Short communication

Multifactorial correspondence analysis of risk factors for sheep and goat brucellosis seroprevalence

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Abstract

This paper reports the investigation of herd characteristics as potential risk factors for sheep and goat brucellosis seroprevalence, based on multifactorial correspondence analysis. The survey was carried out on 4123 herds in Trás-os-Montes e Alto Douro, in the north-east of Portugal. Brucellosis in small ruminants is a disease with Obligatory Notification status in Portugal and is the subject of an Official Eradication Campaign. Multifactorial correspondence analysis identified an association between herds with high seroprevalence (≥5%), intermediate seroprevalence (>0% and <5%), 3 or more positive animals, 2 positive animals, 1 positive animal, and larger herds (150 or more analyzed animals), and this group supplied contrasting results to the group of no positive animals and small herds. Within this study, larger herds were associated with milk production and intermediate seroprevalence values (of >0% and <5%), and contrast with those herds with 3 or more positive animals and high seroprevalence. The significant contribution made by the principal and secondary axes consolidates this explanation. The results of this study suggest that herd size and production type might have an impact on brucellosis seroprevalence.

Keywords: Multiple correspondence analysis; Risk factors; Small ruminants; Brucella; Seroprevalence

1. Introduction

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Brucella melitensis frequently occurs in sheep and goats and is highly pathogenic for humans, causing as it does one of the most serious zoonoses in the world (OIE, 2003; Benkirane, 2006). The disease is responsible for considerable economic losses to the small-ruminant industry (Blasco, 2006). In Portugal, this is a problematic disease in sheep and goats and is under the auspices of a National Eradication Program. The aim of this study was to assess, via a multiple correspondence analysis study, potential risk factors associated with brucellosis seropositivity in the north-east of Portugal (Trás-os-Montes) during 2004. Multifactorial correspondence analysis (MCA) is a method applied to discreet qualitative variables, especially nominal or ordinal ones (Matias, 2006). This analysis method is an exploratory multivariate...
technique that converts a matrix of non-negative data into a graphical display in which the rows and columns of the matrix are depicted as points (Greenacre and Hastie, 1987). In an MCA plot of the data’s attributes, the negative and positive attributes are represented as separate points (Torres and van de Velden, 2007). All multivariate analysis methods work by computing successive axes of decreasing importance called principal axes. MCAs reduce the data contained in large tables and allow us to see them in a vectorial plan. The degree of correlation among variables and/or observations is assessed by their relative proximity. Thus, the closer they are more correlated are they. The number of factor axes to be used is chosen based on a compromise between the degree of explained variability and interpretation simplicity. Scatter-plot clouds of variables and observations may also provide information about the underlying structure of the initial information matrix (Matias, 2006).

2. Materials and methods

2.1. Herds

A list of the herds of small ruminants surveyed for brucellosis by the Ministry of Agriculture’s Committee for the Eradication of Brucellosis was obtained for the north-east of Portugal. According to the list, in 2004 a total of 4707 herds were tested for Brucella melitensis infection in the Trás-os-Montes e Alto Douro region. To be considered eligible for the study all participating herds were required to supply information regarding sanitary interventions (blood sample collection), seropositivity, herd size, species, herd constitution (whether includes just one species or both), and type of production (meat or milk). Herds with incomplete information or with contradictory results (e.g., more seropositive animals than actual number of animals tested) were excluded. The study was carried out for 4707 small-ruminant herds. Herds were stratified based on the number of animals per herd into quartiles of: ≤30 animals; >30 and <150 animals; and ≥150 animals. The first quartile was ≤30 animals, the second and third quartiles >30 and <150 animals, and the fourth quartile ≥150 animals. A herd was considered as a sheep or goat herd if it had more than 50.0% of the predominant species and classified as a meat or milk herd if it had more than 50.0% animals that produced meat or milk. If the herd contained only one species (sheep or goat) it was considered pure, and classified as mixed if it had at least two animals of different species. A herd was considered to have the lowest possible seroprevalence if it had 0% of positive animals, intermediate seroprevalence if it had >0% and <5% of seroprevalence and high seroprevalence if it had ≥5% of seroprevalence. Also taken into consideration were the herds with no animals testing positive (zero), with one positive animal, with two positive animals, and with three or more positive animals. Some herds underwent one or more sanitary interventions (blood sample collections) over the course of the year. In order to avoid repeating the information collected, only the result of the first intervention was counted. This was except in those cases when animals tested positive in subsequent samples after previous blood samples collected had been negative.

2.2. Serology

The serological survey was conducted between January and December of 2004. Sampling was performed during the course of Portuguese National Eradication Program of Brucellosis. In brief, blood samples (10 ml) were collected from the anterior jugular of all adult animals in the herd and placed into EDTA-free glass containers. Blood samples were subsequently transferred to the Official Veterinary Laboratory. The two tests were carried out in series, in accordance with the herds’ brucellosis status. In herds not free from brucellosis, an animal was classified as positive when it was seropositive for antibodies against Brucella species via the Rose Bengal plate-agglutination test (RBT), as described by OIE (2003). The complement fixation test (CFT) was used in all animals with a negative RBT. The animals were classified as positive if the CFT was positive. In flocks free or officially free of brucellosis, the CFT was the test used to decide whether the animal should be sacrificed, and an animal was classified as positive if both the RBT and the CFT were positive. The RBT sensitivity and specificity values were 97.6% and 77.6%, respectively. The CFT sensitivity was 88.1% and was 100% specific (Blasco et al., 1994). Herd seroprevalence was adjusted by taking into account the apparent prevalence (AP) estimate as well as the sensitivity (Se) and specificity (Sp) of the applied tests (RBT and CFT) in the formula introduced by Rogan and Gladen (1978): TP = (AP + Sp − 1)/(Se + Sp − 1).

2.3. Statistical analysis

Multifactorial correspondence analysis (MCA) linked to risk factors in herds and the seroprevalence of sheep and goat brucellosis was carried out using ANDAD version 7.1, developed by the Instituto Superior Técnico, Centro de Valorização de Recursos Minerais/Instituto Superior Técnico de Lisboa, Portugal (CVRM/IST 2000). The correspondence analysis’ main result was a two-dimensional plot of the associations between qualitative, explanatory and outcome variables. It was assumed that the initial data had two clouds in two multi-dimensional vector spaces: one cloud for the columns (the variables studied) and one cloud for the rows (herds), which was not represented due to its high number (4707). The MCA succeeded in constructing factorial axes that enabled the modalities to be positioned according to their coordinates on the selected factorial map. MCA interpretation consists of: (a) assigning a meaning to the factorial axes, depending on the variables they are formed by and (b) interpreting the relationships between herds and variables using the aforementioned factorial axis meanings.

Two factorial axes were taken into consideration in this study. The two factorial axes were those whose variables
Fig. 1. Plot of multifactorial correspondence analysis (MCA) results among sheep and goat herds in the north-east of Portugal during 2004—dimension 1 and 2. Sen1 - Send <30 animals; Sen2 - Send ≥30 and ≤150 animals; Sen3 - Send >150 animals. Po0 - no positive animals; Po1 - 1 positive animal; Po2 - 2 positive animals; Po3 - 3 or more positive animals. Sp1 - sheep specie; Sp2 - goat specie; Co1 - pure constitution; Co2 - mixed constitution. Pro1 - meat production; Pro2 - milk production. Pe0 (% of positives); Pe1 (>0 and <5%); Pe2 (≥5% of positives). Dimension 1 in the analysis is illustrated as the horizontal axis, and dimension 2 is illustrated as the vertical axis.

exhibited the greatest behavioral variability. The plot identifies clusters of associated variables, with those clusters a greater distance from the intersection having stronger associations. Explanatory variables of less than −0.3 and more than 0.3 in the analysis were considered to show a significant association.

3. Results

In this study, the original data enabled the detection of two axes that explained 65.4% of the total variance. The first axis sets herd size, a high number of positives per herd and higher prevalence. The second is characterized by contrasting those larger milk-producing herds to a higher number of positives per herd and a higher prevalence. The results of the correspondence analysis of herd characteristics are shown in Fig. 1. The first two-dimensions accounted for 52.6% (38.5% and 14.1%, respectively) of the data variation. A significant association between herds with high seroprevalence (≥5%), intermediate seroprevalence (>0% and <5%), 3 or more positive animals, 2 positive animals, 1 positive animal, and large herds (150 or more analyzed animals) could be observed. This latter group is opposite to the group of no positive animals and small herds. The variables that made the highest partial contributions to variability were, in decreasing order: intermediate seroprevalence with 1.25; 3 or more positive animals with 1.21; 2 positive animals with 1.19; 1 positive animal with 1.13; high seroprevalence with 0.98 and herds with ≥150 analyzed animals with 0.79 for the positive dimension 1 (F1); opposing this was the no positive animals variable with −0.30 and small herds (≤30 animals), with −0.26 in negative dimension 1/F1 (Table 1). In dimension 2 it was found that larger herds are associated with milk production, and intermediate seroprevalence (>0% and <5%), and are opposite to herds with 3 or more positive animals and high seroprevalence. In decreasing order, in positive dimension 2 (F2) the variables “≥150 animals” with 0.55, and “milk production” with 0.54 in the positive dimension 2 (F2) were observed, and in the negative dimension 2 the variables “3 or more positive animals” with −0.93 and “≥5% of prevalence”, with −1.00, were observed.

4. Discussion

This study was conducted with the aim of identifying herd characteristics as potential risk factors associated with brucellosis seroprevalence in small ruminants in the north-east of Portugal. This information is required in order to outline measures to control zoonotic brucellosis (Lithg-Pereira, 2001). In this study, the herds were not projected on the analysis due to their excessive quantity and inherent difficulty of interpretation. Multifactorial correspondence analysis identified an association between herds with high seroprevalence (≥5%), intermediate seroprevalence (>0% and <5%), 3 or more positive animals, 2 positive animals, 1 positive animal, and larger herds (150 or more analyzed animals), and this group was opposite to the group of no positive animal and small herds. However, when those larger herds were involved in milk production, they were only associated with intermediate seroprevalence values (>0% and

Table 1
Contributions of all variables

<table>
<thead>
<tr>
<th>Variables</th>
<th>Axis 1</th>
<th>Axis 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sen1 (≤30 animals)</td>
<td>0.26</td>
<td>0.08</td>
</tr>
<tr>
<td>Sen2 (&gt;30 and &lt;150 animals)</td>
<td>0.41</td>
<td>0.08</td>
</tr>
<tr>
<td>Sen3 (≥150 animals)</td>
<td>0.79</td>
<td>0.55</td>
</tr>
<tr>
<td>Po0 (no positive animals)</td>
<td>0.30</td>
<td>0.02</td>
</tr>
<tr>
<td>Po1 (one positive animal)</td>
<td>1.13</td>
<td>0.26</td>
</tr>
<tr>
<td>Po2 (two positive animals)</td>
<td>1.19</td>
<td>0.06</td>
</tr>
<tr>
<td>Po3 (three positive animals)</td>
<td>1.21</td>
<td>0.93</td>
</tr>
<tr>
<td>Sp1 (ovine species)</td>
<td>0.03</td>
<td>0.14</td>
</tr>
<tr>
<td>Sp2 (caprine species)</td>
<td>0.09</td>
<td>0.45</td>
</tr>
<tr>
<td>Co1 (herds of only one species)</td>
<td>0.07</td>
<td>0.05</td>
</tr>
<tr>
<td>Co2 (herds of sheep and goats)</td>
<td>0.37</td>
<td>0.29</td>
</tr>
<tr>
<td>Pro1 (meat production)</td>
<td>0.02</td>
<td>0.13</td>
</tr>
<tr>
<td>Pro2 (milk production)</td>
<td>0.08</td>
<td>0.54</td>
</tr>
<tr>
<td>Pe1 (0% prevalence—the lowest)</td>
<td>0.03</td>
<td>0.016</td>
</tr>
<tr>
<td>Pe2 (&gt;0% and ≤5% prevalence—intermediate)</td>
<td>1.25</td>
<td>0.42</td>
</tr>
<tr>
<td>Pe3 (&gt;5% prevalence—high)</td>
<td>0.98</td>
<td>1.00</td>
</tr>
</tbody>
</table>
tion is reduced by vaccination (Koopman and Longini, 2000; Kabagambe et al., 2001; Al-Majali, 2005). Plausible explanations for a positive association between herd size and infectious disease include a greater risk from the introduction of pathogens from outside the herd, a greater risk of transmission of pathogens within and among herds when the herd is large, and the impact of management and environmental factors related to herd size (Gardner et al., 2002). Larger herds were more likely to have at least one positive animal than smaller herds (Al-Majali, 2005). The number of susceptible animals is usually greater in large herds unless their risk of infection is reduced by vaccination (Koopman and Longini, 1994). Another possible explanation could be that larger herds were usually associated with more intensive management practices. These are typically more difficult to control and allow for closer contact between animals and their environment which increases potential exposure to infectious excretions; which can in part be attributed to confinement systems being more frequently used with large herds. These systems in turn increase this exposure. On the other hand, the number of direct and indirect contacts that a small-ruminant herd has with potential outside sources of infection may increase as the herd expands in size. These contacts include the introduction of breeding stock and feeders, the transportation of feed and slaughter animals, and visitors. Consequently, unless the protective management practices outlined above are used, the risk of pathogen introduction will also usually increase (Stegeman et al., 1999; Gardner et al., 2002). Our results could also be related to a higher density of animals per herd. This is because stocking density allows for greater contact between animals, creating a higher bacterial load in the environment and increasing the chances of disease transmission. Area density might have a positive correlation with herd size or stocking density within herds. Greater herd density could be confused with larger herd size (Flori et al., 1995), and therefore might partly explain the reported herd-size effects. However, the variable “stocking density” was not investigated in this study because it is difficult to measure accurately. Though several authors have reported that brucellosis is more prevalent in milk-producing rather than meat herds (Omer et al., 2000; Lithg-Pereira, 2001), this study showed that when larger herds were involved in milk production their seroprevalence dropped closer to intermediate values (>0% and <5%), and contrasted with herds with 3 or more positive animals and high seroprevalence. This association is probably a reflection of the better management practices applied to milk herds in the region, including more stringently applied hygiene practices, which, therefore, reduce the spread of infection. This is because in this region milk is traditionally used to produce a high-quality cheese. As such, this cannot be explained as a true breed predisposition. Meat-producing breeds of sheep and goats were raised more extensively than milk-producing animals in the region and better environmental features were often enjoyed by specialized (milk) large herds. In addition, meat producers introduced new animals into the herd on a more frequent basis, and stock interchange is most frequent when the herd is large. These increase the risk of introducing an infected animal into the herd. Practices that involve movement of animals between herds are also likely to carry risks (Kabagambe et al., 2001). However, there are a number of recent population-based studies which have described the relative frequency of these practices in variously sized herds or in herds used for different types of production (Omer et al., 2000; Lithg-Pereira, 2001). Nevertheless, due to the limitations imposed by our study’s design (cross-sectional), the results must be interpreted carefully. This is because it was not possible to clearly identify a cause-and-effect relationship (Thrusfield, 1995). Our results could make a useful contribution towards preventing brucellosis in small ruminants and decreasing losses in the livestock industry. When herds are large they are associated with high prevalence values, but when they are large and produce milk they are projected on the opposite side to those with higher prevalence, and closer to intermediate prevalence levels. This could be down to the fact that larger herds that produce milk are linked with high-quality milk production, and may also indicate that herd management improves where production is very profitable. Therefore, if we were able to explain the economic effects of eradicating brucellosis to farmers, perhaps we would see improved results.

5. Conclusions

The results of this study suggest that herd size and production type might have an impact on brucellosis seroprevalence. The demonstration of an association between herd size and disease could interest epidemiologists keen to find a basis for future studies. These studies could include a survey of farmers’ needs, regarding information and education for example, and the need to design further epidemiological studies to understand why large, meat herds exhibited high seroprevalence and large milk herds did not. Also, public-health concerns regarding food-borne diseases linked to the meat of small
ruminants are sure to increase interest in the impact of herd size on pathogen prevalence. This is because larger herds contribute the greatest number of slaughter animals for the market place (Gardner et al., 2002). This information could make an important contribution in the future towards appropriately designed strategies aiming to prevent brucellosis infection in the region.

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References