





POPULATION GENOMIC analysis in a BIRD NON-MODEL SPECIES

<u>Riccardo Rossi¹</u>, Guido R. Gallo², Giulio Formenti³ Luca Gianfranceschi²

E-mail: r.rossi44@campus.unimib.it

¹ University of Milan – Bicocca (Milan, Italy)

- ² University of Milan (Milan, Italy)
- ³ The Rockefeller University (New York, NY, USA)

Keywords: genomic, structural variants, birds, bioinformatics, population genomics, barn swallow, bird migration

Abstract:

The barn swallow (*Hirundo rustica*, Hirundinidae, Passeriformes) is an iconic bird and a flagship species for conservation biology. Despite intense research efforts, this bird still poses several fascinating and unresolved scientific questions, such as structure of genetic variation within breeding populations. Similarly, the genes responsible for existing, extensive phenotypic variation at phenological, morphological and behavioural traits, including major fitness components, still have to be identified. Yet, unveiling these genes is of pivotal importance to our understanding of the ecological and evolutionary population processes, especially in an era of human-driven environmental change. Understanding the genetic bases of such adaptations could be crucial for conservation purposes.

Thanks to the long-reads sequencing costs dropping and the improvement of bioinformatic tools, deeper genomic populations analyses are becoming much more affordable, also in non-model species such as the barn swallow.

We performed whole genome sequencing (WGS) of 127 samples of barn swallow, using PacBio High Fidelity (HiFi) long-read sequencing technology. Blood samples came from 3 different countries: Italy, Spain and Israel. The first two populations belong to the subspecies *H. r. rustica*, and their migration over the Sahara, taking two different routes, is well known. The Israeli population belongs to the *H. r. transitiva* subspecies, which is documented as resident or short-distance migrant. HiFi long reads were used to generate a dataset of different types of structural variants for downstream analyses. The final aim of this study is to have a better understanding of barn swallow populations structure and differentiation among subspecies, together with finding genes involved in migration and phenotypic traits.