'Nero' black chokeberry fruits according to different soil water conditions. *Korean Journal of Plant Resources*, *30*(1), 88-95.

2. Oh, Y., Park, J.Y., Shin, H., **Han, H.**, Park, J.H., Kim, D. (2016). Assessment of genetic relationships in Korean bred pears (*Pyrus* spp.) using simple sequence repeat markers. Journal of Agricultural Science Chungbuk National University. 32(1), 63-70.

1. Oh, Y., Shin, H., Kim, K., **Han, H.**, Kim, Y.K., Kim D. (2015). Researches of pear tree (*Pyrus* spp.) genomics.

VI. International Conference

2019. Development of a SNP-derived CAPS marker set associated with pollen fertility in *Pyrus* spp. XV EUCARPIA Fruit Breeding and Genetics Symposium, June 3-7, Prague, Czech Republic.

2019. Development of insertion and deletion markers associated with pollen fertility in pears (*Pyrus* spp.). XV EUCARPIA Fruit Breeding and Genetics Symposium, June 3-7, Prague, Czech Republic.

2019. Three complementary restorer genes confer pollen fertility restoration in *Pyrus* spp. Plant and animal genome conference XXVII, January 12-16, San Diego, CA, USA

2018. Development of a cleaved amplified polymorphic sequence marker associated with presence or absence of pollen in pear (*Pyrus* spp.). 9th international rosaceae genomics conference, June 26-30, Nanjing, China.

2018. Candidate QTL regions associated with fruit size and weight in Mapping population between ʹWhangkeumbaeʹ and ʹMinibaeʹ (*Pyrus* spp.). Plant and animal genome conference XXVI, January 13-17, San Diego, CA, USA.

2018. Development of distinguishable markers among apple sports (*Malus × domestica* Borkh.) from 'Fuji' and 'Hongro' using sequence-specific amplified polymorphism markers. Plant and animal genome conference XXVI, January 13-17, San Diego, CA, USA.

2017. Identification of candidate SNPs for formation or degeneration of pollen in interspecific population in pears (*Pyrus* spp.). Plant and animal genome conference XXV, January 14-18, San Diego, CA, USA.

2017. An InDel and SNP genetic linkage map in interspecific Asian pear using next generation sequencing. Plant and animal genome conference XXV, January 14-18, San Diego, CA, USA.