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Remote sensing based identification of environmental risk factors associated with West Nile disease in horses in Camargue, France

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Abstract

Geographic information system and remote sensing technologies were used to identify landscape features associated with risk of West Nile virus transmission as defined by the presence of confirmed horse cases. SPOT-4 images of Camargue area were used to generate a map of landscape categories of epidemic foci and the geographic information system was employed to determine the proportion of landscape components surrounding 10 horse case sites and 17 control sites.

The spatio-temporal analysis of the cases outbreak gave the best results for a spatial window of 9 km and a temporal window of 18 days. Two clusters were identified (relative risk = 3.35), both in the wet area of Camargue, near the town "Les Saintes Maries de la Mer". The first one was 4 km radius, the second 9 km.

The relationships between the presence of cases and proportions of landscape categories were analyzed using generalized linear model. The best model indicated that rice fields and dry bushes, wet "sansouire" and open water were the major components of the landscape that were associated with the presence of West Nile virus cases.

Keywords: West Nile virus; Horse; Risk factor; Remote sensing; Camargue; France

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1. Introduction

West Nile (WN) fever is a flaviviral infection transmitted by mosquitoes. Transmissions cycles of WN virus involve wild birds as principal reservoir hosts and mosquitoes as vectors (Komar, 2000). The virus has been isolated from 43 mosquito species, mainly of the *Culex* genus. Birds usually do not show any symptoms when infected. Occasional encephalitis, death or long term persistence of the virus have been reported. High, long term viremia, sufficient to infect vector mosquitoes has been observed. Migratory birds are instrumental in the introduction of the virus to temperate areas during spring migrations (Rappole and Hubalek, 2003).

Mammals, including humans and horses are incidental and dead-end hosts. Infected horses can exhibit signs of biphasic fever, followed by encephalomyelitis with staggering gait, hind limb weakness and paralysis, often leading to recumbency and death (Ostlund et al., 2000). The frequency of cases of inapparent infection in association with cases of clinical disease is difficult to establish.

Natural foci of West Nile virus infections are mainly situated in wetland ecosystems (river deltas or flood plains) and are characterized by the bird–mosquito cycle. In Europe, West Nile virus circulation is confined to two basic types of cycles and ecosystems (Komar, 2000):

- rural (sylvatic) cycle: wild, usually wetland birds and ornithophilic mosquitoes, and
- urban cycle: synanthropic or domestic birds and mosquitoes feeding on both birds and humans.

The first European isolations of the virus were recorded in 1963, from patients and mosquitoes in Rhone delta, and from patients and ticks (*Hyalomma marginatum*) in the Volga delta (Hannoun et al., 1964; Platonov et al., 2001). West Nile virus was subsequently isolated in Portugal, Slovakia, Moldavia, Ukraine, Hungary, Romania, Czechland and Italy (Hubalek and Halouzka, 1999). In France, two outbreaks were reported in the Camargue region, Southern France, during the summer of 1962 (Joubert et al., 1970) and during the late summer and autumn 2000 (Murgue et al., 2001). No abnormal deaths of birds were reported.

Since the 2000s outbreak, the Camargue area is considered as an endemic zone for WN virus. The Camargue is a region situated in the south of France, along the Rhone river delta. From an ecological point of view, the Camargue presents diversified environments, consisting of dry areas irrigated by canals, ditches and wetlands (Blondel and Isenmann, 1981; Hoffmann et al., 1968). These biotopes are favourable to both *Aedes* and *Culex* mosquitoes, which are potential vectors for the WN virus and populations of breeding and migratory birds, which are potential reservoirs. More than 300 bird species, including migratory and resident, are observed in this area. Thousands of horses live in this region.

In 1964, WN virus was isolated from *Culex modestus* (Hannoun et al., 1964) determining this species as a vector of WN virus in France. Since then, neither entomological studies nor sequentially collected samples have shown any other infected species (Murgue et al., 2001). Recent studies have investigated the potential of a variety of