Peste des petits ruminants outbreaks in Morocco - 2008

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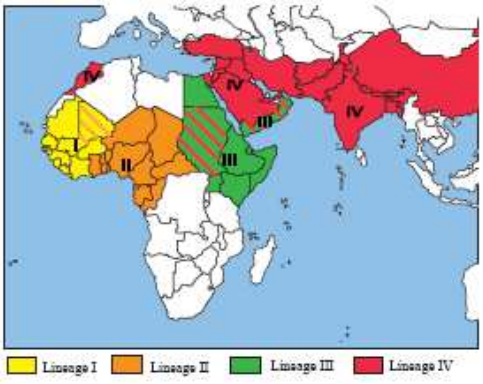

Fig 1 : Extent of PPR in the world

Introduction

Peste des Petits Ruminants (PPR) is a highly contagious and fatal disease of small ruminants such as sheep and goats with high morbidity and mortality. It is endemic in sub-Saharan Africa, Middle East and Asia, but it has never been described in North Africa before (Fig 1). In July 2008 two outbreaks were reported by the Moroccan veterinary services to the World Organization for animal Health (OIE). This notification was based on clinical and basic laboratory diagnostics carried out in Morocco. In CIRAD, Partial sequencing of the amplicons from infected tissue samples from the Moroccan epizootic confirmed that the causative agent was PPRV of lineage IV - a lineage circulating in the Middle East and Asia but not reported before from Africa.

Material and Methods

Due to the status of OIE reference laboratory, CIRAD received blood and organs samples from sick animals sent by the laboratory of vaccines BIOPHARMA Morocco during the first weeks of the outbreaks. A mission with experts in PPR was organised by FAO in August 2008 in this country. New organ samples were collected. Sera were analysed by C-ELISA based either on anti-N (CIRAD) or anti-H Mabs (Pirbright). Detection of PPRV RNA was performed by RT-PCR [1]. PCR products were directly used for sequencing for phylogenetic analysis [2]. Taqman real-time PCR (unpublished) was performed using the AgPath-ID one-step RT-PCR kit (Applied Biosystem). Both tests are using specific PPR primers/probe targeting the 3' end of the N gene. In Morocco, a full-scale campaign of vaccination of sheep and goats started on September 22nd using PPR vaccine produced by BIOPHARMA laboratory with the attenuated Nigeria 75/1 strain obtained from CIRAD and developed in collaboration with IAH.

Results

Twenty one out of 24 sera were positive or doubtful in both tests. Three out of 10 blood samples and 18 out of 24 organ samples were found positive at least in real-time PCR assay. Sequencing of part of the N PPR gene was done on 6 of those samples and the sequences obtain were compared with the other PPR strain sequences from our library. Inclusion of the Moroccan strains in the phylogenetic tree permitted its classification into lineage IV (Fig 3).

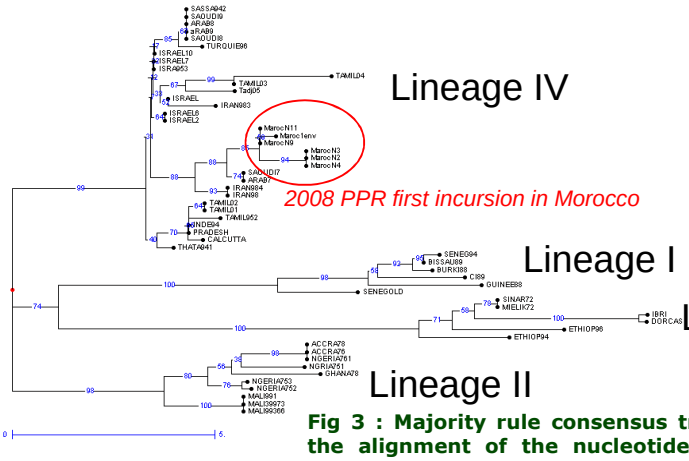

Fig 3 : Majority rule consensus tree of PPRV based on the alignment of the nucleotide sequences of the N protein gene («Neighbour-joining method »)

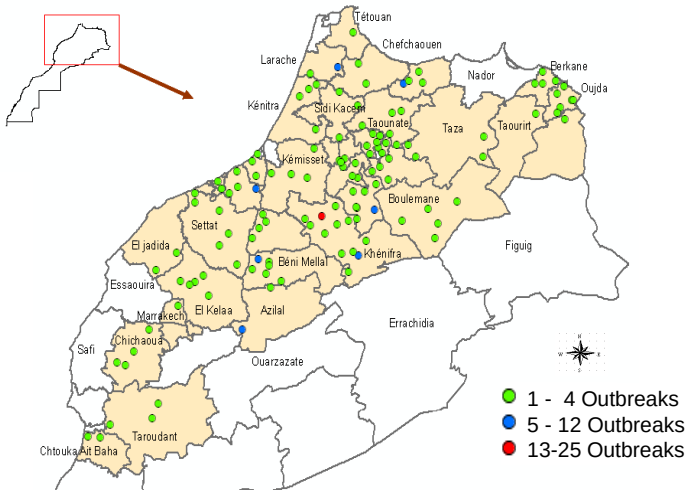

Fig 2 : geographical distribution of outbreaks in November 2008

By mid-November 2008, a total of 257 outbreaks were recorded in 36 provinces (Fig 2). On the 27/01/2009, after the implementation of mass vaccination with the attenuated PPR vaccine that began on the 22 November 2008 , the epidemic was considered as resolved.

Conclusion and discussion

The occurrence of PPR outbreaks in Morocco allowed us to genetically characterize the causal strain and this was shown to be of lineage IV together with other Asian and Middle-East strains whereas the others strains from Africa cluster in three lineages (I – III). The study demonstrate the value of the partial sequence of the N gene as traceability marker of strains to conduct epidemiological field studies. Combined with emergency response it maximizes the prevention of viral spread from infected area.

Acknowledgements

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References

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