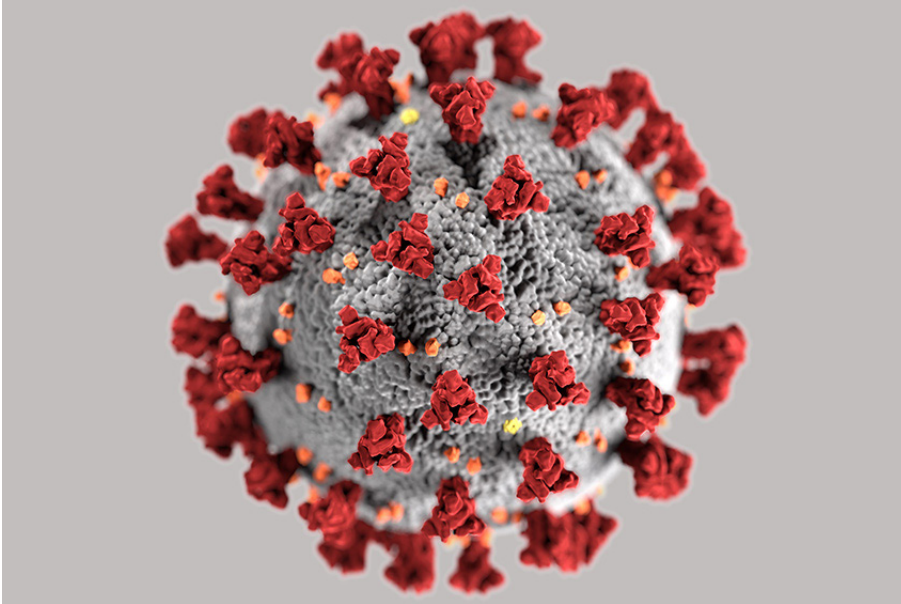




# IEMNews



Several projects on COVID-19 are currently underway at the IEM (see [www.iem.uzh.ch](http://www.iem.uzh.ch)). Among these initiatives is a blog aimed at a wider public audience. The first blog entry by **Prof. Adrian Jäggi** is reprinted here in a shortened version.

## The evolution of the new coronavirus: Where did it come from, and where is it going?

A study published in mid-March argues convincingly that the virus had a natural origin: the scientists examined the genome of SARS-CoV2 and compared it with SARS-CoV, the cause of SARS in 2002, and other related corona viruses found in bats or pangolins. Of particular interest is the DNA sequence responsible for the entry of the virus into the host cell. In SARS-CoV2, this sequence is identical to that of viruses in pangolins, but quite different to SARS.

Furthermore, the identical entry sequence in the pangolin indicates that the virus has been transmitted from these animals to humans. However, the rest of the viral genome is similar to the corona viruses found in bats, suggesting that bats are the original reservoir, as in SARS and MERS. More recent studies confirm the similarity to bat viruses and thus the high probability of a natural origin, but it will probably take some time before the exact transmission chain can be definitively reconstructed (in the case of SARS it took 15 years).

Another debate concerns mutations. Viruses mutate constantly, but this is not in itself a cause for concern, as most mutations do not alter the function of the virus. Comparisons of the virus genome helps to understand the phylogeny of the virus; this approach has shown, for example, that SARS-CoV2 was most likely first transmitted to humans in early December 2019, and in many places has been spreading undetected for a long time. It is possible, but unlikely, that SARS-CoV2 will evolve in a direction that makes it more or less harmful to humans.

Viruses must reproduce as efficiently as possible, just like real living beings – the characteristics of the virus that produces the most copies of itself will prevail in evolution. This means, on the one hand, that viruses should be maximally virulent, i.e. use the host to make as many copies of themselves as possible. On the other hand, the viruses must also make sure that they do not kill the host before they have been able

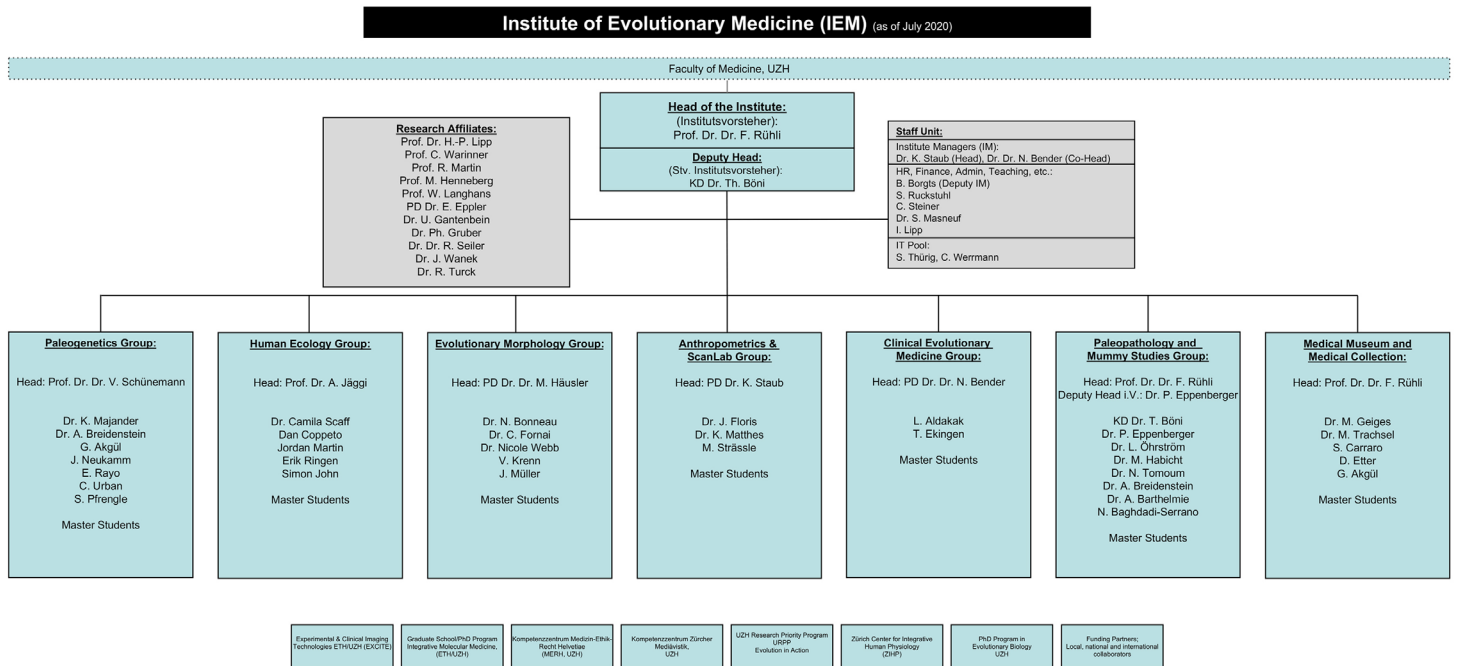
to infect a new host, otherwise they are in an evolutionary virulence and transmission, the dead end. Hence there is a trade-off between so-called «virulence-transmission tradeoff».

So, theoretically, it could be that a mutation occurs that makes a virus more harmful. What happens then depends on how easily this new virus is transmitted. If transmission is easy, the new form of the virus could prevail because it exploits the host more efficiently. This argument is often made in connection with the so-called Spanish flu of 1918/19, when the confined space in the trenches and hospitals of the World War 1 facilitated transmission.

Conversely, a pathogen could become less harmful in the course of evolution if its transmission becomes increasingly difficult. In so far as our behaviour influences the transmission, we can control virulence evolution! This also throws a whole new light on today's measures against COVID-19 such as social distancing, washing hands, etc. - in principle, we are not only protecting ourselves and preventing the pandemic from spreading, but we may even select a «tamer» version of the virus.

*Prof. Dr. A. Jäggi*

# IEM organigram



## Vision and mission statement

We are a leading international and globally connected research, teaching and service institute which is part of the medical faculty at the University of Zurich. We analyse ancient biological material and associated data to better understand modern human health issues and diseases. Due to specialist scientific expertise, excellent infrastructure and state-of-the-art methodologies, we are able to work on various interdisciplinary research questions in the context of the field of Evolutionary Medicine. Our core competencies include:

- In the area of morphology: Clinical Anatomy; Variability and adaptation of body morphology as a function of sex, robustness, time (Microevolution), socio-economic factors (etc.); Macroevolution of joint pathologies.

- In the area of imaging: application of modern imaging techniques (MRI, terahertz) on historical tissues; Radiological diagnosis of pathologies.

- In the area of ancient DNA: Co-evolution of diseases and the human genome (evolution of human pathogens, microbiome analyses etc.).

- Maintaining the historic Medical Collection for both scientific research and inter-museum exchange.

- Ethical considerations for research on historical human tissues.

We will increase the recognition of the research field of Evolutionary Medicine and expand academic teaching of the subject within and outside the Faculty of Medicine. This will be of a sustainable value for our stakeholders at the University of Zurich, in the research community of evolutionary medicine and adjacent areas, to the economy and ultimately for society in general.

## Words from an external collaborator



Matthieu Honegger,  
Professor of Archaeology,  
University of Neuchâtel

I have been working on the pre- and protohistory of the Nile Valley for 25 years, conducting excavations every year in the Kerma region of northern Sudan, which is the centre of the first kingdom of Nubia. My team is composed of researchers (archaeozoologists, bioanthropologists, environmentalists) and students (masters, PhD candidates). In addition to the excavations and research work, we are involved in the protection of the main archaeological sites, as well as their valorisation and mediation, notably through the realisation of the museography of the Kerma museum, founded following a partnership between Switzerland and Sudan. Our activities on site have made it possible, among other things, to excavate four cemeteries from different periods, marking on the one hand the transition between hunter-gatherer societies and Neolithic societies, and on the other hand the transition towards a state society, thanks to the excavation of the first stages of the Royal Cemetery of Kerma. The latter represents one of the major sites in the Nile Valley, covering 70 hectares and containing more than 30,000 tombs. We have thus built up an important anthropological collection consisting of several hundred skeletons.

Three years ago, I was contacted by Frank Rühli to consider a possible collaboration. The panel of analyses proposed by the Institute of Evolutionary Medicine was much wider than our previous work in bioanthropology, both in terms of field study methods (e.g. access to a portable scanner) and analyses, integration of ancient DNA and stable isotopes and also advanced studies of paleopathology. The combination of such approaches made it possible to finally tackle problems linked to the settlement of the region, the health status of the populations, their diet and subsistence patterns, the origin of the individuals and of course the family ties that may unite them. This is how we conceived an interdisciplinary Sinergia project of the SNF, integrating our Institute of Archaeology, that of Frank Rühli (Paleopathology and Mummy Studies Group) and that of Verena Schünemann (Paleogenetic Group). The aim was not to focus solely on the Kerma sites, but to envisage a much broader study, including samples from Egypt and Sudan. The project includes 1200 skeletons from 31 sites, and addresses the issues of settlement and health status in the Nile Valley using a multiscale approach, combining three levels of analysis, from the most global in terms of territory, to the most detailed meaning high precision work on a single, very well documented cemetery. This is an exciting project due to its scale and multidisciplinary scope, and we can only hope that it will soon be accepted for funding to quickly begin this collaboration with the Institute of Evolutionary Medicine.

## Words from a new member of the IEM



Kerttu Majander, Ph.D  
Postdoc Research Assistant  
Paleogenetics Group

I have a background in medical genetics and genetic bioinformatics from my Bachelor's and Master's studies at the University of Helsinki, Finland. Since starting my PhD in the Archaeo- and Paleogenetics group at the University of Tübingen in 2014, I've familiarized myself with several sides of ancient DNA research. In the last years, I have worked on skeletal collections from my native country, inspecting the genetic population history of Finnish people, as well as the bacterial fauna found in historical individuals, spanning from oral metagenomics to infectious agents. In 2016, a Finnish ancient DNA project (SUGRIGE) was founded to investigate the population genetics of North-Eastern Europe through time, especially concentrating on the Finno-Ugrian language speaking groups. This project was the first one in Finland to employ physical remains from archaeological sites, necessitating a collaboration with a more established ancient DNA research centre, Max Planck Institute for the Science of Human History, Jena, Germany,

where I worked on these topics as a visiting researcher for three years. During this time, we revealed novel aspects of the northeastern Europeans, such as an early eastern connection of Finnish and closely related populations, characterized in a Siberian-type ancestry. Last year, I had the opportunity to join the Paleogenetics Group at the Institute of Evolutionary Medicine at the University of Zürich for a new, exciting academic chapter. Together with prof. Verena Schuenemann, and supported by the Swiss National Science Foundation, we embarked on a project "Towards the Origins of Syphilis", which aims to illuminate the past spread of treponemal diseases and their co-evolution with the human host, using ancient human remains from around the world. The pilot study from this project resulted in a recent publication, where the historical North-European individuals proved once more a valuable source of information: The samples from early modern period Finland and Estonia yielded the first genomes of ancient causative agent of syphilis ever recovered from the European continent. Currently, I am looking forward to expanding my research on ancient pathogens in my post-doctoral work and deepen the various collaborations on this front in the highly enjoyable, international atmosphere of the IEM and University of Zürich.

## IEM-publications (selected publications since last IEM News December/2019)

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## New IEM-members

The IEM is happy to welcome the following members to the institute:

- Adam Daniel Hunt, M.A., PhD Student, Human Ecology Group
- Alexander Barthelmie, Dr. med., Assistant, Paleopathology and Mummy Studies Group
- Megan Malherbe, MSc., PhD Student, Evolutionary Morphology Group
- Antoinette Goujon, MSc Student, Evolutionary Morphology Group
- Esther Käch, Dr. med. Student, Paleogenetics Group
- Michela Lanfranchi, Dr. med. Student, Paleopathology and Mummy Studies Group
- Sandra Willi, Dr. med. Student, Clinical Evolutionary Medicine Group
- Mirella Woodert, MSc Student, Evolutionary Morphology Group
- Jonas Müller, Dr. med. Student, Evolutionary Morphology Group

### Editorial

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