

2.1.1. Annual highlights

CEH's fourth year has been one of consolidation, in which we not only made significant progress on addressing the research questions initially outlined in our proposal, but also held our COVID-delayed DNRF Center Conference and performed considerable outreach aimed at both our scientific peers globally, school pupils and the general public in Denmark. The conference was held at Rungstedgaard in May, thanks to an additional financial award from the DNRF and involved 20 invited experts from all around the world, who spent two days with our CEH staff to discuss the future potential of evolutionary hologenomics. With regards to outreach at the public level, in addition to contributions to events such as Forskningens Døgn and Kulturnatten, and teaching at schools and Folkeuniversitet, we are particularly pleased with the release of a complete theme issue on hologenomics (in Danish) for Biologiforbundets magazine, 'Kasketot' read by science school teachers. The theme issue consists of five articles, with content spanning a general introduction to the new field of hologenomics, human health, and the applied aspects of how hologenomics can make food production more sustainable, as well as an assignment about the microbes in the everyday life of the pupils. We further entered a collaboration with the largest digital learning platform in Denmark, Alinea, to develop 6.5 lectures of online teaching in hologenomics aimed at 8th-9th graders, which was released in early 2024.

In the context of research and education, CEH's staff continue to be productive. Not only did many of our staff attract grants, including three Marie Curie Fellowships, but we also saw an increasing number of BSc and MSc students trained, as well as four PhDs graduated. Overall, research is moving forward on almost all of our initial proposed goals. In RL1, implementing our Full Hologenomics approach, we have continued technical development in both the lab and computationally, allowing us to take the lead in several reference genome and microbiome dataset generations, e.g. Yggdrasil and the Earth Hologenome Initiative (EHI), as well as make publicly available workflows for all steps from sample collection to data analysis. In RL2, our central Metagenomic Space concept is in the final review, and we are making major steps forward with regards to deciphering what shapes this space, including through novel use of genome editing and epigenetics as well as organoid and gut-on-a-chip technology, and the development of mathematical models to describe the process. In RL3, which examines ongoing eco-evolutionary processes, our expanded team means we are applying our approaches to a broad range of vertebrates (principally, although occasionally other systems such as plants that provide complementary insights), in questions ranging from competition to behaviour, to the parallel evolution of adaptive traits. In RL4, which explores the hologenomic basis of major evolutionary transitions, we have made major progress on one of our two key themes - domestication. In particular, through systems including foxes, chickens, and dogs, we have shown how domestication-related behaviour can be rapidly shaped through hologenomic interactions. While progress attacking our other RL4 theme, evolution of herbivory, is lagging due to challenges in the available public datasets, thanks to the progress of the EHI we anticipate that within the next year we will be able to use our standardised and curated datasets to make major advances here. And our last central Research Line (RL5) continues to develop novel insights into the role of fermentation in expanding the human metagenomic space. Lastly, we continue to complement our central Research Lines with ongoing developments in the more applied and medical contexts, with multiple papers on a range of relevant agricultural systems, including fish and chickens.