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FACTORS ASSOCIATED WITH OCCURRENCE OF *SALMONELLA* IN BROILER AND LAYER FLOCKS OF CHICKENS IN KAMPALA DISTRICT, UGANDA

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L'étude portait sur le rôle d'élevage de poulets (n = 29) et de poules pondeuses (n = 45) comme sources possibles de Salmonella pour l'Homme dans le district de Kampala et sur l'identification des principaux facteurs de risque d'infection dans ces troupeaux, grâce à une étude transversale.
Des salmonelles ont été isolées d'un nombre significativement plus élevé d'élevages de poulets que d'élevages de pondeuses (p = 0,04). Les grands troupeaux étaient plus souvent infectés que les petits (p = 0,09). La période de vide des locaux était associée au statut salmonellique des troupeaux de poulets. Lorsque le temps de vide des locaux était plus long, l'infection salmonellique était plus faible (p = 0,04). En plus de l'identification des sources de Salmonella pour la volaille, des études futures portant sur un plus grand nombre de troupeaux devraient porter sur ces facteurs lors de l'évaluation de l'importance de la gestion et des autres facteurs de risque de portage de Salmonella chez les poulets du district de Kampala et de l'ensemble de l'Ouganda.

INTRODUCTION

Among foods of animal origin, poultry meat and eggs are important sources of food-borne *Salmonella* for humans (Todd, 1992). The recent increase in isolation of *Salmonella enteritidis* as a predominant serotype recovered from humans and poultry in all continents has led to a heightened international interest in this pathogen and other *Salmonella*. This has created a need to provide accurate information on *Salmonella* in the poultry industry worldwide (Rodrigue et al., 1990).

Most of the published epidemiological studies on *Salmonella* (other than *Salmonella pullorum* and *Salmonella gallinarum*) have been conducted in the large, integrated poultry production systems found in developed countries. Few studies, however, have employed multivariable analyses to identify quantitative management risk factor profiles for *Salmonella* infection in chicken flocks (Renwick et al., 1992; Henken et al., 1992), and these studies are often useful in understanding problems of a multifactorial nature. Few published reports from Africa including Uganda, have described the magnitude, phenotypes and risk factors for *Salmonella* occurrence in the poultry industry. The objective of this study, therefore, was to identify important risk factors for *Salmonella* infection within commercial layer and broiler chicken flocks in Kampala district, Uganda.

MATERIALS AND METHODS

Sampling and sample size considerations

No useful sampling frame of chicken flocks existed in the study area, therefore two veterinarians working with poultry in this region were asked to compile a list of broiler and layer chicken operations (at least 80 of each type) to a total of 300 flocks. Using the lists as a sampling frame, sixty chicken flocks of each type were randomly sampled for the study during the month of January 1996. The number of flocks sought for this study was based upon a global estimate of the prevalence of *Salmonella* in broiler or layer flocks of 50% with an allowable error of 10%, and an estimated total population of chicken operations of 500 of each type in Kampala district (Kampala District Veterinary Office monthly returns, 1994). One flock per operation was randomly selected for sampling in those operations that had more than one barn. The *Salmonella* status of each flock was determined by culture of pooled litter and feed samples. Six litter samples, each of which was composed of a pool of two 10 g litter samples, were collected from each study chicken unit. Using this number of litter samples, we could be 95% certain of detecting *Salmonella* if present in 50% of the samples (Cannon and Roe, 1982; Martin et al., 1987). The samples were delivered within six hours of collection to the laboratory (Department of Veterinary Public Health and Preventive Medicine, Faculty of Veterinary Medicine, Makerere University, Kampala-Uganda).

The methods used to isolate *Salmonella* from the litter and feed samples followed those reported by Poppe et al. (1991a). Positive cultures were then forwarded to a reference laboratory (Health of Animals Laboratory, Agriculture Canada, Guelph, Ontario) for serotyping, biochemical testing, antibiotic resistance pattern determination, phagetyping and plasmid analysis. The methods have been described in detail elsewhere (Nasinyama, 1996).

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Data collection, handling and analysis

Information on flock management was collected by administration of a questionnaire (available on request) to the flock manager (or a family member who sometimes managed the birds) by personal interview. The questionnaire was administered at the time of collection of the litter and feed samples. The questions used in this study were based in part on the literature pertaining to studies on *Salmonella* in poultry (Henken et al., 1992; Renwick et al., 1992), especially those factors that were thought to have a meaningful and/or biological association with presence of *Salmonella* in chicken flocks.

The questionnaire information and culture results from the broiler and layer flock studies were entered into a computer database. Statistical analyses were carried out with standard software (SAS Institute Inc., Cary, North Carolina, USA). The unit of interest and analysis was the flock, and was coded 1 if positive or 0 if negative for *Salmonella*. Flocks were considered to be positive if *Salmonella* organisms were isolated from either the litter or the feed samples or both, otherwise they were negative. Survey questions were summarised using simple descriptive statistics, and frequency distributions were determined for various response categories. The logistic procedure was utilised to model flock salmonella-status as a function of the potential risk factors. Variables found to be associated with salmonella-status of the flocks ($p<0.25$) on screening were offered into a multiple logistic regression model. Significance in the final model was set at $p\leq0.1$ level. The goodness of fit and usefulness of the final model were assessed (Hosmer and Lemeshow, 1989).

RESULTS

Although sixty chicken operations of each type were randomly selected for this study, only 45 layer and 29 broiler chicken flocks participated and were surveyed and sampled. The remaining operations were not available to the study because they had sold off their birds and cleaned poultry houses of the litter in preparation for the next batch of birds.

On screening, variables that were associated ($p<0.25$) with salmonella-status of the study chicken flocks included restriction of visitor entry into chicken houses ($p=0.11$), the type of birds, with broiler flocks more likely ($p=0.15$) to be salmonella-positive than layer flocks. Larger flocks were also more likely ($p=0.19$) to be salmonella-positive than small ones. However, operations that reported presence of pest droppings in the poultry feed or had a shorter downtime (< 4 weeks) were less likely ($p=0.21$) to be salmonella-positive than those that did not or had a longer downtime, respectively.

In the multivariable logistic regression models, the type of bird, flock size and downtime were significantly ($p<0.1$) associated with flock salmonella-status (Table I).

Table I
Results of the final logistic regression model of flock and management risk factors for flock Salmonella-status of chicken flocks in Kampala district.

Variable	Parameter	SE	p-value	Odds	90%CI (OR)
Intercept	0.491	0.873	0.573	-	-
Bird type	-1.404	0.669	0.036	0.25	0.08,0.74
Flock size	0.002	0.001	0.090	1.00	1.00,1.00
Downtime	-1.680	0.827	0.042	0.17	0.05,0.72

However, both the linear and quadratic components of the age variable were not significant ($p=0.69$). Multicollinearity among the explanatory variables was not important, therefore the final model was considered to contain the three variables (Table I). The goodness of fit of the final model was poor, as assessed by the Hosmer-Lemeshow statistic ($C=14.29$ on 8df, $p=0.07$). This was probably due to presence of zero cells among some categories of the classification table. The sensitivity and specificity of the final model were 25% and 83.8%, respectively.

DISCUSSION

Salmonella were recovered from significantly more broiler flocks than the layer flocks, a finding that is in agreement with other studies (Poppe et al, 1991a; Poppe et al., 1991b). One of the factors that might explain this difference was the age of the birds. However, in the separate analyses examining the potential risk factors for occurrence of *Salmonella* in litter among broiler and layer flocks, the age of the birds at sampling showed no significant association with the salmonella status of the litter. Other workers have shown a significant but negative age effect (Linton et al., 1985; Renwick et al., 1992). The broiler and layer flocks in this study had a median age of 6 and 36 weeks. The lack

of an age effect within each bird type could have been a result of sample size rather than variability in the age structure of the study flocks.

Downtime was identified as a significant risk factor for *Salmonella* infection of chicken flocks in this study. Operations reporting a longer downtime (more than 4 weeks) were significantly more likely to be salmonella-positive than those that reported a shorter duration. The significance of this finding is open to question, however, since downtime could actually be a surrogate for efficiency of cleaning and disinfection of the poultry houses after disposal of all the birds. The efficiency of disinfection practices therefore requires investigation among the poultry operations in Kampala district.

The sampling frame of the flocks involved in this study was purposively chosen by veterinarians in the poultry industry in the district. Nevertheless, given that there were an estimated 500 flocks of each type of bird in the district, and we selected the study flocks from a list of 300, we believe that the sampled flocks were a fair representation of the entire flock population in the district. Exposure information bias is a possibility in studies utilising questionnaires and requiring recall. Interviews in this study were conducted within the chicken house and information was validated for some study variables by observation therefore limiting misclassification bias.

In conclusion, results of this cross-sectional study showed that *Salmonella* organisms were more often isolated from broiler flocks than layer flocks (p=0.04) in Kampala district. Although limited by sample size, the study identified some factors to be significantly associated with the salmonella-status of the flocks studied, including downtime, flock size and bird type. In addition to identifying sources of *Salmonella* for poultry, future studies involving a large number of flocks should focus on these factors when assessing the importance of management and other flock-level risk factors for salmonellosis in Kampala district and Uganda as a whole.

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