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Risk factors for sanitary condemnation in broiler chickens and their relative impact: application of an original multiblock approach

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SUMMARY

An innovative and well-adapted statistical method, called multiblock redundancy analysis, is proposed for a complex health-event analysis to account for the thematic block organization of variables. The outcome block contained the condemnation rates of 404 broiler chicken flocks, distinguishing infectious and traumatic condemnation categories. Explanatory variables were organized in blocks related to the different production stages (farm structure and routine husbandry practices; on-farm flock history and characteristics; catching, transport and lairage conditions; slaughterhouse and inspection features). The aim was to determine risk factors for both condemnation categories, and the relative impact of the different production stages on the whole condemnation rate. Results showed that significant factors were either specific to one condemnation category or related to both categories, and each of the explanatory blocks was involved in the explanation of infectious and traumatic condemnation rates. On-farm flock information explained 40% of the overall condemnation process whereas the other explanatory blocks had similar relative impacts.

Key words: Complex modelling, condemnation, food safety, multiblock redundancy analysis, poultry.

INTRODUCTION

Our aim was to investigate the sanitary condemnation process in the context of food safety, i.e. withdrawal from the food chain of any carcass diagnosed as unfit for human consumption on the basis of macroscopic lesions, during meat inspection at poultry slaughterhouses [1]. A better understanding of the factors influencing the condemnation process would facilitate food safety control and implementation of the most appropriate measures at the production level [2]. Factors pertaining to primary production were shown to be associated with the condemnation process in broiler chicken flocks using a classical modelling approach [3]. However, it has not been possible to accurately predict the condemnation rate with the production risk markers identified [3]. The predictive value of the model may have been reduced by the heterogeneity of the outcome considered [3], as the overall condemnation rate may incorporate different reasons for condemnation [4, 5], involving different sets of explanatory variables (e.g. ascites and fractures may be related to different risk factors).

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Giving consideration to this heterogeneity in the analysis would clarify the relationships between variables, and the factors related to rare reasons for condemnation would not be neglected [3]. However, the commonly adopted statistical methods are unable to account for multiple outcomes [3] so, as an alternative, most studies have focused on and selected a particular reason for condemnation, e.g. cellulite [6–9], cyanosis [10], or ascites [11]. It is, however, difficult to integrate the results from these separate analyses into an overall approach to food safety control and determine the most appropriate focus for containment or management measures.

Considering a heterogeneous outcome composed of different variables is an approach which can be extended to the structure of the explanatory variables. Investigation of the risk factors for sanitary condemnation in poultry revealed that the condemnation process was consistently multifactorial [3, 7–9, 12, 13], resulting from complex interactions between variables which can usually be organized into different thematic blocks (i.e. farm characteristics, husbandry management practices, health status of the animals, transport conditions, slaughtering).

Our objectives were to model the relationships between the condemnation rate as a composite outcome (i.e. composed of different reasons for condemnation) and the explanatory variables organized in thematic blocks. In particular, we attempted to assess the relative impact of each thematic block of explanatory variables in explaining the overall outcome, and which variables within these blocks had an impact on any one of the component outcomes. For this purpose we used an innovative and well-adapted statistical method, especially developed for epidemiological data, called multiblock redundancy analysis [14, 15].

METHODS

Data

Study sample

The study population consisted of a two-step cohort of broiler chicken flocks slaughtered during 2005, from all the European Union-licensed slaughterhouses in the main French regions of production (i.e. Bretagne and Pays de la Loire [16]).

The epidemiological unit was the slaughtered flock. A flock was defined as a group of birds placed in the same house, shipped to the same slaughterhouse and processed together on the same day. The dataset included 404 flocks, randomly selected by two-stage sampling, stratified per slaughterhouse and based on random selection of the day of slaughter and of the flock sequence number in the slaughtering schedule of that day. Study population details, sampling design, flock selection and sample size have been described previously [3, 4].

Data collection

The first step in the study was prospective. Each flock was followed from its arrival at the slaughterhouse until the condemnation rate and official sanitary reasons for condemnation were obtained after the regulatory meat inspection. The seven official reasons for condemnation [17], i.e. emaciation; congestion; arthritis/polyarthritis; infected skin lesions; significant wounds and bruises; abnormal colour, odour or conformation; and ascites were considered. The main macroscopic lesions on a sample of carcasses condemned for each official reason, were also reported by the official veterinary meat inspectors at the post-mortem examination [4]. The second step was retrospective and involved the collection of on-farm information during an appointment with the farmer. This consisted of a personal interview and examination of the on-farm records by four previously trained investigators from the AFSSA laboratory.

Data were collected for each flock using standardized questionnaires, official documents, routine slaughterhouse records, measurements, and on-farm records. Information was collected about conditions during the rearing period, health history, catching and loading, transportation to the slaughterhouse, and slaughtering conditions [3].

Definition of the outcome variables

The overall condemnation rate was divided into two continuous outcome variables by grouping the official reasons for condemnation in two distinct categories. The first outcome (Infect) grouped the official reasons for condemnation corresponding to health-related problems of presumed infectious or metabolic origin and exhibition of acute or chronic evolution (i.e. emaciation, congestion, arthritis/polyarthritis, ascites). The second outcome (Trauma) grouped the official reasons for condemnation corresponding to problems of presumed traumatic origin, whether secondarily infected or in the process of healing (i.e. infected skin lesions; bruises and wounds; abnormal colour, odour or conformation).

This grouping was based on previous findings [4]: the lesions observed during the post-mortem examination of carcasses condemned for each condemnation reason [4] were analysed and revealed two distinct sets. Carcasses condemned for emaciation, congestion, arthritis/polyarthritis, and ascites mainly exhibited macroscopic lesions of the viscera, whereas carcasses condemned for infected skin lesions; bruises and wounds; and abnormal colour, odour or conformation tended to exhibit external lesions, such as scratches or broken legs [4].

For each flock, the outcomes were calculated as the percentage of carcasses condemned for each condemnation category (i.e. Infect and Trauma), by dividing the number of carcasses condemned for the corresponding official condemnation reasons in a given flock by the total number of birds slaughtered in this flock.

Data organization

The collected variables were organized into five logical blocks (Table 1). The outcome block contained two quantitative variables, i.e. the condemnation rates classified as Infect and Trauma. The potential explanatory variables were organized in four thematic blocks related to farm structure and routine husbandry management practices (15 variables), flock specific on-farm history and characteristics (17 variables), flock catching, transport and lairage conditions (11 variables), and slaughterhouse and inspection features (four variables).

These thematic blocks were relevant and consistent with an operational application. Information pertaining to farm structure and husbandry practices rarely change between two flocks and are the farmer's responsibility. On-farm history and events which occur during rearing are specific to each flock. Transport features and slaughtering characteristics occur during the final steps of production and cannot be controlled by the farmer, but are under the control of professionals.

These 47 potential explanatory variables were selected from the total collected variables on the basis of the main factors reported in the literature [7, 8, 10, 12] and earlier univariate screening using a generalized linear mixed Poisson regression analysis, applied to the overall condemnation rate [3], and to each of the Infect and Trauma outcomes. Only variables with sufficient variation, i.e. a minimal category frequency of 10%, were considered.

All the variables under study were first described in terms of a frequency distribution (qualitative data) or as the mean and S.D. (quantitative data). The categorical variables were coded as dummy variables for the purpose of statistical processing. As all the variables were expressed in different units, they were column centred and scaled to unit variance [18].

Statistical analysis

The first objective of the statistical treatment was to identify those risk factors within the four explanatory blocks X_1 (farm structure and routine husbandry management practices), X_2 (flock specific on-farm history and characteristics), X_3 (flock catching, transport and lairage conditions) and X_4 (slaughterhouse and inspection features), which simultaneously explain each outcome Y (Infect and Trauma). The second objective was to estimate the relative impact of each explanatory block $X_{k=(1,\ldots,4)}$ on the explanation of the outcome block Y, i.e. the condemnation rate.

Multiblock redundancy analysis [14, 15] was applied. This method is suitably adapted to a setting in which a block Y of several outcomes is explained from K several blocks of explanatory variables (X_k). The statistical basis of this method has already been described in detail [14, 15], therefore only the main principles are presented in this paper.

Multiblock redundancy analysis combines factor analysis and regression. This method can be considered as a regression of Y upon linear combinations of the X variables or as a factor analysis of the Y variables on components, constrained to be a linear combination of X. Multiblock redundancy analysis is a direct extension of redundancy analysis [19], to a multiblock setting where K several explanatory blocks X_k explain a block Y containing several outcomes.

Principle of the method

The information from all the explanatory variables, i.e. the merged dataset called $X=[X_1|,\ldots,|X_k]$, is summarized with global components t oriented towards the Y explanation. The components are ordered so that each successive component contains a decreasing proportion of the total variation between the outcomes. Consequently, the first global component (i.e. the first dimension) contains the largest amount of information while the last may contain very little additional information. For each dimension, the method seeks a global component $t=Xw$, which is a linear combination of all the variables

Table 1. *Definition and distribution of data collected to identify potential factors related to carcass condemnation in broiler chickens (404 flocks, France, 2005)*

Definition of variables	% or mean (S.D.)
Y block: outcomes	
Condemnation rate for 'infectious' categories: Infect (%)	0·53 (0·55)
Condemnation rate for 'traumatic' categories: Trauma (%)	0·28 (0·19)
X_1 block: farm structure and husbandry management practices	
Cemented access to the chicken house	
Yes	73·8
No	26·2
Age of the chicken house	
>12 years, without renovation	53·0
⩽12 years or >12 years and renovated	47·0
Total area for chicken (m^2) on the farm	2184 (1336)
Heating system in the chicken house	
Gas heaters	35·2
Radiants	64·8
Lighting in the chicken house	
Dark	62·6
Semi-bright	12·1
Bright	25·3
Type of ventilation in the chicken house	
Dynamic	48·3
Static	51·7
Soaking step in cleaning of chicken house	
Yes	18·8
No	81·2
Pest control of the chicken house	
Yes	77·7
No	22·3
Use of specific clothes on-farm	
Yes	61·1
No	38·9
Number of people devoted to chicken production	
Several	37·1
One	62·9
Frequency of farmer's visits during the starting period (number/day)	3·6 (1·3)
Frequency of farmer's visits during rearing (number/day)	2·5 (0·99)
Sorting practice	
Yes	43·6
No	56·4
Drinking water acidification	
Yes	24·3
No	75·7
Source and quality of drinking water	
Main or well with disinfection	82·7
Well without disinfection	27·3
X_2 block: flock's characteristics and on-farm history	
Production type	
Standard	66·8
Certified	10·6
Heavy	11·9
Light	10·7
Chick density at placement (number of chicks/m^2)	22·5 (3·4)
Genetic strain	
A	55·0
Others	45·0

Table 1 (*cont.*)

Definition of variables	% or mean (S.D.)
Size of the flock (number of chickens)	14 479 (8434)
Average bird weight at slaughter (kg)	1·9 (0·4)
Stress occurrence during rearing*	
Yes	20·0
No	80·0
Heat stress occurrence during rearing	
Yes	13·4
No	86·6
Homogeneity of chicks at placement	
Yes	77·5
No	22·5
Homogeneity of chickens at the end of rearing	
Yes	77·0
No	23·0
Respiratory disorder observed	
Yes	17·8
No	82·2
Locomotor disorder observed	
Yes	9·9
No	90·1
Early† mortality (%)	1·3 (1·0)
On-farm mortality (%)	2·7 (2·0)
Sanitary visit during the rearing period (veterinarian or technician)	
Yes	25·3
No	74·7
Copper administration	
Yes	14·6
No	85·4
Previous loading	
Yes, <1 week before slaughter	16·3
Yes, ⩾1 week before slaughter	24·3
No	59·4
Previous thinning	
Yes	17·8
No	82·2
X_3 block: catching, transport and lairage conditions	
Crating practices	
Specific operator	31·2
Catchers	68·8
Presence of the farmer during loading	
Yes	79·7
No	20·3
Stocking density in transport crates (kg/m²)	57·4 (6·9)
Meteorological conditions during lairage	
No rain and no wind	80·9
Rain and/or wind	19·1
Sun during lairage	
Yes	40·1
No	59·9
Time of lairage (hours:minutes)	3:53 (2:11)
Time of feed withdrawal (hours:minutes)	12:29 (3:57)
Time spent in transport crates (hours:minutes)	5:29 (2:13)
Dirty feathers at exit of crates	
Yes	26·2
No	73·8

Table 1 (*cont.*)

Definition of variables	% or mean (S.D.)
Clinical signs observed at ante-mortem inspection	
Yes	27·7
No	72·3
Dead on arrival (%)	0·18 (0·26)
X_4 block: slaughterhouse and inspection characteristics	
Localization of the withdrawal of carcasses	
Defeathering and evisceration	43·8
Defeathering	56·2
Localization of the condemnation of carcasses	
Defeathering and evisceration	46·3
Defeathering	53·7
Number of carcasses inspected by operator for an individual flock	8260 (6577)
Slaughter line speed (number of carcasses/hour)	7634 (2193)

* For example: heat stress, feed chain failure.
† During the first 10 days following placement.

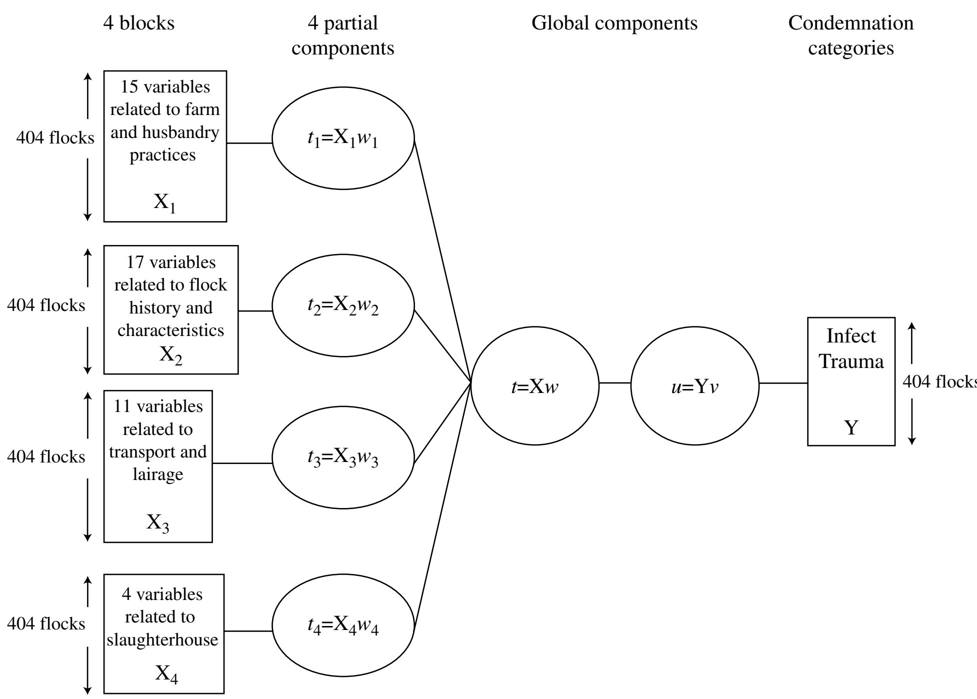

Fig. 1. Conceptual scheme highlighting the relationships between the four blocks (X_1, X_2, X_3, X_4) and the Y block, and their associated components.

derived from the X block. This component summarizes K partial components $t_k = X_k w_k$, respectively associated with the blocks X_k. The global component t is closely related to a component $u = Yv$, which summarizes the outcomes and is a linear combination of the Y variables. These components are computed to maximize a criterion based on the squared covariance between the global component t and component u. The solution is given by the eigenanalysis of a matrix which involves the blocks Y and X_k [14, 15]. Figure 1 shows the relations between tables and components in our analysis.

Explanation of Y from several blocks ($X_1, \ldots, X_k$)

A model is obtained by regressing the Y variables on the global components t, which are constrained to be orthogonal with each other. These can be directly used as predictors for the Y variables, replacing the explanatory variables X in the regression to

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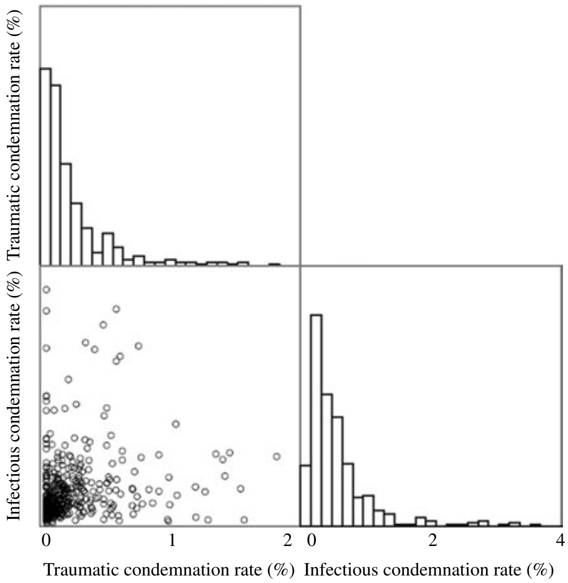

Fig. 2. Distribution of the infectious and traumatic condemnation rates, 404 broiler chicken flocks, France, 2005.

obtain regression coefficients [20]. The number of components, i.e. number of dimensions, to retain in the model was determined by cross-validation procedure [21], which consists of splitting the whole dataset into two sets, i.e. a calibration set and a validation set. The calibration set (representing two thirds of the whole dataset) was used to estimate the regression coefficients β of the model linking explanatory variables X and outcomes Y, and the root mean square error of calibration which reflects the fitting ability of the model. The validation set (representing the remaining third) was used to compute the root mean square error of validation which reflects the prediction ability of the model. This procedure was repeated 500 times. The two errors can be seen as functions of the number of dimensions introduced in the model. The optimal number of components is a compromise that optimizes both the fitting and prediction abilities of the model.

All 47 potential explanatory variables were included in a multivariate model, fitted with a manual backward-selection procedure. Standard deviations (S.D.) of the regression coefficients were computed using the results from the repeated cross-validated regressions. Each explanatory variable was considered to be significantly associated with any variable from Y when the 95% confidence interval (CI) associated with the regression coefficient did not contain the value 0. The exponentiated regression coefficient (e^{β}) was interpreted as an incidence rate ratio (IRR), representing the proportional increase in condemnation rate for a unit change in the explanatory variable [22].

Importance of each block X *in the* Y *explanation*

The importance of each block X_k in explaining block Y is reflected by the coefficient a_k^2. The coefficients a_k are the normalized covariances between the partial components t_k and the component u, under the constraint $\Sigma a_k^2 = 1$.

Statistical procedures were conducted using SAS software [23] (descriptive analysis) and Matlab [24] (multiblock redundancy analysis).

RESULTS

Descriptive analysis

The average within-flock condemnation rate for the Infect condemnation category was 0·53% (S.D. = 0·55), ranging from 0% to 3·71%, and for the Trauma category was 0·19% (S.D. = 0·28), ranging from 0% to 1·72%. Flocks were generally condemned for both Infect and Trauma condemnation categories (Fig. 2). Only 19% (75/404) of the flocks were condemned solely for the Trauma category (one flock) or, more frequently, only for the Infect category (74 flocks). The explanatory variables are described in Table 1.

Explanation of the condemnation rate

The optimal model, with both correct fitting ability and good prediction ability, was one with two global components. Table 2 shows the explanatory variables which were significantly associated with the condemnation rates for the infectious category (Infect) and for the traumatic category (Trauma). Variables pertaining to each of the four thematic blocks were involved in the explanation of both outcomes. The Infect condemnation rate was significantly related to 18 explanatory variables: five pertaining to farm structure and routine husbandry practices, seven to flock characteristics and history, three to catching, transport and lairage conditions, and three to slaughterhouse features. The Trauma condemnation rate was significantly associated with 15 variables, of which six, four, four, and one, respectively were related to the above-mentioned blocks (i.e. X_1–X_4). Certain variables were only associated with one outcome: 11 variables were specifically associated with the Infect condemnation rate and eight variables were

Table 2. *Significant regression coefficients* of the explanatory variables related to infectious (Infect) and traumatic (Trauma) condemnation categories obtained with multiblock redundancy analysis† (404 broiler chicken flocks, France, 2005)*

	Infect				Trauma			
Explanatory variables	β	S.D.	IRR	95% CI	β	S.D.	IRR	95% CI
X_1 block: farm structure and husbandry management practices								
Cemented access: yes (*vs.* no)					−0·33	0·13	0·72	0·56–0·93
Age of the chicken house: >12 years (*vs.* recent or renovated)	0·28	0·09	1·32	1·10–1·58	0·33	0·13	1·39	1·07–1·79
Soaking step in cleaning of house: yes (*vs.* no)					−0·46	0·10	0·63	0·52–0·76
Lighting in the house: dark *vs.* semi-bright *vs.* bright‡					−0·38	0·14	0·68	0·52–0·90
Frequency of farmer's visits during the starting period	−0·32	0·08	0·73	0·63–0·84	−0·33	0·09	0·72	0·61–0·85
Sorting practice: yes (*vs.* no)	0·28	0·09	1·32	1·10–1·59				
Number of people devoted to chicken production: several (*vs.* one)	−0·32	0·07	0·73	0·64–0·83				
Drinking water acidification: yes (*vs.* no)	−0·33	0·08	0·72	0·62–0·84				
Drinking water: main or well with disinfection (*vs.* well without disinfection)					−0·53	0·14	0·59	0·44–0·78
X_2 block: flock's characteristics and on-farm history								
Production type: standard (*vs.* others)	−0·29	0·10	0·75	0·62–0·90	−0·34	0·12	0·71	0·56–0·91
Homogeneity of chickens at the end of rearing: yes (*vs.* no)	−0·65	0·11	0·52	0·42–0·65				
Sanitary visit: yes (*vs.* no)	−0·21	0·10	0·81	0·67–0·98				
Respiratory disorder observed: yes (*vs.* no)	0·34	0·10	1·41	1·15–1·72				
Locomotor disorder observed: yes (*vs.* no)	0·40	0·11	1·48	1·19–1·86				
Chick density at placement					0·80	0·24	2·23	1·39–3·57
Genetic strain: A (*vs.* others)	−0·67	0·08	0·51	0·43–0·60				
Size of the flock	−0·39	0·08	0·68	0·57–0·80	0·46	0·11	1·59	1·27–1·98
Average bird weight at slaughter					0·25	0·13	1·29	1·01–1·65
X_3 block: catching, transport and lairage conditions								
Crating practices: specific operator (*vs.* catchers)					−0·16	0·08	0·85	0·73–0·99
Presence of the farmer during loading: yes (*vs.* no)					−0·52	0·11	0·60	0·48–0·73
Dirty feathers at exit of transport crates: yes (*vs.* no)	0·47	0·07	1·60	1·39–1·84				
Dead on arrival	0·20	0·07	1·23	1·07–1·40	0·39	0·15	1·48	1·11–1·97
Time of lairage	−0·21	0·06	0·81	0·72–0·92	−0·32	0·07	0·73	0·64–0·84
X_4 block: slaughterhouse and inspection characteristics								
Withdrawal at the evisceration line: yes (*vs.* no)	0·39	0·06	1·48	1·32–1·66	0·39	0·10	1·47	1·20–1·80
Carcasses condemnation place: defeathering and evisceration (*vs.* defeathering)	−0·14	0·07	0·87	0·76–0·99				
Number of carcasses of the flock inspected by operator (1000-carcasses increments)	−0·13	0·04	0·88	0·82–0·94				

* β, Regression coefficient; S.D., standard deviation; IRR, incidence rate ratio; CI, confidence interval.

† Model with two global components, root mean square error of calibration = 0·0365; root mean square error of validation = 0·0554.

‡ The risk of traumatic condemnation of a flock reared in a dark house was 32% lower than in a semi-bright house, which was 32% lower than in a bright house.

specifically associated with the Trauma condemnation rate.

Importance of each thematic block in the condemnation rate explanation

Variables related to flock characteristics and history (block X_2) had the greatest impact on the overall condemnation rate Y, with a relative weight of 40%. The relative weights of the three other explanatory blocks: catching, transport and lairage conditions (22%), farm structure and routine husbandry practices (20%), slaughterhouse and inspection characteristics (18%), were very similar.

DISCUSSION

Multiblock redundancy analysis

Generalized linear regression models have usually been used to model the condemnation rate, e.g. linear regression [12], logistic regression [6, 7], Poisson regression [3, 8, 10] or negative binomial regression [25]. Such methods can quantify the association between the outcome and a set of explanatory variables, and may account for interactions between explanatory variables and for potential clustering [3, 9]. Alternative statistical strategies, such as using an artificial neural network [11] or factor analysis [13], have been tested to overcome structural multicollinearity between variables which cannot be adequately addressed by regression [26, 27], leading to often unstable results [26]. In any case, the outcome variables considered corresponded either to a specific reason for condemnation [6–11] or to the overall condemnation rate [3, 12, 25], exposing the identified risk factors to be partial or related to the major reason for condemnation [3]. In effect, the less frequent manifestations of a complex outcome can sometimes be masked by the more dominant, with the result that some of the specific determinants may be neglected.

Multiblock redundancy analysis appears to be well-adapted for handling complex epidemiological data [14, 15]. It combines factor analysis and regression, and has the advantages of both statistical approaches. First, it is insensitive to multicollinearity within the explanatory blocks which usually leads to confounder bias in analysis. The information within the blocks of explanatory variables is summarized into components, which are linear combinations of the original variables and constructed in such a way as to be mutually orthogonal, i.e. uncorrelated [26, 28]. Second, the structure of the explanatory variables within the thematic blocks can be used to estimate their respective weights in the outcome explanation. Above all, the prediction of several variables can be handled simultaneously. This avoids the need to build several models, or to combine several outcomes into a single variable, which can otherwise lead to loss of information.

As in our application, a complex health event may be composed of distinct manifestations. It can also be defined by different occurrences of the same event in sub-populations, e.g. the seroconversion towards porcine circovirus type-2 of different pigs in a swine herd [29]. The multiblock modelling method could therefore be extended to similarly structured data that pertain to other fields of application, e.g. chemometrics, sensometry or ecology.

Study design and limitations

Selection bias was limited by sampling broiler chicken flocks at random and information bias was minimized as much as possible by standardizing data collection [30]. More detailed limitations of the study design have been discussed previously [3]. However, a potential misclassification bias could not be excluded because the attribution of each condemned carcass to one of the official reasons for condemnation was based on visual, so subjective, criteria [17]. In particular, a reddish carcass might be classified under either congestion or abnormal colour. Risk of misclassification was minimized by considering two condemnation categories in the outcome block rather than each of the seven official reasons for condemnation. The official condemnation reasons were indeed grouped into a composite outcome according to logical categories, i.e. 'infectious' or 'traumatic', based on post-mortem examination of the macroscopic lesions of the condemned carcasses [4]. Condemned carcasses in the 'infectious' category were effectively more likely to have visceral rather than external lesions whereas in the 'traumatic' category the reverse was observed [4]. These 'infectious' and 'traumatic' categories were adopted to simplify analysis of the complex outcome, and these labels did not prejudge the causes or the conditions related to the official reasons for condemnation.

Our study arranged the explanatory variables into relevant and useful thematic blocks, which were consistent with decision-support purposes. This multiblock structure of the data might help to determine which of the different stakeholders in poultry production (i.e. farmers, transporters, slaughterers) has the greatest responsibility in the process leading to carcass condemnation, and the stages of primary production where control and prevention efforts should be focused. In particular, information pertaining to farm structure and husbandry practices rarely change between two flocks and may be used to identify the best points of focus when designing prevention and control programmes. Flock-related information may be accurately and continuously monitored, and be of particular use in determining the most appropriate risk indicators [31] to anticipate inspection organization at the slaughterhouse [3, 12].

Risk factors for the condemnation process

Flocks were usually condemned for both 'infectious' and 'traumatic' condemnation categories but much less frequently for the 'traumatic' category. Rarer flocks were condemned mainly or even only for 'traumatic' category. The former more frequently observed flocks would have been depicted in a classical model of overall condemnation, whereas the rare flocks mainly condemned for 'traumatic' category would have gone unnoticed. However, the risk factors specifically associated with the rarer 'traumatic' category might be different, which could be important for identifying a suitable course of action. These could be of benefit to all types of flock. Multiblock redundancy analysis was able to take into account their presence within the overall condemnation process. The observed dominance of the 'infectious' condemnation category could explain why 'infectious' risk factors have tended to predominate in explaining the condemnation rate as a whole in previous analyses [12, 25], particularly in the previous classical modelling approach of the present dataset [3].

Most risk factors, in both the Infect and Trauma condemnation categories, were on-farm parameters, i.e. pertaining to farm structure and routine husbandry practices or to flock characteristics and history. The observed effects of farm-related factors were biologically relevant and consistent with previous findings [4, 7, 8, 13, 25, 32–36]. Similarly, associations between factors pertaining to transport conditions [8, 13, 25, 33] and the condemnation process have already been reported. Conversely, the widely reported association between litter characteristics and condemnation for cellulitis [6–8] was expected but not observed. The litter characteristics in our dataset showed little variation and their impact could not be explored.

New biologically relevant relationships were observed. The application of good hygiene practices and basic rules of biosecurity, e.g. routine sanitary visit, cemented access to the chicken house or inclusion of a soaking step during cleaning, were associated with a lower risk of condemnation. These may reflect improved farmers' awareness and attitude towards hygiene and disease prevention. Similarly, the application of good catching and loading practices, e.g. presence of the farmer during loading or having a specific operator for crating, were associated with a lower risk of 'traumatic' condemnation.

Although all the four thematic blocks had been previously evoked with a classical modelling approach, multiblock redundancy analysis has revealed new risk factors for the 'traumatic' condemnation category, related to hygiene practices and biosecurity, catching and loading practices.

CONCLUSIONS

Farm, bird, transport and slaughterhouse features have all been shown to significantly affect the condemnation process in broiler chickens. This previously reported multifactorial origin of condemnation [3, 7–9, 12] was further highlighted by the relative impact (18 %) of the least important primary production stage in explaining the condemnation process. Such information could be used to design, organize, implement or evaluate control or prevention programmes, when an overall analysis of an adverse health event is required so that appropriate action can be implemented at the most relevant stages of production. Decision-makers may need to determine which of the different actors in poultry production (i.e. farmers, transporters, slaughterers) have the greatest responsibility in the process leading to carcass condemnation. This may be useful in global management decisions, whereas professionals may be more interested in the specific risk factors related to each condemnation category in order to accurately assess and improve their current practices. In particular, this might help to provide to the farmer with relevant feedback on the flock's meat inspection results, in accordance with current European regulations related to food chain information [37]. The full heterogeneity of the health event must be taken into account so that different manifestations are not neglected when targetting appropriate control measures and changes in current practices to limit the risk of condemnation.

These operational conclusions were reached by using multiblock redundancy analysis. This innovative statistical method, as shown by this investigation of the condemnation process, is well adapted to public health issues. The risk factors specific to each manifestation of a complex health event can be identified from a single dataset and a single analysis and the relevant steps of the process on which to focus can be determined, as a decision-support aid in health event management. This responds to the specific expectations of the various actors in the poultry production chain confronted with the complexity of health events.

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DECLARATION OF INTEREST

None.

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