JOHAN HALLIN

I am a dedicated scientist with an eye for details. I have managed large projects with close collaborators and have positioned myself at the intersection of computational and molecular biology

contact

✉ johan.h.hallin@gmail.com

🖥 j-hallin.github.io

G scholar.google.com/citations?user=rtnFHLUAAAAJ&hl

☎ +1 418 520 4836

🏠 795 Avenue Monk, app 2
G1S 3M7 Quebec

EDUCATION

BSc	MSc	PhD	HFSP Fellow
Biology	Molecular biology	Université Côte d'Azur	Université Laval
Göteborgs Universitet	Göteborgs Universitet	2014 - 2018	2018 -
2010 - 2013	2013 - 2014		

EXPERIENCE

During my Bachelor's and Master's thesis I worked in the lab of Jonas Warringer. During my Bachelor conducted a large experimental evolution project which was later taken over by a PhD student. My Master's was also focused on experimental evolution, looking into the different evolutionary trajectories of isogenic and non-isogenic colonies. During my time in Gothenburg I supervised master students and the occasional postdoc and also helped set up the novel phenotyping methodology Scan-o-matic[3].

After my Master's I was granted an Erasmus Placement Program scholarship to go to Gianni Liti's lab at the institute for research on cancer and aging, Nice (IRCAN). During this period I enhanced my molecular biology skills and was key in finalizing a project in the lab by constructing a large phenotyping experiment[5].

I enrolled in the competitive LabEx Signalife PhD program and joined Dr. Liti's team as a PhD student. It resulted in two successful papers stemming from a large experiment I performed[1,2]. The two papers were highly collaborative with close collaborations between labs in France, Sweden and the U.K. During this period I further advanced my programming and analytical skills by handling large amounts of data and by spending two weeks as a visiting researcher in Leopold Parts lab at the Sanger Institute. I am continuing my work with Gianni by working on the nature of gamete inviability.

I am now a postdoctoral fellow with Christian Landry. Funded by the HFSP, I am working with potential de novo genes that we found in natural Saccharomyces paradoxus populations[6] in order to understand how genes can emerge from intergenic regions.

PAPERS

1. K. Märtens*, J. Hallin*, et al. Predicting quantitative traits from genome and phenome with near perfect accuracy. *Nature Communications*, 2016

2. J. Hallin*, K. Märtens*, et al. Powerful decomposition of complex traits in a diploid model. *Nature Communications*, 2016

3. M. Zackrisson, J. Hallin, et al. Scan-o-matic: High-resolution microbial phenomics at a massive scale. *G3*, 2016

4. J. Yue, [..2..], J. Hallin, et al. Contrasting evolutionary genome dynamics between domesticated and wild yeasts. *Nature Genetics*, 2017

5. I. Vazques-Garcia, [..4..], J. Hallin, et al. Background-dependent effects of selection in subclonal heterogeneity. *Cell Reports*, 2017

6. E. Durand, [..1..], J. Hallin, et al. Turnover of ribosome-associated transcripts from de novo ORFs produces gene-like characteristics available for de novo gene emergence in wild yeast populations. *Genome Research*, 2019

Skills

R programming ●●●●●

Unix bash ●●●○○○

Python ●○○○○○

Yeast genetics ●●●●●

Writing ●●●●○

Presenting ●●●●○

Supervising ●●●○○

Design ●●●●○

English

Swedish

Spanish ●○○○○

AWARDS & SCHOLARSHIPS

2019	HFSP long-term postdoctoral fellowship
2019	Banting postdoctoral fellowship (*declined*)
2017	Poster Prize 28th ICYGMB
2016	Oral Presentation Prize Signalife Student Conference
2016	Visiting researcher Sanger Institute, U.K. Doctoral school ED85

REFEREE

Molecular Biology and Evolution

Nature Ecology and Evolution

Current Biology

Plos Biology

Science

PNAS

Yeast

eLife