Due to globalization (trade and tourism) and global warming, novel introductions and establishments of exotic mosquito species (EMS) in Belgium are expected to occur, based on interception data and suitability models developed for some invasive species in Europe. The introduction of potential disease vector species constitutes a threat to human and animal health. In this context, the Belgian government and regional authorities are funding a monitoring project (MCO) which aims at detecting and evaluating the occurrence of EMS in Belgium (focusing on six EMS with high invasive potential). The project is coordinated by the Institute of Tropical Medicine of Antwerp (ITM). Such species monitoring, however, requires reliable identification. Within this framework, the Barcoding facility for Organisms and tissues of Policy Concern (BopCo project - the Belgian federal in-kind contribution to LifeWatch), which aims at facilitating identifications of biological samples of policy concern, will collaborate with the ITM and validate the morphological identification of a subset of samples using DNA-based methods. Therefore, the present contribution evaluates diagnostic DNA RFLP and sequence data for each mosquito species (N=37; native and potentially invasive) recorded in Belgium, and elaborates a workflow for the identification of the collected mosquito samples.

Each dataset (DNA sequences from the online repositories and new barcodes) was subject to NJ tree reconstruction (K2P, 500 BS) and DNA barcoding gap analysis. From the 37 mosquito species, 24 can be identified with high reliability using the COI Folmer region exclusively (65%), including all six EMS of main concern. For six other species (16%), additional DNA data are proposed in the identification workflow presented hereunder. In the case of the *Aedes caspius / Ae. dorsalis and Ae. cantans / Ae. anulipes* species complexes, further study to develop specific identification techniques is required. A third species complex, *Ae. cinereus / Ae. geinus*, cannot yet be resolved due to the lack of available material for *Ae. geinus*. Finally, for Culiseta subochrea, not enough DNA data could be retrieved (N_r=1).

All native Belgian mosquito species (except seven), and the six investigated exotic mosquito species can be reliably identified using DNA-based methods, based upon data analyses of online repositories and subsequent testing. Further specific identification techniques for the seven remaining native species are currently investigated and/or developed in order to complete the identification workflow. Early interceptions of EMS and a rapid DNA-based identification are thus feasible and will help the authorities in their decision process. Ultimately, the project will build a DNA-reference collection of all life stages of Belgian native and exotic mosquito species.

**Monitoring of Exotic MOsquitoes in Belgium (MEO)**

Molecular validation of morphological species identifications

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