Curriculum Vitae – Lena Birgitta Marie Granehäll

Education since leaving school

- 2017- 2020 - PhD studies in Ancient microbiomes and pathogens, Eurac Research / LMU Munich
- 2013-2015 **Degree of Master of Science**, Main Field of study: Biology, Uppsala University
  Title of Degree Project: “Detection and isolation of STEC in food”
- 2010-2013 **Degree of Bachelor of Science** with a major in Biology, Swedish University of Agricultural Sciences
  Title of Degree Project: “Assessment of defense responses in finger millet to the blast inciting fungus *Magnaporthe oryzae*”

Present appointment

Research Assistant (Bioinformatician)
01/05/2024 – 30/04/2025
Micro4food, Free University of Bozen-Bolzano (Unibz)

- Project: “P*asta and bakery products: integrity, wholesomeness and sustainability - Process and product innovation (INTEGRI)”*
- System administrator for the Micro4food workstation
- Bioinformatic analysis on NGS data for several food and gut microbiome-related projects within the lab group

Professional experience

Research Assistant (Bioinformatician)
15/03/2023 – 14/03/2024
Micro4food, Free University of Bozen-Bolzano (Unibz)

- Project: *“Future-proof bioactive peptides from food by-products: an eco-sustainable bioprocessing for tailored multifunctional foods (PROACTIVE)”*
- System administrator for the Micro4food workstation
- Bioinformatic analysis and statistics on NGS and metabolic data for several food and gut microbiome-related projects within the lab group

Research Assistant (Bioinformatician)
Micro4food, Free University of Bozen-Bolzano (Unibz)
01/03/2022 - 09/03/2023

- Project: “*Smart Protein for a Changing World. Future-proof alternative terrestrial protein sources for human nutrition encouraging environment regeneration, processing feasibility and consumer trust and acceptance (SMART PROTEIN*)”
- Bioinformatic analysis and statistics on NGS data for several food and gut microbiome-related projects within the lab group
- System administrator for the Micro4food workstation

PhD student, Post-graduate
Eurac Research, Institute for Mummy Studies/Faculty of Biology, LMU Munich
06/11/2017- 05/11/2020

- Research on molecular detection and analysis of infectious diseases and microbiomes in ancient human remains using NGS computational analysis.
- Development of target capture enrichment for detection of low-abundant *H. pylori* from ancient human remains.
- DNA extraction and library building for Illumina sequencing.
- Indexing adapter development

Research assistant, Post-graduate
Human Evolution, Uppsala University
2015-2017

- Laboratory work preparing ancient and modern human samples.
- DNA extraction and library building for Illumina and sanger sequencing.

Research assistant, Post-graduate
Swedish National Food Agency
06-07/2015

- Laboratory work, isolating cultures of Enterohaemorrhagic E. coli (EHEC) for a project in mapping pathogens in unpasteurized milk.

Research assistant, Under-graduate
Swedish University of Agricultural Sciences
06-08/2013

- Computational work mapping the genome of the agricultural pathogen *Plasmodiophora brassicae*.

Experience in academic teaching

- Teaching assistant 2024: Starter and functional microbes for innovation, authenticity and healthy status (course code: 44706B) – Module: The food - human axis for driving the gut microbiome (16h). Free University of Bozen-Bolzano. Post-graduate course.
- Supervision of several master students thesis' work, both in the lab and computationally

Skills

- Laboratory: BSL3** laboratory, Ancient DNA (aDNA) clean lab, ISO accredited lab.
- Molecular: DNA extraction, **NGS library preparation (Illumina platform)**, **target capture enrichment, PCR**, **qPCR**, microbial cell culture
- Computer and programming: Linux/Unix shell scripting (BASH), computer cluster environment (SLURM), R and python programming languages. Version control systems (Git, Bioconda, snakemake). Next Generation Sequencing data analysis and bioinformatics pipelines, eg. short-read sequence alignment (e.g. samtools, bbmap, BWA, bowtie), multiple sequence alignment, variant and SNP analysis, PCA, de novo assembly (megahit, metaspades), functional genomics, 16S metabarcoding analysis (Qiime, DADA2, phyloseq, vegan, Bioconductor), transcriptomics (FeatureCounts, Deseq2), taxonomic classification, etc. Bioinformatics tools and public databases, e.g. BLAST, NCBI, Genbank, SILVA, KEGG. Predictive modeling with artificial neural networks and random forest (keras and tensorflow).

Other academic responibilities

- Responsible for the organization of the group and bioinformatics meetings of the Institute for Mummy Studies.
- Organizing member of PhD writing meetings at Eurac Research

Publications

Granehäll L., Sarhan, M.S., Thorell, K., et al. Reconstructing the ancient *Helicobacter pylori* genome of an 18th century mummy from Basel, Switzerland. *In review*.

Seersholm, F.V., Sjögren, KG, Julia Koelman, J. et al. Repeated plague infections across six generations of Neolithic Farmers. Nature (632) 114–121. https://doi.org/10.1038/s41586-024-07651-2

Gretzinger, J., Schmitt, F., Mötsch, A. et al. Evidence for dynastic succession among early Celtic elites in Central Europe. Nature Human Behaviour (8) 1467–1480. https://doi.org/10.1038/s41562-024-01888-7

Tlais, A.Z.A., Polo, A., **Granehäll, L.** et al. Sugar lowering in fermented apple-pear juice orchestrates a promising metabolic answer in the gut microbiome and intestinal integrity. Current Research in Food Science (9) 100833 https://doi.org/10.1016/j.crfs.2024.100833

Mastrolonardo, F., Costantini, A., Polo, A., Verni, M., Wilson, J., Tlais, A. Nikoloudaki, O., **Granehäll, L.,** Gobbetti, M., Pontonio, E., Di Cagno, R. New fermented plant-based ingredients in sourdough breads enhanced nutritional value and impacted on gut microbiota (2024). Future Foods. https://doi.org/10.1016/j.fufo.2024.100498

Nikoloudaki, O., Celano, G., Polo, A., Cappello, C., **Granehäll, L.,** Constantini, A., Vacca, M., Speckmann, B., Di Cagno, R., Francavilla, R., De Angelis, M. & Gobbetti, M. Novel probiotic preparation with in vivo gluten degrading activity and modulatory effects on the gut microbiota (2024). Microbiology Spectrum. https://doi.org/10.1128/spectrum.03524-23

Galli, B., Nikoloudaki, O., **Granehäll, L**., Carafa, I., Pozza, M., De Marchi, M., Gobbetti, M & Di Cagno, R. Comparative analysis of microbial succession and proteolysis focusing on amino acid pathways in Asiago-PDO cheese from two dairies (2024). International Journal of Food Microbiology. https://doi.org/10.1016/j.ijfoodmicro.2023.110548

Larena, M., McKenna, J., Sanchez-Quinto, F., Bernhardsson, C., Ebeo, C., Reyes, R., Casel, O., Huang, J.-Y., Hagada, K. P., Guilay, D., Reyes, J., Allian, F. P., Mori, V., Azarcon, L. S., Manera, A., Terando, C., Jamero, L., Jr., Sireg, G., Manginsay-Tremedal, R., Labos, M. S., Vilar, R. D., Latiph, A., Saway, R. L., Marte, E., Magbanua, P., Morales, A., Java, I., Reveche, R., Barrios, B., Burton, E., Salon, J. C., Kels, M. J. T., Albano, A., Cruz-Angeles, R. B., Molanida, E., **Granehäll, L**., Vicente, M., Edlund, H., Loo, J.-H., Trejaut, J., Ho, S. Y. W., Reid, L., Lambeck, K., Malmström, H., Schlebusch, C., Endicott, P., Jakobsson, M., Philippine Ayta possess the highest level of Denisovan ancestry in the world. Current Biology 2021, (31), 1-12. https://doi.org/10.1016/j.cub.2021.07.022

* ***Granehäll L***., Huang K.D., Tett, A., Manghi, P., Paladin A., O'Sullivan N., Rota-Stabelli, O., Segata N., Zink A., Maixner F. Metagenomic analysis of ancient dental calculus identifies a yet unexplored evolutionary complex diversity of oral archaeal *Methanobrevibacter*. 2021. Microbiome 9:197. https://doi.org/10.1186/s40168-021-01132-8

Larena, M., Sanchez-Quinto, F., Sjödin, P., McKenna, P.J., Ebeo, C.,Reyes, R., Casel, O., Huang, J.-Y., Hagada, K. P., Guilay, D., Reyes, J., Allian, F.P., Mori,V., Azarcon, L. S., Manera, A., Terando, C., Jamero, L., Sireg, G. Manginsay-Tremedal, R., Labos, M. S., Vilar, R. D., Latiph, A., Saway, R. L. , Marte, E., Magbanua, P., Morales, A., Java, I., Reveche, R., Barrios, B., Burton, E., Salon, J. C., Kels, M. J. T., Albano, A., Cruz-Angeles, R. B., Molanida, E., **Granehäll, L.**, Vicente, M., Edlund, H., Loo, J.-H., Trejaut, J., Ho, S. Y. W., Reid, L., Malmström, H., Schlebusch, C., Lambeck, K., Endicott, P. & Jakobsson, M. (2021). Multiple migrations to the Philippines during the last 50,000 years. Proceedings of the National Academy of Sciences, 118(13), e2026132118. https://doi.org/10.1073/pnas.2026132118

Hollfelder, N., Babiker, H., **Granehäll, L**., Schlebusch, C. M. & Jakobsson, M. (2021). The genetic variation of lactase persistence alleles in Sudan and South Sudan. Genome Biology and Evolution. 13(5) https://doi.org/10.1093/gbe/evab065

Maixner, F., Thorell, K., **Granehäll, L**., Linz, B., Moodley, Y., Rattei, T., Engstrand, L. & Zink, A. (2019). *Helicobacter pylori* in ancient human remains. World J Gastroenterol, 25(42), 6289-6298. http://dx.doi.org/10.3748/wjg.v25.i42.6289

Further data

Oral presentation: Granehäll, L. Exploring ancient dental calculus: uncovering the diversity of the oral microbiome through metagenomic analysis. GEM-CAP Symposium, Cairo, Egypt. November 30 – December 02

Oral presentation (selected): Granehäll L., Huang K.D., Tett, A., Manghi, P., Paladin A., O'Sullivan N., Rota-Stabelli, O., Segata N., Zink A., Maixner F. Metagenomic analysis of ancient dental calculus reveals unexplored diversity of oral archaeal *Methanobrevibacter*. WMC 2022: 10th World Congress on Mummy Studies, September 5-9th 2022

Oral presentation (selected): Granehäll L., Huang K.D., Tett, A., Manghi, P., Paladin A., O'Sullivan N., Rota-Stabelli, O., Segata N., Zink A., Maixner F. Metagenomic analysis of ancient dental calculus reveals unexplored diversity of oral archaeal *Methanobrevibacter*. ISBA9: 9th International Symposium on Biomolecular Archaeology, June 1st-4th 2021

Poster presentation (selected): Granehäll L., Huang K.D., Tett, A., Manghi, P., Paladin A., O'Sullivan N., Rota-Stabelli, O., Segata N., Zink A., Maixner F. Metagenomic analysis of ancient dental calculus identifies a yet unexplored evolutionary complex diversity of oral archaeal *Methanobrevibacter*. ISME Virtual Microbial Ecology Summit, 11-12 November 2020

Statement of interest

I am applying to the position of commissioned researcher with Prof. Raffaella Di Cagno as my professional experience with molecular genomic laboratory work and experience in food microbiology would enable me to make an excellent contribution to the project.

I have extensive experience with preparing metagenomic libraries for NGS sequencing within the Illumina platform both from my PhD studies at the Institute for Mummy Studies at Eurac research and from my time as a research assistant at the Human Evolution group at Uppsala University. In both instances I extracted DNA from hundreds of samples, prepared dual-index libraries which were pooled for multiplex Illumina sequencing. I also organized and ordered the indexed primers for the entire Institute, and increased reducing the risk of index-hopping and within each sequencing run.

Furthermore, I have excellent knowledge of detecting low-abundant species from complex matrices, e.g. different food matrices, but also ancient human remains. My master thesis was conducted at the Swedish National Food Agency, where I worked on the validation of detecting enterohemorrhagic *Escherichia coli* (EHEC) markers in different food matrices, a project I continued working on as a research assistant. Working at the Mummy Institute, I improved the detection of *Helicobacter pylori* in complex metagenomic matrices from ancient human remains by developing an in-solution enrichment capture for low-abundant target DNA. By including multiple reference genomes as genetic targets, I increased the chance of detecting unknown strains of the bacteria.

All together, I am an excellent candidate for the commissioned researcher position due to my knowledge on working with Illumina libraries species detection in food. I have a strong personal interest in food microbiomes, and would love to work on this project to further the research in this area. I am looking forward to using what I learned during my work and implementing my knowledge in your research project.

Language competence	**Swedish** (Native) **English** (C1); Internal Unibz certification (Language center of Free University of Bozen-Bolzano) **Italian** (B1); Internal Unibz certification (Language center of Free University of Bozen-Bolzan)
Driving license	AM B