[32] SPREAD OF HPAIV H5N1 FROM SOUTH CHINA AGRO-ECOSYSTEMS THROUGH WILD BIRDS MIGRATION: A MULTIDISCIPLINARY APPROACH

Julien Cappelle (1)(2), Delong Zhao (2), John Takekawa (3), Scott Newman (4) and Xiangming Xiao (2)

(1) CIRAD-ES, UR AGIRs, F34398 Montpellier, France; (2) Oklahoma University, Center for Spatial Analysis, Norman OK, USA; (3) US Geological Survey, Western Ecological Research Center, Vallejo CA, USA; (4) FAO, EMPRES Wildlife Unit, Infectious Disease Group Animal Health Service, Animal Production and Health Division, Rome, Italy

Agricultural intensification in South China has increased densities of domestic ducks raised on intensively irrigated paddy fields, an important factor of the persistence of H5N1 highly pathogenic avian influenza virus (AIV) persistence. Some major wild bird congregation wetlands in South China have been partly turned into paddy fields where millions of free-grazing domestic ducks are raised. This may facilitate the contact and the circulation of AIV between poultry and wild waterbirds, reservoir of AIV. In this study we combined epidemiological, ecological, agricultural and virological data to investigate the potential role of wild birds in the long-distance spread of H5N1 HPAIV virus from South China. We used new technologies such as satellite-tracking of Wild birds, GPS tracking of domestic ducks, remote sensing of irrigated paddy fields, phylogenetic analysis of H5N1 strains isolated in wild and domestic birds. Our results show that: (i) wild birds share paddy fields, wetlands and AIV strains with free-grazing domestic ducks when wintering in South China, (ii) spring migration of wild birds from South China match spatially and temporally with the long-distance spread of HPAIV H5N1, (iii) epidemiological and virological data support the role of wild birds in this long-distance spread. This multidisciplinary study brings together different elements in favour of the long distance spread of H5N1 AIV from South China agro-ecosystems through wild ducks migration.