

Frontiers in DNA sequencing

On June 28th from 14.30 to 17.30 at the University of Milan the latest developments in plant and animal genomics will be discussed.

The meeting, sponsored by the Ordine Nazionale Biologi, will be articulated into two phases. In the first part, representatives of two leading companies will present the most up-to-date technologies they have developed for sequencing and assembly of genomes: long-reads (Pacific Biosciences) and optical maps (Bionano genomics). These technologies allow to generate high-quality genome assemblies and many other applications that will be covered during the event.

In the second part, the Vertebrate Genomes Project (VGP, <https://www.rockefeller.edu/research/vertebrate-genomes-project/>) will be presented. This is one of the most ambitious and fascinating ongoing international genomic projects in the world. The VGP employs the above technologies to produce reference level genomes for all 66,000 living vertebrate species. Due to their complexity and size these genomes are the hardest to sequence.

VGP members include several world-renowned research centers, comprising the Vertebrate Genomes Laboratory at Rockefeller University (New York, US) the Wellcome Sanger Institute (Hinxton, UK) and the Max Planck Institute of Molecular Cell Biology and Genetics (Dresden, GE).

From the beginning of 2018, Prof. Nicola Saino and Dr. Giulio Formenti, from the Department of Environmental Science and Policy of the University of Milan, actively collaborate to the VGP with the aim of producing an ultra-high quality genome assembly for the European barn swallow (*Hirundo rustica rustica*). Currently, they are the only Italian partners of the project.

The VGP will be presented directly by its coordinator, Prof. Erich Jarvis (Rockefeller University), who will illustrate the reasons that prompted this tremendous effort and its implications. The presentation will be introduced by the experimental data on the barn swallow genome obtained by Prof. Nicola Saino and Prof. Luca Gianfranceschi, and subsequently manipulated by two bioinformaticians of the Department of Bioscience of the University of Milan, Prof. David Horner and Dr. Matteo Chiara. During the event, representatives from the Functional Genomics Center of Zurich, the sequencing facility of the ETH (Zurich, CH) that generated the sequencing data, will present the technologies and applications available at their center.