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Presentation Abstract

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Presentation:	P260 - A meta-population model to explain an endemic Rift Valley fever transmission in Northern Senegal
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Abstract:	Rift Valley fever (RVF) is known to be endemic in the Ferlo area (northern Senegal) caracterized by temporary pools. In this region, *Aedes vexans arabiensis* and *Culex poicilipes* are known as the two main vectors of RFV, and the transmission of the virus is seasonal with a peak at the end of the rainy season. This seasonality and the persistence of the virus during inter-epizootic periods may be explained by 2 non-exclusive mechanisms:(i) each year, the virus may be introduced in the Ferlo area at the beginning of the rainy season by transhumant herds coming from northern and southern neighboring regions; (ii) the virus may survive in the area in dessicated and diapausing *Aedes* eggs. We represented this epidemiological system by a Susceptible Latent Infectious (SEI) model for both vector populations combined with a Susceptible Infectious Removed (SIR) model for small ruminant hosts. **A generic deterministic model of mosquito population dynamics forced by rainfall and temperature was adapted to both vector populations. This model incorporates eggs, larvae, pupae and adults stages biological parameters. It was calibrated, based on literature data, for population dynamic parameters: mortality rate of eggs, larvae, pupae and adults, sex ratio when hatching, and gonotrophic cycle duration.** This model provides the dynamics of both populations using local rainfall and temperature data. Predicted dynamics of both species were compared to trapping data collected in Senegal during 2014 and 2015 rainy seasons. For small ruminant hosts, the SIR model was structured according to sex and age, and incorporated the main host population dynamic processes: seasonal births, age-dependent mortality. It was parametrized using local field data and literature data for the incubation and viremia period durations. Transmission parameters (direct transmission rate, host/vector ratio) were estimated as in Nicolas et al 2014 Once calibrated, the model assesses different scenarios that may explain RVF endemicity in this area.