

CURRICULUM VITAE

10/2022

PERSONAL DETAILS

Name	Tuomas Hämälä
Nationality	Finland
Email address	tuomas.hamala@gmail.com
Public profiles	Google Scholar , ResearchGate
ORCID ID	0000-0001-8306-3397
Webpage	thamala.github.io

EMPLOYMENT

4/2022 – present	University of Nottingham, UK Marie Skłodowska-Curie individual fellow Supervisor: Levi Yant
9/2021 – 3/2022	University of Oulu, Finland Academy of Finland postdoctoral fellow
8/2018 – 7/2021	University of Minnesota Twin Cities, USA Postdoctoral associate Supervisor: Peter Tiffin

EDUCATION

1/2014 – 7/2018	University of Oulu, Finland PhD in population genetics Thesis title: “Ecological genomics in <i>Arabidopsis lyrata</i> : local adaptation, phenotypic differentiation, and reproductive isolation” Supervisor: Outi Savolainen
9/2011 – 12/2013	University of Oulu, Finland MSc in genetics
9/2008 – 5/2011	University of Oulu, Finland BSc in bioscience

PUBLICATIONS

*equal contribution, #corresponding author

11. **Hämälä T[#]**, Ning W, Kuittinen H, Aryamanesh N* & Savolainen O* (2022). Environmental response in gene expression and DNA methylation reveals factors influencing the adaptive potential of *Arabidopsis lyrata*. *eLife* 11:e83115.
10. Epstein B, Burghardt L, Heath K, Grillo M, Kostanecki A, **Hämälä T**, Young N & Tiffin P[#] (2022). Combining GWAS and population genomic analyses to characterize coevolution in a legume-rhizobia symbiosis. *Molecular Ecology* in press.
9. **Hämälä T^{*,#}**, Wafula EK*, Guiltinan MJ, Ralph PE, dePamphilis CW & Tiffin P[#] (2021). Genomic structural variants constrain and facilitate adaptation in natural populations of *Theobroma cacao*, the chocolate tree. *PNAS* 118: e2102914118.
8. Takou M, **Hämälä T**, Koch E, Steige KA, Dittberner H, Yant L, Genete M, Sunyaev S, Castric V, Vekemans X, Savolainen O & de Meaux J[#] (2021). Maintenance of adaptive dynamics and no detectable load in a range-edge out-crossing plant population. *Molecular Biology and Evolution* 38: 1820–1836.
7. **Hämälä T[#]** & Tiffin P (2020). Biased gene conversion constrains adaptation in *Arabidopsis thaliana*. *Genetics* 215: 831–846.
6. **Hämälä T^{*,#}**, Gorton AJ*, Moeller AD & Tiffin P[#] (2020). Pleiotropy facilitates local adaptation to distant optima in common ragweed (*Ambrosia artemisiifolia*). *PLOS Genetics* 16: e1008707.
5. **Hämälä T[#]**, Guiltinan MG, Marden JH, Maximova S, dePamphilis C & Tiffin P[#] (2020). Gene expression modularity reveals footprints of polygenic adaptation in *Theobroma cacao*. *Molecular Biology and Evolution* 1: 110–123.
4. **Hämälä T[#]** & Savolainen O[#] (2019). Genomic patterns of local adaptation under gene flow in *Arabidopsis lyrata*. *Molecular Biology and Evolution* 36: 2557–2571.
3. Mattila TM*, Laenen B*, Horvath R, **Hämälä T**, Savolainen O & Slotte T[#] (2019). Impact of demography on linked selection in two outcrossing Brassicaceae species. *Ecology and Evolution* 9: 9532–9545.
2. **Hämälä T[#]**, Mattila TM & Savolainen O (2018). Local adaptation and ecological differentiation under selection, migration, and drift in *Arabidopsis lyrata*. *Evolution* 72: 1373–1386.
1. **Hämälä T[#]**, Mattila TM, Leinonen PH, Kuittinen H & Savolainen O (2017). Role of seed germination in adaptation and reproductive isolation in *Arabidopsis lyrata*. *Molecular Ecology* 26: 3484–3496.

FUNDING

- 2021 European Commission, Marie Skłodowska-Curie individual fellowship, 213 000€
- 2021 Academy of Finland, postdoctoral fellowship, 330 000€
- 2019 MPGI, travel grant, \$800
- 2018 Emil Aaltonen foundation, travel grant, 3000€
- 2018 SMBE, young investigator travel award, \$2000
- 2017 Emil Aaltonen foundation, research fellowship, 13 350€
- 2017 UniOGS, travel grant, 1500€
- 2015 PGDP, travel grant, 500€

SKILLS AND EXPERTISE

Population genetics: local adaptation, polygenic adaptation, structural variants, genome evolution, speciation

Bioinformatics: > 10 years of experience with high-performance computing and next-generation sequence analysis; familiar with both model (whole-genome, transcriptome, assemblies) and non-model (transcriptome, RAD-Seq) organism; extensive experience with individual-based simulations (coalescent and forward-in-time); fluent in programming language C

Statistics: fluent in R; regression analysis (e.g., linear mixed models, model selection); machine-learning (e.g., random forest, neural networks); data visualization

Field and laboratory experiments: designed and maintained large-scale reciprocal transplant, common garden, and growth-room experiments

TEACHING AND MENTORING EXPERIENCE

- 2015 – 2016 Master's thesis supervision
Margarita Takou, ecology and population genetics
- 2013 – 2016 Practical trainee supervision
Petri Vänni, Weixuan Ning, Elina Haataja, Margarita Takou, Rami-Petteri Apuli, Paul DuBray, Toni Jenfors
- 2015 Co-instructor
Graduate-level workshop on population genomics, 6 h
- 2014 Teaching assistant
Basics in genetics, 15 h

SELECTED PRESENTATIONS

8/2022	Oral presentation, ESEB, Prague, Czech Republic
1/2022	Oral presentation, PopGroup55, Online
11/2021	Invited online talk, Agricultural Genomics Institute at Shenzhen, China
11/2020	Invited online talk, University of Oulu, Finland
1/2020	Oral presentation, PAG, San Diego, California
8/2019	Poster presentation, ESEB, Turku, Finland
8/2018	Oral presentation, Midwest PopGen meeting, Saint Paul, Minnesota
7/2018	Poster presentation, SMBE, Yokohama, Japan
2/2018	Oral presentation, Arabis symposium, Cologne, Germany
7/2017	Oral presentation, SMBE, Austin, Texas
8/2015	Poster presentation, ESEB, Lausanne, Switzerland

REFERENCES

- Levi Yant (postdoctoral supervisor)
Professor at University of Nottingham, UK, levi.yant@nottingham.ac.uk
- Peter Tiffin (postdoctoral supervisor)
Professor at University of Minnesota Twin Cities, USA, ptiffin@umn.edu
- Outi Savolainen (PhD supervisor)
Emerita professor at University of Oulu, Finland, outi.savolainen@oulu.fi

OTHER

Journal referee
eLife, Evolution, Evolutionary Applications, Evolutionary Ecology, Frontiers in Plant Science, G3: Genes | Genomes | Genetics, Journal of Heredity, Molecular Biology and Evolution, Molecular Ecology, Molecular Ecology Resources, New Phytologist, PLOS Genetics, PNAS

Programs and scripts written for NGS data analysis: [GitHub](#)