A two steps sampling model to access OIE status of "list A bovine disease free zone" in areas where few data are available on bovine population and herd size.

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a) Summary

The model proposed takes into account the lack of information on bovine population characteristics in a zone where sampling has to be done to reach the OIE "disease free" status (7). It allows to assess the probability of identifying a positive zone before any field sampling is launched, depending on the status infected or not of that zone. Applied on data of a developing country zone, West Wellega (Ethiopia), the model seems effective for several values of its parameters. Prevalence distribution (within and between herds) and characteristics of the serological diagnostic test (especially specificity) mainly condition its effectiveness.

b) Introduction

Many developing countries having economic comparative advantage in livestock trade want to reach the OIE List A bovine disease free status. However lack of livestock-related organizations and weak health infrastructures make the use of OIE pathways difficult (8). Many sampling procedures have been suggested taking into account several parameters (herd diagnostic test, sensitivity and specificity of the diagnostic test, within herd prevalence…) (3,4,9,1, 5). All these methods rely on good field information's. The study area which data originated from, situated in the west of Ethiopia, was chosen because of availability of appropriate dataset from a census undertaken by researchers (CIRAD-EMVT/ILRI). It is a border zone with Sudan, a still infected country for some list A diseases and as such represents a sensitive zone when looking at transboundary animal movements between the two countries.

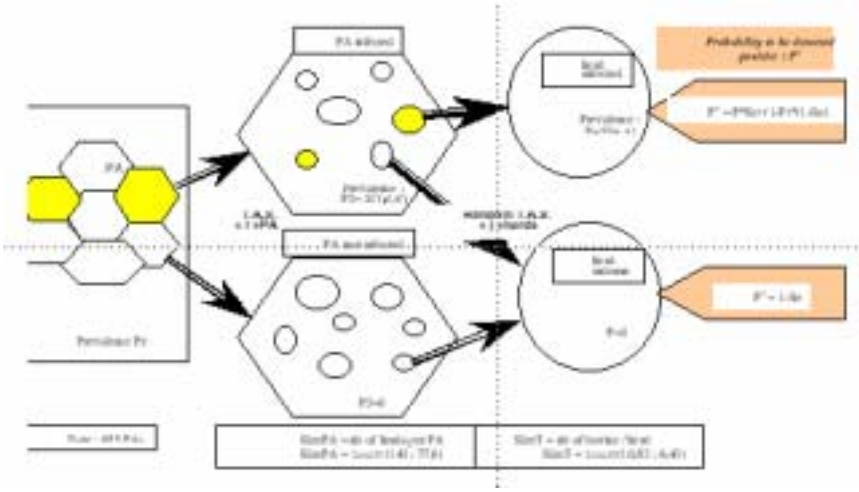
c) Objectives

The aim of this study was to propose and discuss a sampling method, usable where a few livestock data are available, and that could allow the qualification of zone "free" in accordance with the OIE requirements.

d) Materials & Method

In this two stages sample geographic or administrative units are firstly drawn and secondly herds are considered, after census is done in the secondary units selected (Figure1). The sampling units are described by distribution functions, different serological diagnostic test parameters are tested, the herd test is described by herd sensitivity (Se) and herd specificity (Sp) (6,4). The prevalence distributions (within and between herds) are described by Beta functions. The model shows the probability of identifying the area "positive" or "negative", according to its infected or free real status. Statistical analysis has been carried out using SAS©.

Figure 1 : schematic description of the model.



e) Results

This two stage sampling appears really efficient when the specificity of the diagnostic test used is very high (Sp=0,999), when the prevalence distributions are homogeneous and if we admit a cut-off at 1. A lower specificity definitely reduces the efficiency of the model. The influence of the prevalence distributions is clear (Table 1).

Table 1 : Results of the model in infected area according the sampling form and prevalence distributions p et p2. (Sp=0,999 ; Se=0,98 ; k=1)

		Probability of detecting the area "infected" (%)	
p2	p	10 herds/30PAs	30 herds/10PAs
B'1	B1	98,2	94,2
	B2	93,8	88,2
	B3	86,8	78,4
B'2	B1	95,2	89,2
	B2	89,4	82,8
	B3	81,6	67,2
B'3	B1	95	89,2
	B2	91,8	80,2
	B3	82,4	67

In infected and free zones, the best results were obtained for an homogeneous infection distribution in the area, even if there is a high correlation between herds in some secondary units. The sensitivity of the model decreases when the correlation between herds increases. The efficiency of the model is influenced by the number of primary and secondary units sampled. In a logical way the results show that in infected zone, model works better when there is more secondary units and less primary units for the same amount of tests. The difference is clearer when the correlation coefficient of the within herd prevalence distribution is high. Without any cut-off, this model can't show a difference between infected and free zones. A cut-off at "1" (the area is considered negative even if one herd is declared positive) leads to interesting results if the test chosen has a very good specificity.

f) Discussion

The results above show the influence of the parameters' choice on the efficiency of the model. According to the hypothesis made on these parameters, it is possible to test ex ante the efficiency of the method. That could be of a help for the planning of sampling. If the parameters which characterize the area of interest are those for which the model is efficient, it can be used. One of the main parameter, the correlation coefficient represents the evolution and the transmission of the agent infection in the sampling unit we consider. The quality of this data depends on our knowledge on the disease (here we mimic Rinderpest) to be identified and the risk of transmission (contacts between herds). We should be able to identify homogeneous groups of animals at given risk level and use it as a stratification modality in the model. Few parameters where arbitrary chosen. A better knowledge of the breeding context might slightly modify the interpretation in the area, leading to more strategic choices. Some others depend on hypothesis that need to be confirmed (10). The efficiency of the model could be estimate by the measurement of its negative predictive value: higher it would be, lower would be the error on the negative results of the model (2).

g) References

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