To the editor:

P. Ravanini et al. recently detected a small fragment of Japanese encephalitis virus (JEV)-like RNA in a Culex pipiens mosquito pool collected in autumn 2010 in northern Italy [1].

JEV is the prototype of a group of closely related flaviviruses which include West Nile virus (WNV) and Usutu virus (USUV). These viruses are circulating in birds, which are amplifying hosts, and in Culex sp. mosquitoes. Ardeid wading birds and pigs are amplifying hosts for JEV in Asia; humans and horses are sensitive hosts. Five genotypes of JEV have been described in Asia and some of them are widely distributed and most frequently associated with JE outbreaks and epidemics [2].

The spread of WNV in Europe over the last two decades with co-circulation of different viral lineages, as well as the emergence of USUV, initially in Austria in 2001, demonstrate that arboviral diseases of tropical origin may spread in temperate regions [3]. Environmental and climatic changes may also influence the distribution of these viruses in relation with migration patterns of birds.

As a consequence of the recent spread of WNV, entomological, and human/animal surveillance has increased in the recent years in several European and neighbouring countries. In addition, the use of generic PCR amplification techniques has widened the spectrum of viral investigations in collected specimens. Meanwhile the single detection of an RNA fragment of 157 bp with a sequence compatible with JEV has to be treated very cautiously in the absence of additional genomic amplifications of JEV RNA from the initial positive mosquito pool. In addition, contamination of the PCR cannot be completely excluded. This finding requires complementary studies to confirm the presence of JEV in Europe.

Previously Mani et al. [4] had reported JEV-like infection in passerine birds collected in Tuscany in 1996. The authors claimed that fragments on the viral E gene amplified from the organs of these birds were closely related to the Nakayama strain of JEV. This strain has been commonly used for vaccine production in Asia. Additional studies in Tuscany were inconclusive.

Research into the possible introduction of JEV to Europe should be conducted. Entomological investigations should be strengthened in habitats potentially suitable for JEV transmission in Europe and the use of generic flavivirus RT-PCR assays should be extended. Serological surveys in birds (in particular Ardeid wading birds) should include the differential diagnosis between WNV, USUV and JEV antibodies. Suspected neuroinvasive infections in humans and/or horses not confirmed as WNV or USUV infections, should be tested for JEV. As a second priority, serosurveys in pig-breeding farms located in the proximity of potential mosquito-breeding habitats such as rice paddies may also be conducted.

If the presence of JEV is confirmed in northern Italy, a risk assessment at the human/animal interface would need to be conducted to evaluate the public health consequences. As a result, the strategy for the laboratory differential diagnosis of neuroinvasive cases occurring in humans and also horses during the mosquito season may have to be modified to include JEV in the panel of viruses under investigation.

References