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### **S.29** AEROBIOLOGY. ADVANCES IN THE ATMOSPHERIC POLLEN RESEARCH AND CHALLENGES IN THE CONTEXT OF GLOBAL CHANGE. SESSION 1

#### **S.29.1** Metabarcoding and metagenomics techniques in monitoring airborne pollen

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The importance of monitoring the concentration of pollen in the atmosphere has been widely demonstrated from the environmental, ecological and agronomic point of view, as well as from the perspective of human health, since allergenic pollen represents the most important cause of pollinosis globally. Traditionally, pollen concentrations in the air are estimated from analyses based on identification and quantification using optical microscopy. However, the classification of pollen types at the species level using this procedure is limited. This is due to the morphological characteristics of the pollen grains used for their recognition, often shared within genera, families, and even taxonomic orders. An alternative approach is the identification of pollen through molecular sequencing and DNA analysis. Different high-throughput sequencing (HTS) technologies have been used to massively analyse environmental DNA and therefore the airborne pollen. This process requires, before sequencing, the preparation and amplification of the specific library for each sequencing platform. "Ion Torrent" (ThermoFisher), "GenapSys" technology and above all "Ilumina", represent several platforms that sequence with the metabarcoding procedure short DNA fragments (reads) up to a few hundred base pairs in length. Other platforms called "third generation sequencing" such as "PromethION", "GridION" and "MinION" from "Oxford Nanopore Technology" and "PacBio CCS" from "Pacific Biosciences", generate much longer reads (LR) than those obtained in the previous ones, however they are still little used in aerobiology. This study presents a review and the state of the art of airborne pollen studies based on metabarcoding and metagenomics, as well as the limitations of these molecular analyses.

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