

CURRICULUM VITAE

1/2025

PERSONAL DETAILS

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

EMPLOYMENT

1/2024 – present	Natural Resources Institute Finland (Luke), Finland Senior scientist
4/2022 – 12/2023	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

15. Vlček J, **Hämälä T**, Vives Cobo C, Curran E, Šrámková G, Slotte T, Schmickl R, Yant L ✉ & Kolář F ✉ (2025). Whole-genome duplication increases genetic diversity and load in outcrossing *Arabidopsis*. *bioRxiv* preprint.
14. Bray SM, **Hämälä T**, Zhou M, Busoms S, Fischer S, Desjardins SD, Mandáková T, Moore C, Mathers TC, Cowan L, Monnahan P, Koch J, Wolf EM, Lysak MA, Kolář F, Higgins JD, Koch MA & Yant L ✉ (2024). Kinetochore and ionic adaptation to whole genome duplication in *Cochlearia* shows evolutionary convergence in three autopolyploids. *Cell Reports* 43: 114576.
13. **Hämälä T** ✉, Moore C, Cowan L, Carlile M, Gopaulchan D, Brandrud MK, Birkeland S, Loose M, Kolář F, Koch MA & Yant L ✉ (2024). Impact of whole-genome duplications on structural variant evolution in *Cochlearia*. *Nature Communications* 15: 5377.
12. Winters NP*, Wafula EK*, Knollenberg BJ, **Hämälä T**, Timilsena PR, Perryman M, Ralph PE, Prewitt S, Leandro-Muñoz LE, Delgadillo-Duran DA, Altman NS, Tiffin P, Maximova SN, dePamphilis CW, Marden JH & Guiltinan MJ ✉ (2024). A combination of conserved and diverged responses underlies *Theobroma cacao*'s defense response to *Phytophthora palmivora*. *BMC Biology* 22: 1–24.
11. Epstein B, Burghardt L, Heath K, Grillo M, Kostanecki A, **Hämälä T**, Young N & Tiffin P ✉ (2023). Combining GWAS and population genomic analyses to characterize coevolution in a legume-rhizobia symbiosis. *Molecular Ecology* 23: 3798–3811.
10. **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.
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 MPG, 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, ecology, and genomics: 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, long-reads, 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; familiarity with basic wet-lab techniques

TEACHING AND MENTORING EXPERIENCE

- 2023 MSc thesis supervision
Xiuzhiping Quan (bioinformatics major)
- 2022 MSc thesis co-supervision
Ana Da Silva, Matthew Gaskins (bioinformatics majors)
- 2015 – 2016 MSc thesis supervision
Margarita Takou (ecology and population genetics major)
- 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

PRESENTATIONS

Invited departmental seminars and conference talks

1/2025	PAG conference, San Diego, California
8/2023	Department of Ecology & Evolution, University of Sussex, UK
5/2023	Department of Evolution, Ecology & Behaviour, University of Liverpool, UK
3/2023	Milner Centre for Evolution, University of Bath, UK
11/2021	Agricultural Genomics Institute at Shenzhen, online
11/2020	Department of Ecology & Genetics, University of Oulu, online
1/2020	PAG conference, San Diego, California

Contributed conference talks and posters

7/2023	Oral, SBE, Ferrara, Italy
8/2022	Oral, ESEB, Prague, Czech Republic
1/2022	Oral, PopGroup, online
8/2019	Poster, ESEB, Turku, Finland
8/2018	Oral, Midwest PopGen meeting, Saint Paul, Minnesota
7/2018	Poster, SBE, Yokohama, Japan
2/2018	Oral, Arabis symposium, Cologne, Germany
7/2017	Oral, SBE, Austin, Texas
8/2015	Poster, 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
- Otti Savolainen (PhD supervisor)
Emerita professor at University of Oulu, Finland, otti.savolainen@oulu.fi

OTHER

Journal referee

Annals of Botany, eLife, Evolution, Evolution Letters, Evolutionary Applications, Evolutionary Ecology, Frontiers in Plant Science, G3: Genes | Genomes | Genetics, Journal of Ecology, Journal of Heredity, Molecular Biology and Evolution, Molecular Ecology, Molecular Ecology Resources, Molecular Plant, Nature Communications, New Phytologist, The Plant Cell, PLOS Genetics, PNAS

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