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Selection of Traits in Poultry Breeding Using Cluster Analysis

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Abstract: This study aimed to select representative traits from phenotypic variability between broiler chicken grandparent lines using cluster analysis. Chicks from four dam lines and two sire lines of broiler grandparents were housed to assess performance traits (body weight, eviscerated carcass yield, breast yield and leg yield) and morphometric traits (back and leg feathering), which were used to calculate the Mahalanobis' distance, between chicken line pairwise. Phenograms were obtained based on those distances using UPGMA method in cluster analysis. The smallest relative contribution of traits for divergence between chicken lines was assessed to eliminate them. Body weight at 35 days, all carcass traits and back feathering at 28 days were the most representative traits to explain phenotypic variability between chicken lines. From observed clusters and the largest heterogeneity between chicken lines from different clusters, crosses between sire lines SL1 and SL2 with dam lines DL3 and DL4 might result in strain combinations with the largest heterosis. Cluster analysis on performance and morphometric traits is suitable to study phenotypic variability between broiler chicken grandparent lines. We suggest analyzing data from poultry breeding using cluster analysis.

Key words: Feathering, selection index, multivariate analysis, phenotypic variability

Introduction

Broiler producers have used commercial poultry production system that combines high productivity with high efficiency. To attend this aim, chicken lines with high potential performance have been selected on economical traits, such as growth rate, feed efficiency, slaughter weight, carcass conformation and meat quality through phenotypic selection (Yang and Jiang, 2005). Additionally, feathering rate has also been considered to obtain an integrated carcass that no present cutaneous lesions, which mainly occurred in rearing due to high density of chickens and in transportation from farmer house to slaughterhouse. Often, these lesions cause partial or total carcass condemnation, resulting in economical losses (Estevez, 2007).

According to Flock *et al.* (2005), chicken strains with high performance present high body weight (about 2.5-2.8 kg at 41 days) with feed intake increased, but feed efficiency reduced that has allowed obtain high efficiency in commercial poultry production system. These strains also present year by year a decreasing on slaughter age, today about 40-41 days. High performance of these strains is resulted from poultry breeding that has been based on univariate phenotypic selection.

Although the use of classical animal breeding methodologies based on univariate phenotypic variability measurements have allowed to develop specialized lines that are used to obtain chicken strains, the application of new methodologies need to be

investigated to select the best combination between chicken lines to assure the best indexes in world poultry as purposed by Rosário *et al.* (2005; 2007). If selection of some more representative traits on phenotypic variability from several economical traits could be make routinely, this strategy might not only reduce time, but also reduce cost to evaluate and select poultry genetic resources.

It is impossible accept that all economical poultry traits are independent in their biological nature because these traits present phenotypic and genetic correlations caused by linkage or pleiotropy (Minvielle *et al.*, 2005; Aerts *et al.*, 2007; Dodgson, 2007). If is linkage, it is possible to manipulate crosses between lines and obtain better chicken strains, but if is pleiotropy, it is unable any strategy for useful manipulation. Therefore, multivariate analysis can be implemented to assess breeding resources based on account of major part of total phenotypic variability from all traits.

Several multivariate analysis methods are available, depending on the aim of the study: principal components, factor analysis, canonical correlation, correspondence analysis, multidimensional scaling analysis, redundancy analysis, canonical discriminant analysis and cluster analysis. The term cluster analysis (Tryon, 1939) encompasses a number of different algorithms and methods for grouping objects of similar kind into respective categories. In other words, cluster analysis is an exploratory data analysis tool which aims

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Table 1: Parameters and feed types used during experimental period

Parameters	Diets			
	Pre-Starter	Starter	Grower	Finishing
Catering age (days)	0-11	12-21	22-35	36-42
Particle size type	Mash	Mash	Mash	Mash
Crude Protein (%)	23.0	22.0	20.0	20.0
Metabolizable energy (kcal/kg)	3000	3080	3180	3260

at sorting different objects into groups in a way that the degree of association between two objects is maximal if they belong to the same group and minimal otherwise (Johnson and Wichern, 1992).

Examples for using of multivariate approaches were showed by Dobek *et al.* (2000) e Szwaczkowski *et al.* (2001) using mixed inheritance model via Gibbs sampling, by Szydlowski and Szwaczkowski (2001) using segregation analysis of production traits through Bayesian inference and Lahav *et al.* (2006) using marker-assisted selection based on a multitrait economic index.

Also, phenograms can be constructed from cluster analysis using Mahalanobis' distance that considers intra-specific variation and correlations between traits and not only tendency of sample mean (Barbosa *et al.*, 2005). The purpose of this analysis is cluster, according to some classification criteria, chicken lines in several groups where there is homogeneity within group and heterogeneity between groups. Alternatively, this analysis also aims to discriminate, from an original cluster, several clusters, following some similarity or non-similarity criteria. Another interesting characteristic of this analysis is that allows the selection of most important traits, which participate on clustering (Johnson and Wichern, 1992).

The aim of this work was to select representative traits on phenotypic variability between broiler chicken grandparent lines, becoming easier selection of better genotypes using cluster analysis.

Materials and Methods

Animals and experimental conditions: Four experiments were carried out according to animal welfare international laws (Canadian Council on Animal Care, 1993). A total of 12,000 chicks (3,000 for each experiment) from six broiler chicken grandparent lines were used. Four of these lines were dam lines (DL1, DL2, DL3 and DL4) and two were sire lines (SL1 and SL2), which were used in crosses to obtain chicken strains.

Birds were housed in farmer house, without sex separation, in six pens (one per line), equal density in 12 chicks.m². In addition, natural ventilation, controlled with lateral curtains handling, fans and nebulizators were used to control temperature and humidity environment. Feed and water were available *ad libitum* during whole experimental period, which was from 1 to 42 days of age

for all experiments. Mortality or deficient chicks were removed daily.

Different feed types were available at several ages (Table 1). All feeds offered in each period were formulated with basic ingredients such as fine ground corn, soybean, soy oil, limestone and specific premix.

Evaluated traits: Birds were weighed weekly, from 7 to 42 days, taking randomly 50 birds from each line and from each experiment. At 42 days there were taken random samples of 10 birds from each line and each experiment, which were weighed and slaughtered to assess carcass and part yields. Traits measured were: eviscerated carcass weight (without viscera, head, neck, feet and abdominal fat), breast and legs (thighs and drumsticks) weights. Carcass yield was considered as percentage of eviscerated carcass weight than body weight. Part yields were considered as being percentages of breast weight and legs weight than eviscerated carcass weight.

At 28, 35 and 42 days, 50 birds from each line and each experiment were taken randomly for visual evaluation of morphometrical traits of back and leg feathering. A score range from 0 to 10 was used, where 0 corresponds to back and legs completely no feathering and 10 corresponds to back and legs completely covered by feathering.

Statistical analysis and selection of traits: Firstly, analyses of variance from four experiments were accomplished jointly, in order to verify significant differences between experiments. These differences were not verified and for this reason, data obtained from four experiments were considered as being only one dataset. Therefore, this strategy increased total replicate number, resulting in 200 replicates of each line for body weight, back and leg feathering, and 40 replicates for carcass and part yields.

To accomplish phenotypic variability study, Mahalanobis distances (D^2), between lines pairwise, were calculated in agreement with formula defined by Mahalanobis in 1936 and presented by Rao (1952). After, phenograms were obtained based on those distances using UPGMA method – unweighted pair-group method using arithmetic average (Sneath and Sokal, 1973) – for cluster analysis between chicken lines.

The procedure adopted to select traits is described as follows:

- i) cluster analysis of lines was obtained, considering body weight at 7, 14, 21, 28, 35, 42 days traits.
- ii) exclusion of the trait that presented the smallest relative contribution for divergence between chicken lines, according to method described by Singh (1981).
- iii) cluster analysis was repeated, according to step i), excluding the detected trait according to step ii). This analysis was compared with result of initial cluster obtained in step i).
- iv) if results were similar, i.e. the cluster was not modified, the trait detected in step ii) was excluded. On the other hand, the trait was maintained in the cluster analysis and selection of traits was finished, because it was assumed the assumption that if a trait with the smallest contribution altered cluster, other trait with higher contribution would modified it too.

Procedure described (steps i to iv) was accomplished until all traits with the smallest relative contributions for divergence between lines, considering the initial contributions, were excluded from analysis without affecting initial cluster obtained from all traits in step i). This procedure was also repeated considering eviscerated carcass, breast and legs yields at 42 days of age traits and after, considering morphometric traits (back and leg feathering at 28, 35 and 42 days of age) separately.

Results

Relative contribution of body weight at 7, 14, 21, 28, 35 and 42 days for divergence between six broiler chicken grandparent lines is presented in Table 2. It was observed that body weight at 35 days presented the largest contribution (36.62%), while body weight at 7 days showed the smallest contribution (1.77%) for divergence between chicken lines.

Considering all body weights, three initial clusters could be observed: one composed by DL1 and DL2 lines (cluster 1), other composed by DL3 and DL4 lines (cluster 2) and one other composed by SL1 and SL2 lines (cluster 3). Following the analysis, clusters 1 and 2 linked to cluster 3. This fact may be explained due to weight differences between dam and sire lines (Fig. 1A). In Fig. 1B, it could be observed that after removal the smallest relative contribution traits for divergence between broiler chicken grandparent lines, the phenogram was obtained only with body weight at 35 days, where both initial and final clusters were similar than that obtained when was considered all body weights jointly (Fig. 1A). It was evidence that distances between clusters 1 and 2 were reduced when was compared with Fig. 1A. Therefore, body weight at 35 days might be considered to represent phenotypic variability between the six broiler chicken grandparent lines studied.

Table 2: Relative contribution (%) of body weight at 7 (BW7), 14 (BW14), 21 (BW21), 28 (BW28), 35 (BW35) and 42 (BW42) days of age for divergence between six lines

Trait	Contribution (%)
W7	1.77
W14	14.29
W21	5.88
W28	33.07
W35	36.62
W42	8.37

Table 3: Relative contribution (%) of eviscerated carcass yield (ECY), breast yield (BY) and leg yield (LY), at 42 days, for divergence between six lines

Trait	Contribution (%)
ECY	64.68
BY	29.60
LY	5.72

Table 4: Relative contribution (%) of back feathering at 28 (BF28), 35 (BF35) and 42 (BF42) days and leg feathering at 28 (LF28), 35 (LF35) e 42 (LF42) days, for divergence between six lines

Trait	Contribution (%)
BF28	65.43
BF35	10.40
BF42	0.35
LF28	13.75
LF35	2.12
LF42	7.95

Table 3 presents relative contributions of eviscerated carcass, breast and leg yield at 42 days, for divergence between the six broiler chicken grandparent lines. Eviscerated carcass yield presented the largest relative contribution (64.68%) while leg yield trait presented the smallest contribution (5.72%), being for this reason firstly removed from cluster analysis.

Four clusters were constituted in Fig. 2A: one composed by DL1 and DL2 lines, other composed by DL3 line, one more constituted by DL4 and last one composed by SL1 and SL2 lines. After, two clusters were constituted: one by DL lines and other by SL lines, discriminating clearly dam and sire line lines, when carcass traits were considered. It found in phenogram presented in Fig. 2B, where leg yield was removed, modification of initial clusters, when all yield traits were considered (Fig. 1A). Therefore, all yield traits must be used for representativeness of phenotypic variability between the six broiler chicken grandparent lines.

When morphometric traits were considered, back feathering at 42 days presented the smallest relative contribution (0.35%) for divergence between six broiler chicken grandparent lines and because of this it was eliminated from initial analysis (Table 4).

Initial cluster on morphometric traits (Fig. 3A) showed three clusters. The first constituted by DL1 and DL2 lines, the second by DL3 and DL4 lines, and the third by SL1 and SL2 lines were similar for body weights, but with different clusters in following analysis, where were

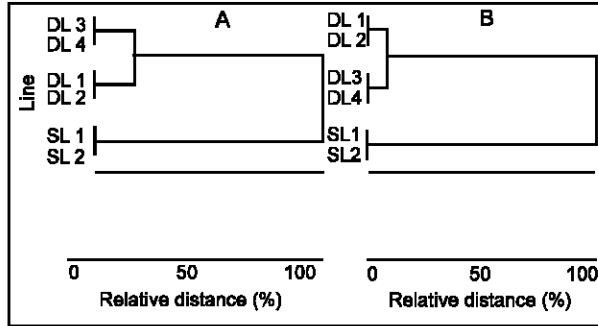


Fig. 1: Phenograms obtained from Mahalanobis distance (D^2) between lines, by UPGMA method: A) considering body weight at 7, 14, 21, 28, 35 e 42 days; and B) considering only body weight 35 days.

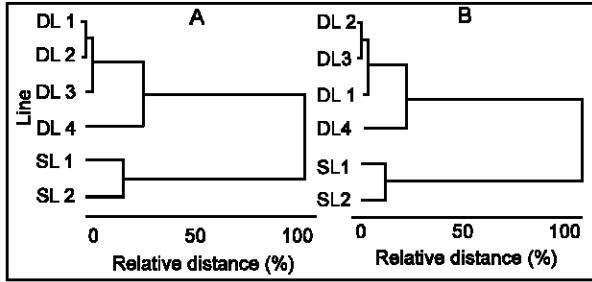


Fig. 2: Phenograms obtained from Mahalanobis distance (D^2) between lines, by UPGMA method at 42 days: A) considering eviscerated carcass yield, breast yield and leg yield; and B) considering only eviscerated carcass yield and breast yield.

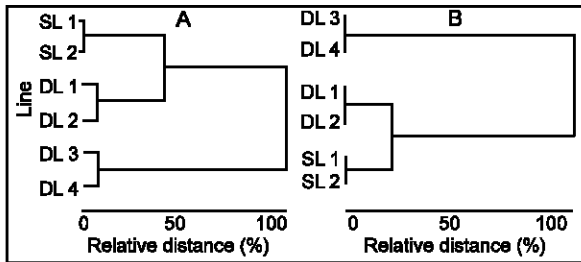


Fig. 3: Phenograms obtained from Mahalanobis distance (D^2) between lines, by UPGMA method: A) considering back and leg feathering at 28, 35 e 42 days; and B) considering only back feathering at 28 days.

constituted two clusters: one by SL1, SL2, DL1 and DL2 lines, and other by DL3 and DL4 lines, preventing the discrimination between DL and SL lines. Back and leg feathering at 42 days presented the smallest relative contribution (0.35%) for divergence, being initially removed of cluster analysis between lines,

without modification in initial and subsequent cluster composition considering all morphometric traits (Fig. 3A). After, other traits with small contribution were removed, obtaining a cluster composed by only back feathering at 28 days without modifications (Fig. 3B). Therefore, back feathering at 28 days can be used for representativeness of phenotypic variability between the six broiler chicken grandparent studied.

Discussion

This work investigated two points using cluster analysis: (1) selection of more representative traits in poultry breeding and (2) selection of better combinations between broiler chicken grandparent lines more divergent on phenotypic variability.

Among performance traits, only body weight at 35 days was select to represent the major part of phenotypic variability between the six broiler chicken grandparent lines studied. Indeed, this trait has been an important trait when the univariate analysis is used to assess broiler chicken performance, because it represents suitably chicken growth phenomenon. Among carcass traits, all traits must be used to explain phenotypic variability between the six broiler chicken grandparent lines studied. Our results are consisted with Berri *et al.* (2001), who studied the effect of selection for improved body composition on muscle and meat traits.

Back feathering was the most important trait to explain the major part of phenotypic variability between the six broiler chicken grandparent lines. Feathering traits have been studied by Proudfoot *et al.* (1979) who showed that higher densities (range 0.037, 0.055, 0.074, 0.0927m²/bird) resulted in lower final body weight, increased carcass damage, poorer feathering condition, and a linear increase in the percentage of downgrades related to breast blisters. Estevez (2007) suggested that science consistently indicates that the health and welfare of broilers can be achieved at a range of densities (rather than at a single density) most likely varying between 34 to 38 kg/m² to avoid feathering problems and losses in chicken performance.

Selecting these most representative traits was possible to select better combinations between broiler chicken grandparent lines more divergent on phenotypic variability. In fact, this selection is an important step in poultry breeding if the aim is select the best chicken lines whose crosses among them may create strains with high heterosis effect.

Indeed, heterosis has been used by poultry breeders who consistently practice directional phenotypic selection with some level of culling to eliminate Mendelian deleterious or unwanted alleles (Barbato, 1999). It may be beneficial to view heterosis for economic traits as coefficients of variation and as deviations from parental means. This approach may enhance improvements in performance as well as

uniformity, which is becoming increasingly important with greater mechanization in production and processing (Williams *et al.*, 2002).

Additionally, the use of cluster analysis became easier selection of chicken lines that probability to obtain better strains because were discriminated clusters with larger divergence. Thus, with observed results from clusters and considering the largest heterogeneity between broiler chicken grandparent lines from different clusters, the crosses between SL1 and SL2 lines with DL3 and DL4 lines might result in strain combinations with higher heterosis.

Our results may be also useful to establish a selection index in poultry breeding. Selecting the most important traits that explain the major part of total phenotypic variability between broiler chicken grandparent lines a necessary step to purpose a selection index. This index is characterized by combination of all economical traits in only one equation increasing the efficiency of selection process. In the most cases, designing selection index is very complex because a high number of calculations and of traits is included in index. Hence, it seems to be necessary more studies to determine what traits with higher representativeness of phenotypic variability between chicken lines must be used in development these indexes, allowing the maximization of selection process to obtain better genotypes and the minimization of time expended in this process.

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References

- Aerts, J.H., J. Megens, T. Veenendaal, I. Ovcharenko, R. Crooijmans, L. Gordon, L. Stubbs and M. Groenen, 2007. Extent of linkage disequilibrium in chicken. *Cytogenet. Genome Res.*, 117:338-345.
- Barbato, G.F., 1999. Genetic relationships between selection for growth and reproductive effectiveness. *Poult. Sci.*, 78: 444-452.
- Barbosa, L., A.J. Regazzi, P.S. Lopes, F.C. Breda, J.L.R. Sarmiento, R.A. Torres and T.A. Torres Filho, 2005. Evaluation of genetic divergence among lines of laying hens using cluster analysis. *Braz. J. Poult. Sci.*, 7: 79-83.
- Berri, C., N. Wacrenier, N. Millet and E. Le Bihan-Duval, 2001. Effect of selection for improved body composition on muscle and meat characteristics of broilers from experimental and commercial lines. *Poult. Sci.*, 80: 833-838.
- Canadian Council on Animal Care, 1993. Guide to the use of experimental animals (Ottawa: CCAC).
- Dobek, A., K. Moliński, M. Szydlowski and T. Szwaczkowski, 2000. Analysis of single gene multitrait effects in livestock by the use of Gibbs sampling. *J. Appl. Gen.*, 41: 275-283.
- Dodgson, J.B., 2007. The chicken genome: Some good news and some bad news. *Poult. Sci.*, 86: 1453-1459.
- Estevez, I., 2007. Density allowances for broilers: Where to set the limits?. *Poult. Sci.*, 86: 1265-1272.
- Flock, D.K., K.F. Laughlin and J. Bentley, 2005. Minimizing losses in poultry breeding and production: how breeding companies contribute to poultry welfare. *World's Poult. Sci. J.*, 61: 227-237.
- Johnson, R.A. and D.W. Wichern, 1992. Applied multivariate statistical analysis (New Jersey: Prentice Hall).
- Lahav, T., G. Atzmon, S. Blum, G. Ben-Ari, S. Weigend, A. Cahaner, U. Lavi and J. Hillel, 2006. Marker-assisted selection based on a multi-trait economic index in chicken: experimental results and simulation. *Anim. Gen.*, 37: 482-488.
- Minville, F., B.B. Kayang, M. Inoue-Murayama, M. Miwa, A. Vignal, D. Gourichon, A. Neau, J.L. Monvoisin and S. Ito, 2005. Microsatellite mapping of QTL affecting growth, feed consumption, egg production, tonic immobility and body temperature of Japanese quail. *BMC Genomics*, 6: 87.
- Proudfoot, F.G., H.W. Hulan and D.R. Ramey, 1979. Effect of 4 stocking densities on broiler carcass grade, the incidence of breast blisters, and other performance traits. *Poult. Sci.*, 58: 791-793.
- Rao, C.R., 1952. Advanced statistical methods in biometric research (New York: John Wiley).
- Rosário, M.F., M.A.N. Silva, A.A.D. Coelho and V.J.M. Savino, 2007. Estimating and predicting feed conversion in broiler chickens by modeling covariance structure. *Int. J. Poult. Sci.*, 6: 508-514.
- Rosário, M.F., M.A.N. Silva, V.J.M. Savino, A.A.D. Coelho and M.C. Moraes, 2005. Evaluation performance of the broiler chicken genotypes through repeated measures. *Braz. J. Anim. Sci.*, 34: 2253-2264 (Suppl. 5). (in Portuguese).
- Singh, D., 1981. The relative importance of characters affecting genetic divergence. *Ind. J. Genet. Plant Breed.*, 41: 37-245.
- Sneath, P.H. and A.R.R. Sokal, 1973. Numerical taxonomy (San Francisco: Freeman).
- Szwaczkowski, T., M. Szydlowski, K. Moliński and A. Dobek, 2001. Multivariate analysis of mixed inheritance model of performance traits in layers using Gibbs sampling. *J. Anim. Breed. Gen.*, 118: 205-211.
- Szydlowski, M. and T. Szwaczkowski, 2001. Bayesian segregation analysis of production traits in two strains of laying hens. *Poult. Sci.*, 80: 125-131.
- Tryon, R.C., 1939. Cluster analysis (New York: McGraw-Hill).
- Williams, S.M., S.E. Price and P.B. Siegel, 2002. Heterosis of growth and reproductive traits in fowl. *Poult. Sci.*, 81: 1109-1112.
- Yang, N. and R.S. Jiang, 2005. Recent advances in breeding for quality chickens. *World's Poult. Sci. J.*, 61: 373-381.