

## Deciphering Urban Adaptation: Multi-omics insights from Italian pollinators

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### Abstract:

Pollinator insects, such as bees, play a crucial role in ecosystem functioning and food security. However, in the last decades their biodiversity and wellbeing have been affected worldwide by different anthropic stressors, such as urban expansion. To understand how pollinators adapt, both phenotypically and genotypically, to urban habitats, we collected a solitary bee, namely *Osmia cornuta* (Latreille, 1805) and two bumblebee species, namely *Bombus terrestris* (Linnaeus, 1758), *Bombus pascuorum* (Scopoli, 1763) in 4 Italian cities. The sampling campaign was concluded last summer with a total of 300 bee individuals from 24 sampling sites in Milan, Rome, Turin, and Florence, including both urban and semi-natural areas. To address our aim, we are using a multi-omic approach combining genomic, transcriptomic and metabolomic analyses. Through whole genome sequencing we are aiming to assess the presence of regions under selection by urban habitats. With mRNA sequencing we are focusing on identifying differentially expressed genes between urban and semi-natural populations of the 3 different species. Finally, using LC-MS, we are investigating the influence of urbanization on metabolites production to evaluate if metabolisms were influenced by anthropic stressors.

Preliminary results from metabolomic and transcriptomic analyses confirm clear differences between urban and semi-natural populations. Regarding bumblebees collected in Milan, we obtained promising results showing possible signs of phenotypic adaptation. Specifically, lysophospholipids, metabolites of phospholipases, are more abundant in individuals coming from urban areas. This is plausible in the light of their role in response to higher temperature, pollutants and pathogens, factors known to be characteristic of cities. For what concerns gene expression, it is evident from our data that a pool of differentially expressed genes is present in individuals coming from urban areas and each species analysed has a characteristic pool. As a future perspective, we plan on conducting bioinformatic analysis to integrate transcriptomic and metabolomic data so that we can identify the different metabolisms driving mechanisms of adaptation to urban environments. Our findings will be able to inform policymakers in managing urbanization processes' effect on wildlife and ecosystems. Specifically, our results will help in define new biomarkers able to assess Nature Based Solution and policies regarding urban green areas' effect on wildlife's health and wellbeing.