



ER-VEC 1.1, AN EMBRYONIC WEB APPLICATION FOR VECTOR-BORNE DISEASES DATA MANAGEMENT IN THE EMILIA-ROMAGNA REGION, ITALY

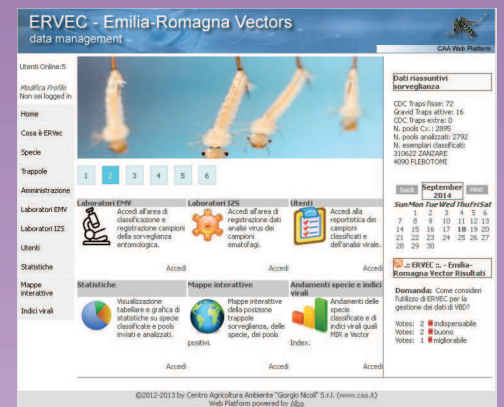
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Introduction

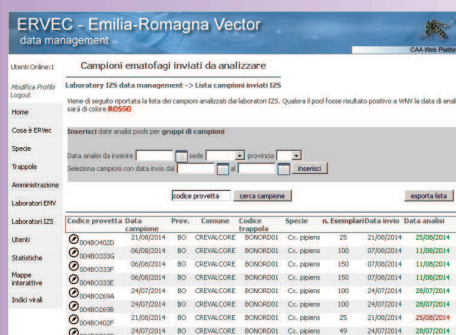
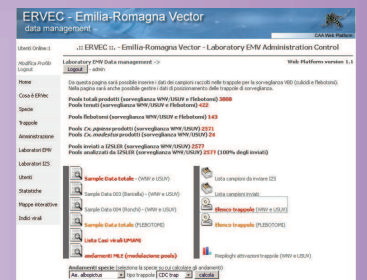
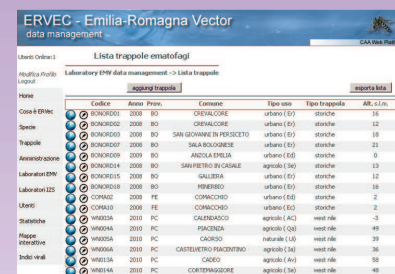
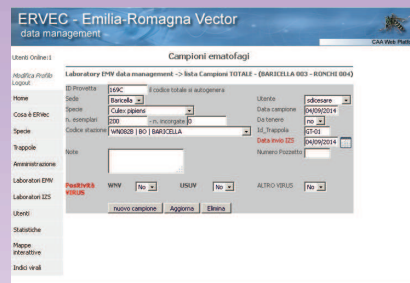
The data management in Vector Borne Diseases (VBD) surveillance may take advantage from structured databases where to store information produced by different entities. For this purpose we are developing an application for entomological data management for West Nile (WNV) and Usutu virus (USUV) and Toscana Virus (TOSV) surveillance in Emilia-Romagna region, Italy.

The application ER-Vec 1.1 (Emilia-Romagna Vectors), on-line from 2014 (ervec.caa.it), allows real time data sharing between entomological laboratories that collect field data throughout the network of 72 CO₂ and 16 gravid traps regularly activated during the season such as: geographical data (station coordinates), collected vector species (mosquitoes and sandflies), trap type (CO₂ traps or gravid traps), and virus laboratory screening results such as: identification dates and virus type identified (e.g. WNV, USUV or TOSV). Virus).



ER-VEC features

EMV LABORATORY (VECTOR SPECIES IDENTIFICATION)



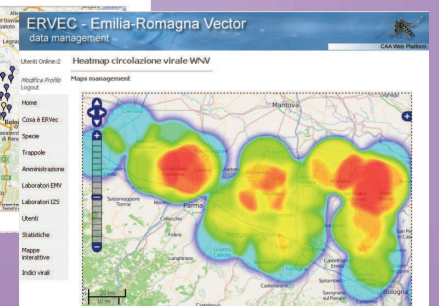
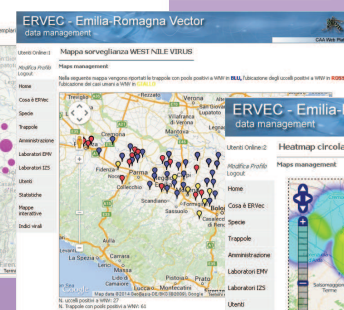
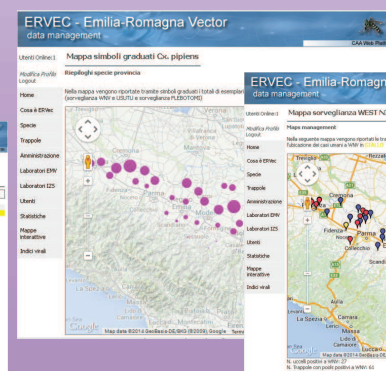
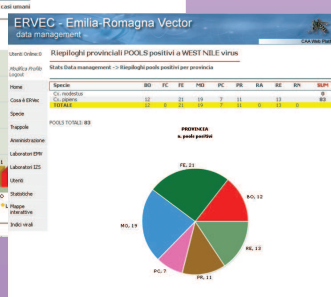
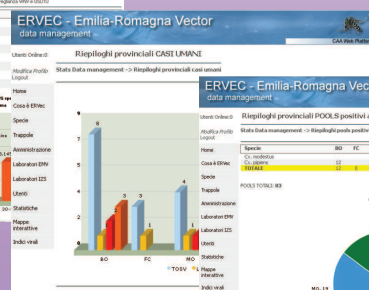
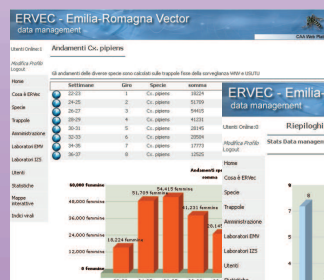
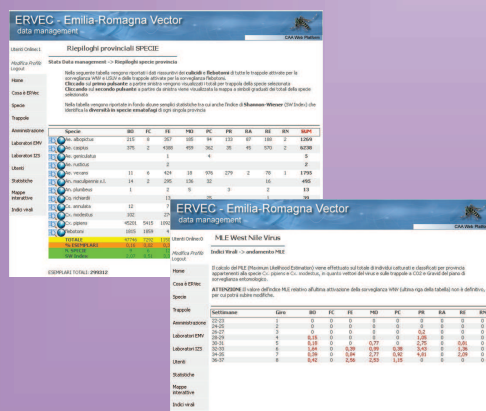
IZS LABORATORY (VIRUS IDENTIFICATION)

ER-VEC SYSTEM

USERS

USERS

USERS



REPORTS AND TABLES

INTERACTIVE GRAPHS

INTERACTIVE MAPS (graduated symbol maps, point maps, heatmaps)

All the data collected were entered in Er-Vec by specific forms to reduce errors. The web application was also integrated with interactive maps developed with Google Map APIs and OpenLayer, table statistics on species collected, pools analyzed, pools positive to WNV or USUV per province, vector species density trends, MIR (Minimum Infection Rate) and MLE (Maximum Likelihood Estimation) provincial trends for WNV and USUV and all these data, processed automatically, were shared with the surveillance involved institutions.

The application is under development to improve statistics outputs, automatic virus circulation maps and species distribution maps creation.