IMPROVING THE EFFICIENCY OF TURKEY BREEDING PROGRAMS
THROUGH SELECTION INDEX DESIGN, TECHNOLOGICAL
ADVANCEMENTS, AND MANAGEMENT OPTIMIZATION

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LINDSAY ANNE CASE

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ABSTRACT

IMPROVING THE EFFICIENCY OF TURKEY BREEDING PROGRAMS THROUGH SELECTION INDEX DESIGN, TECHNOLOGICAL ADVANCEMENTS, AND MANAGEMENT OPTIMIZATION

Lindsay Case
University of Guelph, 2011

Advisors:
Dr. Stephen P. Miller
Dr. Ben J. Wood

Breeding objectives in the turkey industry are heavily weighted towards improving growth traits. This thesis focused on methods to efficiently select for other important production traits such as reproduction, feed efficiency, and meat yield. Based on bivariate and random regression modeling it was determined that egg production, fertility, and hatchability were influenced by genotype by environment interactions and, as a result, the regulation of reproductive traits is by some unique genes in the summer and winter. This may be due to changes in day length and temperature. Feed efficiency is another important consideration in a breeding objective and feed conversion ratio and residual feed intake were both moderately heritable. Residual feed intake was also more independent of production traits than feed conversion. Feed intake, body weight, and weight gain were moderately heritable and progress can be made in feed efficiency by appropriately weighting these traits in an index. Infrared measures of surface temperature were then investigated to determine if they can be used to select for feed efficiency. Temperatures of the distal metatarsus, eye, neck, and head did not show a strong relationship to feed efficiency and therefore offer limited advantages to a breeding program. Selection for breast meat yield (BMY) is important and it was determined that
breast muscle depth, measured with ultrasound technology, is heritable and highly correlated to the carcass trait. As a result, ultrasound traits can compliment conformation scoring and sibling testing in a breeding program to increase the accuracy of selection for BMY and increase response to selection. A deterministic model was also developed and could be used to determine optimum slaughter weight. This would optimise profits in an integrated system, enabling the industry to account for and capitalize on genetic gains. Overall, the population parameters and selection criteria identified for reproduction, efficiency, and meat yield traits identified in the present thesis could be used to increase selection efficiency in turkey breeding programs. Further, the developed production model can be used by the industry to slaughter turkeys at a time that maximizes profits, based on performance levels.
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Chapter 1

General Introduction

The turkey industry is an important segment within the livestock production sector of the economy and the top ten turkey-producing countries generate approximately 6 billion kilograms of turkey meat annually (Agriculture and Agrifoods Canada, 2007). In 2009, 1.2 million tons of poultry meat was produced in Canada and consumption of poultry meat has increased by 1.9 kg per person over the past decade (Statistics Canada, 2009; 2011). Turkey consumption by Canadians has increase by 6% per person over this time period, which is a promising trend as chicken consumption in Canada has remained stable and the consumption of red meat has decreased (Statistics Canada, 2009). The market value of turkey meat in the Canadian quota system has also increased by 1.1% since 2007, despite an economic recession (Statistics Canada, 2011). While there has been a recent decline in turkey consumption in US markets, per capita consumption is forecasted to stabilize in 2011 (Johnson, 2010). On a global scale, poultry will represent the world’s most popular meat by 2030 (Executive Guide to World Poultry Trends, 2010).
While consumption of turkey meat is increasing, the number of companies managing pure-line breeding stock has decreased over the past 30 years and, currently, only two companies control the world’s commercial genetic stock. As a result, there is a large responsibility for these companies to develop appropriate breeding objectives and selection programs to meet market requirements and to generate genetic progress that will enable turkey products to most efficiently meet demands while managing line bio-security for the safe preservation of genetic stocks.

In the turkey industry, primary breeders have developed many pure bred lines, each with a specialized breeding objective, and the commercial turkey is a four-way cross. Specialized male and female pure lines are selected to contribute to unique final products, each of which is tailored to meet the needs of different markets. Based on this industry structure, the turkey breeding industry has been successful at achieving genetic gains and increasing performance levels. From 1966 – 2003 growth rate to market age has approximately doubled in the turkey and feed efficiency has increased by approximately 20% (Havenstein et al., 2007b). While limited turkey studies have not clearly distinguished the relative impact of genetics and management to the improved performance levels, it has been estimated that 85 – 90% of the improvements in broiler performance have been due to an increase in the genetic potential of birds (Havenstein et al., 1994; Havenstein et al., 2007a).

Genetic gains in the turkey industry are accomplished by selection in the pure lines. Body weight remains the most prominent trait for selection due to its high impact on carcass value, meat production cost, and the ease of selection due to its high heritability and breeding programs also balance selection for production and reproductive
traits. As a result, the relationship of other economically important traits to body weight must be carefully considered as it will have a strong influence on rates of gain as well as overall economic return. For example reproduction is important, particularly in the female lines. Egg production, fertility, and hatchability of the hen impact industry efficiency as performance levels reflect the number of dams required to meet production needs. Improvement of reproductive traits will thus have benefits to both an integrated company as well as independent growers. Selection for feed efficiency is also important and the trait has a large impact on profit levels for production, especially at the downstream industry segments which manage the largest proportion of birds in the production system. Increasing growth performance without a large increase in feed requirements for the birds is, as a result, an important consideration in a breeding goal. Consumer demands are a further consideration for primary breeding companies and the popularity of white meat, based on consumer desirability, has made increasing breast meat yield valuable. Overall, the genetic gains in growth that are the focus of turkey breeding must be balanced by improvements in other traits that impact production efficiency, financial gains, and consumer desires.

The turkey industry relies on the cooperation of the primary breeder, multiplier, commercial producer, and processor. The number of birds within each industry segment increases exponentially and, as a result, the design of a selection program is critically important. This necessity of an effective breeding program is amplified in the turkey industry due to the limited number of primary breeding companies, as discussed. As a result, there is a large responsibility for each primary breeder to maintain and improve
their genetic stock in a responsible manner to ensure a stable supply of high-quality
turkey products.

Modeling of the traits in a breeding program as well as population parameters for
traits must be accurate to optimize the rate of genetic gain. Accordingly, reliable
estimates of genetic parameters in the population are essential to develop a selection
index with the optimal selection criterion and the appropriate weights on traits. Genetic
parameters are also required to predict both direct and correlated responses to selection,
which will have an impact on overall progress in a breeding program. While improved
performance levels over time have shown the success of traditional selection criteria, it is
also important to investigate novel traits that can be used to accelerate gains in the
breeding objective. In the turkey industry, birds are selected at commercial age and,
therefore, generation interval is not practically reduced. As a result, novel selection
criteria that increase the accuracy of selection are important to identify and new
technologies offer the opportunity to more accurately measure turkey performance and
accelerate the rate of genetic gain. While decisions made at the primary breeder level
flow downstream to affect all segments of the industry, it is essential for commercial
producers to optimize their flock management. Tools to help producers make the best
decisions to maximize financial gains will thus improve industry efficiency as a whole.

An accurate selection index is the foundation of a successful breeding program.
The goal of the first two studies in this thesis was to investigate the modelling of egg
production, fertility, and hatchability in the turkey to determine if the consideration of
each of reproductive phenotype as a single trait across seasons was optimal for selection.
Increasing the efficiency of selection for reproductive traits is of particular importance
due to the antagonistic relationship between these traits and body weight, which is a primary focus of selection.

Genotype by environment (GxE) interactions invalidate the assumption that superior genes in one environment are superior in another environment. Consequently, genetic progress based on single trait selection is not efficient. Turkey egg production, fertility, and hatchability performance levels fluctuate seasonally. If these trends are caused by an underlying change in the genes controlling each trait throughout the year, a genotype by environment interaction is influencing reproduction in the turkey hen.

Through the investigation of these trends the objective of the first study was to use a bivariate model to evaluate a GxE interaction for reproductive traits in the turkey. Study two aimed to support the bivariate conclusions by studying individual variation in phenotypic plasticity using a random regression modelling approach. Study two also had an objective to identify if changes in day length or temperature could be contributing to this effect. Once identified, a GxE interaction could be considered in the development of breeding programs to maximize genetic progress.

Feed efficiency is an economically important trait and must be considered in a breeding program due to the positive correlations between bodyweight traits and feed intake. As a result, it is necessary to limit the increase in production costs related to feed as growth rate improves. Genetic parameters of feed efficiency measures in the turkey are not widely published and there is a need to determine the heritability of direct measures of feed efficiency as well as the relationship of efficiency to growth traits and efficiency constituent traits. Feed conversion ratio and residual feed intake are both commonly considered measures of feed efficiency in livestock (Herd and Bishop, 2000;
Cai et al., 2008; Aggrey et al., 2010). The aim of study three was to determine the genetic parameters of these direct measures of feed efficiency as well as their relationships to body weight, growth, and feed intake. This information is required for the development of a selection index to determine selection index weights and predict responses to selection. These parameters are also necessary to develop an index that will improve growth performance while controlling any correlated acceleration in the required feed levels.

To meet the increasing global demands for poultry meat, primary breeders must aim to continuously improve selection efficiency. To this end, it is important to investigate novel selection criteria that can increase progress in the breeding objective. The number of selection candidates with individual feed efficiency estimates in a turkey breeding program is limited by the high cost of feeding trials. Consequently, a correlated trait would be advantageous to incorporate into a selection index to improve the accuracy and intensity of selection, which will help control feed efficiency.

Heat is produced as a by-product of metabolism and heat exchange in birds occurs across the skin surface. Thus, variation in surface temperature may be correlated to turkey feed efficiency. If a relationship between infrared images of surface temperature and feed efficiency exists, temperature traits could be incorporated into a selection index. With the potential to capture infrared images on all selection candidates, not just those in a feeding trial, selection intensity would be increased. Consequently, the objective of the fourth study was to determine if infrared imaging could be used to measure surface temperature of the turkey and to estimate the correlation between infrared traits and feed efficiency.
Balancing improvements in traits related to feed efficiency and reproduction will have a general and widespread positive influence on the turkey industry, which is driven by the benefits associated with increased body weight and growth traits. It is also important, however, for breeders to consider consumer demands in the final turkey product. This has made selection for increased breast meat yield valuable. The positive relationship between the absolute weight of the breast muscle and body size is inherent, however increasing the percentage of breast meat on the carcass is a profitable aim for turkey breeders. Consequently, it would be extremely valuable to identify methods that will improve the evaluation of breast meat yield in the live turkey. The current in vivo selection criterion for breast meat yield is based on conformation scoring and a limited amount of cut-up information is also available on siblings of selection candidates. While this technique has been successful, conformation scoring is subjective and requires discretion by the individual taking the measurement. As a result, it is important to identify new in vivo traits that can be objectively measured to increase the rate of gain in meat yields.

Ultrasound can be used to quantitatively measure the depth of tissues on a live bird. As a result, this technology has the potential to estimate the depth of the turkey breast. If this measure is heritable and highly correlated to true breast meat yield, ultrasound measured breast depth can be used to compliment or replace conformation scoring in a selection program. The objective of the fifth study was to determine if an ultrasound measure of muscle depth could be used to increase the accuracy of selection for breast meat yield by considering new sources of information. Accelerating the
increase in breast meat yield, relative to overall body weight, would have a positive effect on profitability and would produce a turkey product that better meets consumer needs.

The initial studies of this thesis consider the design of a breeding program to optimize the rate of genetic gain in reproduction, efficiency, and meat yield traits. This genetic progress would be reflected by an increase in production profitability. Improvement in the gross margin, however, is also greatly affected by flock management. Tools to identify the most optimum time to slaughter a turkey, based on the parameters that change as the bird grows, are therefore useful. Models that describe a turkey production system have been developed and include all of the financial inputs and outputs, as related to turkey biological traits. These sets of equations can be adapted to model the change in financial inputs and returns as a reflection of the biological changes that occur as a bird develops. The point during production when the gross margin is maximized can therefore be identified and, as a further advantage, the framework for such a model can be adapted to reflect the current economic climate. Modelling tools can therefore be used at the commercial producer level to make decisions that will compliment advances in genetics to improve the profitability of turkey production.

The turkey industry is highly integrated and, as outlined, increasing body weight and growth while balancing improvements in other economically important traits is the primary goal of a breeding program. To continually increase overall efficiency of the industry progress in reproductive traits, feed efficiency, and consumer appeal must also be carefully considered. The design of a breeding program must therefore balance selection for all of these traits. To optimize response to selection, traits must be properly modelled and the genetic parameters in the population must be understood. The traits
included in the selection program must also be considered and, as technology develops, there is an opportunity to identify novel selection criteria that will accelerate progress in the breeding objective. Producers must also be conscientious as proper management decisions are required to capitalize on the genetic gains. As a result, the studies in this thesis provide information and methods to improve the success of turkey breeding programs by ensuring selection indexes optimize selection for reproductive, efficiency, and meat yield traits as these all impact industry efficiency. The thesis further develops tools that can be used at the producer level to maximize financial gains.
Chapter 2

Genotype by environment interaction as it relates to egg production in turkeys (Meleagris gallopavo)

L. A. Case,* M. J. Kelly,* S. P. Miller,* and B. J. Wood*†

*Department of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada;

†Hybrid Turkeys, Suite C, 650 Riverbend Drive, Kitchener, Ontario, Canada

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2.1 Abstract

Genotype by environment (GxE) interactions can reduce the accuracy of a model to predict an animal’s performance and have an undesirable influence if not accounted for when estimating breeding values. Consequently, identification of these GxEs is necessary when considering a turkey breeding program. If a GxE exist, re-ranking based on the genetic prediction of turkey egg production, fertility, and hatchability in different seasons would occur. Quantification of the GxE interactions was based on the genetic correlation estimated when traits were expressed in different seasons. Egg production was expressed as the percentage of days with an egg produced, fertility represented the proportion of hatched eggs that contained a fertile embryo, and hatchability was defined as the percent of fertile eggs that produced a live bird. Variance components and heritability for egg production, fertility, and hatchability were estimated using ASReml. The heritability ($h^2$) of egg production was calculated to be 0.32 for both lines with the phenotypic ($\sigma^2_p$) and genetic ($\sigma^2_g$) variance, 141.3 and 45.58 (percent days with egg produced)$^2$ and 118.3 and 38.35 (percent days with egg produced)$^2$ for female and male lines, respectively. The $h^2$ estimates for fertility were 0.08 in both lines with $\sigma^2_p$ and $\sigma^2_g$ of 293.3%d and 24.03%d, and 576.9%d and 48.43%d for female and male lines, respectively. The hatchability $h^2$, $\sigma^2_p$ and $\sigma^2_g$ estimates were 0.09, 267.1%d, and 24.44%d, respectively for the female line and 0.15, 582.2%d and 90.01%d for the male line. Based on an animal model, the variance components were used to calculate estimated breeding values for each trait. The annual fluctuation in estimated breeding values resulted in the need to evaluate egg
number, fertility, and hatchability as two traits; summer and winter lay. The correlation between the two traits was less than unity (female line: $r_{\text{egg production}}=0.76$, $r_{\text{fertility}}=-0.20$, $r_{\text{hatchability}}=0.75$ and male line; $r_{\text{egg production}}=0.86$, $r_{\text{fertility}}=0.19$, $r_{\text{hatchability}}=0.68$) suggesting a GxE interaction and animals will significantly re-rank in genetic predictions for these reproductive phenotypes in different seasons of lay. Egg production, fertility, and hatchability in turkeys could be considered as two distinct traits in an animal model based on season of lay.

2.2 Introduction

The turkey breeding industry is driven by increasing growth rates, while balancing improvement in other economically important traits, as this results in a more profitable turkey product. Due to the negative relationship between growth traits and production traits (Nestor et al., 2000) it is important for breeding objectives to balance selection for reproductive performance as well. Reproductive traits are more heavily weighted in female line turkeys, and the traits should be properly modelled in a selection index to ensure optimal selection efficiency.

Environmental sensitivity refers to the different phenotypic expression of a genotype in response to different environments (Kolmodin et al., 2003). Reproductive traits can fluctuate annually (Horn and Perenyi, 1974; Tona et al., 2007) and this may be due to phenotype regulation by different genetic controls in different seasons. If environmental sensitivity is not consistent for all individuals, a genotype by environmental interaction (GxE) will result. Due to the varying magnitude of phenotypic change between environments there is a re-ranking of individuals for trait expression and,
consequently, selection for superior performance in one environment will not necessarily result in enhanced performance under other sets of environmental conditions (Falconer and Macay, 1996).

Genotype by environment interactions have been detected for egg production in layer hens and body weight traits in broiler chickens (Mathur and Horst, 1994; Settar et al., 1999). High performance genotypes in the spring were associated with low EBVs under the heat stresses of summer. As seen with body weight, seasonal environmental changes may be producing the GxE observed for egg production in layer chickens. Currently, there is no documented literature investigating seasonal GxE interactions for turkey reproductive traits.

The aim of the current study was to estimate reproductive trait genetic parameters in male and female turkey lines and to investigate if a GxE interaction existed for egg production, fertility, and hatchability in different seasons. Identification of any interactions could lead to the consideration of distinct seasonal traits in selection decisions to more effectively manage the selection for egg production.

2.3 Materials and methods

2.3.1 Study Population and Management

The populations used were a commercial large white female (n_{total} = 430,975, n_{sire} = 2,195, n_{dam} = 10,471) and male (n_{total} = 423,159, n_{sire} = 1,772, n_{dam} = 15,949) line with a breeding objective balanced between commercial and reproductive traits. Full pedigree information was available for each line. A stronger selection emphasis was placed on reproductive traits in the female line compared with the male line. Traits were
recorded between 1995 and 2007 and trait values for egg production (n \text{female line} = 8,809, n \text{male line} = 13,875), fertility (n \text{female line} = 8,787, n \text{male line} = 15,735), and hatchability (n \text{female line} = 8,765, n \text{male line} = 15,631) were recorded. The male to female ratio in the female and male lines was 1 to 5 and 1 to 10, respectively. Artificial insemination was used for all matings, with 203 flocks across the 13 year period and a consistent number of hens starting lay throughout the year. All eggs were stored for between 4 and 14 days.

Rearing until 20 weeks of age was under a standard commercial production environment and feeding regime. After 20 weeks of age hens were placed onto a commercial parent stock bodyweight restriction diet. Lighting programs, designed to induce lay, were controlled in dark-out barns and lighting consisted of equal 12 hourly periods of light and dark with a light intensity of approximately 107 LUX. From 16 – 30 weeks birds were exposed to 6 hourly periods of dark and 18 hours of light with an intensity of approximately 88 LUX. Light intensities could be varied with flock requirement, bird temperament and other management factors. From 30 weeks of age the light conditions consisted of 16 hours of light with an intensity of approximately 107 LUX and 8 hourly periods of dark.

Egg production was evaluated as percentage days with egg produced between 30 and 60 weeks of age. Fertility was measured as the proportion of eggs that were candled fertile. Hatchability was calculated as the percentage of fertile eggs that produced a live poult. Based on these trait definitions, hens had a single record for each reproductive trait.
2.3.2 Statistical Analysis

Variance components and heritability for egg production, fertility, and hatchability were estimated with ASReml (Gilmour et al., 2002). Values were preliminarily estimated within line for each reproductive trait in a single trait model. The following animal model was used to estimate additive genetic effects for all traits as a single annual trait:

\[ y = \mu + flock + b(\text{age}) + a + e \]

where \( y \) was the evaluated trait (egg production, fertility and hatchability) and \( \mu \) the average trait value of all animals. \( Flock \) was a fixed classification factor incorporated to account for the temporary environmental effects influencing each group of hens laying in a barn at the same time and the \( age \) regression accounts for the age of the hen. These fixed effects were included in all single and multiple traits models. \( a \) and \( e \) represent the random animal additive genetic effect and residual random effect, respectively. Analysis of variance of the animal model was used to determine the significance of fixed effects.

EBVs from the single trait models were plotted and seasonal partitioning of the data was based on observed EBV transition patterns. Based on more consistent values associated with the performance levels from January—May and July—November, these periods were defined as the summer lay (GxE Summer) and winter lay (GxE Winter) seasons, respectively. June and December were considered transitional periods.

A single trait analysis for the summer and winter lay traits was conducted by treating traits across the seasons as uncorrelated and genetic parameters were estimated. A bivariate model was then used to generate parameter estimates incorporating the
covariance between the traits, within line. The random animal and residual effects were assumed to be normally distributed with a mean of zero and a covariance:

\[
\text{Var} \begin{pmatrix}
a_{\text{GxEWinter}} \\
a_{\text{GxESummer}} \\
e_{\text{GxEWinter}} \\
e_{\text{GxESummer}} \\
\end{pmatrix} = 
\begin{pmatrix}
A\sigma^2_{a\text{GxEWinter}} & A\sigma_{a\text{GxEWinter},\text{GxESummer}} & 0 & 0 \\
A\sigma_{a\text{GxEWinter},\text{GxESummer}} & A\sigma^2_{a\text{GxESummer}} & 0 & 0 \\
0 & 0 & I\sigma^2_{e\text{GxEWinter}} & I\sigma^2_{e\text{GxESummer}} \\
0 & 0 & I\sigma^2_{e\text{GxEWinter}} & I\sigma^2_{e\text{GxESummer}} \\
\end{pmatrix}
\]

where \( A \) represents the relationship matrix. A genetic correlation between summer and winter lay, calculated based on the covariance between seasons \((A\sigma_{a\text{GxEWinter},\text{GxESummer}})\), of less than 1 would indicate a GxE is impacting the reproductive traits.

To account for genetic trends in the EBVs estimated by BLUP for egg production, fertility, and hatchability as the result of selection over time, monthly average EBVs from the bivariate model were adjusted as:

\[
EBV = \mu + \text{hatch\_year} + \text{hatch\_month}
\]

where \( EBV \) equals \( EBV_{\text{all}} \), \( EBV_{\text{GxEWinter}} \) or \( EBV_{\text{GxESummer}} \) and \( \mu \) was the average breeding value for all animals. \( \text{Hatch\_year} \) was a fixed classification effect representing the hatch year of the turkey and \( \text{hatch\_month} \) was a fixed class effect representing the month a poult was hatched. These time adjusted EBV values were used to calculate annual EBV fluctuations as the difference between the highest monthly EBV value and the lowest monthly EBV value.
2.4 Results

Heritability estimates from the single trait, uncorrelated seasonal trait, and bivariate models are shown in Table 2.1, Table 2.2, and Table 2.3 for egg production, fertility, and hatchability, respectively. The flock and age effects in the animal model were significant for all reproductive traits (P < 0.05), except for the effect of age on hatchability (P < 0.12 for the male line and P < 0.17 for the female line). Based on the initial single-trait model analysis, phenotypic performance for turkey reproductive traits fluctuated annually as shown in Figure 2.1. The patterns of EBVs, used to determine appropriate season definitions, showed that the EBVs for June and December were not consistent with either summer (January - May) or winter (July - November) EBVs. These two months were, therefore, considered transitional and were not included in either seasonal trait definition. As the correlation between seasons is the focus of the present study, the omission of this data in the bivariate model will not greatly impact the analysis of a GxE.

Plotting of the egg production phenotype in both the female and male lines resembled a normal distribution, with a slightly elongated tail towards lower trait values. The annual breeding value fluctuations for egg production are shown in Figure 2.2a. Breeding value estimates were not consistent between the summer lay season and the winter lay season in either line and these trends persisted when seasonal traits were plotted independently in Figure 2.3a. Analysis using a bivariate model resulted in higher heritability values for the seasonal traits, indicating a larger proportion of phenotypic variance was explained by genetic factors (Table 2.1). The correlation between summer and winter lay traits was 0.76 and 0.86 for the female and male lines, respectively. These
values depart from a correlation of unity (r = 1) and indicate that selection decisions made on one environment would decrease the accuracy of selection in the other environment due to ranking inaccuracies of selection candidates.

Variance component and heritability estimates for fertility are shown in Table 2.2. Using a bivariate model did not change heritability estimates, however incorporating a GxE interaction reduced the level of difference between variance components in the summer and winter traits. Breeding values were not consistent annually in both the single trait and multiple trait analysis, and EBVs were higher in the winter season than the summer season (Figure 2.2b and Figure 2.3b). The average fertility value was higher and phenotypic standard deviation smaller in the female line ($\mu = 85.7\%$, $SD = 12.2\%$) than the male line ($\mu = 75.4\%$, $SD = 24.7\%$). The high mean value and low standard deviation resulted in a non-normal distribution of fertility in the female line, as shown in Figure 2.4. The correlation between seasonal fertility traits was -0.20 for the female line and 0.43 for the male line. These values are lower than one which is indicative of a GxE for fertility.

The hatchability phenotype followed a normal distribution, however there was a truncation of the upper tail at the maximum value of 100%. This truncation of the tail was not as severe as the pattern seen for fertility and was assumed to not have largely influenced the parameter estimates. Incorporating a GxE into the model increased heritability estimates for the seasonal traits in both lines, except for winter lay in the female line. The range in EBVs for the female and male lines is shown for a single annual trait in Figure 2.2c and from the multiple trait model in Figure 2.3c. Breeding value estimates from both models showed elevated values in the summer lay season.
relative to the winter lay season. The correlation between hatchability expressed as a summer and winter lay trait (female line, $r = 0.75$ and male line, $r = 0.68$) indicates that a GxE interaction will result in a ranking discrepancy for one seasonal trait when selection decisions are based on performance in the other season (Table 2.4).

### 2.5 Discussion

The impact of GxE interactions on a breeding program must be considered, because genetic correlations between environments that are lower then unity can result in a re-ranking of selection candidates between environments (Falconer and Macay, 1996). Robertson (1959) suggested that genetic correlations of less than 0.8 were indicative of a significant GxE. More recently, Smith and Banos (1991) and Mulder and Bijma (2006) investigated GxE interactions in dairy cattle populations and determined that if genetic correlations between environments are lower than 0.8 to 0.9, genetic gain can be increased by selection across environments. The calculated genetic correlations for reproductive traits in the turkey ranged from -0.20 to 0.86 indicating that single-trait selection is limiting the possible rate of genetic progress (Table 2.4). This is because each reproductive phenotype is controlled by different genes to some extent, or different emphasis on an overlapping set of genes in the summer and winter, which will result in the re-ranking of performance levels in one environment when EBVs are based on measurements taken in the other season. As a result, the structure of selection programs related to turkey reproductive traits should be considered to increase rates of genetic progress in both seasons.
Once induced to lay at approximately 30 weeks of age, hens are routinely in production for between 24 and 30 weeks and as a consequence many turkeys will lay across seasons, which necessitates the genetic improvement of both seasonal traits. When genetic correlations are greater than 0.61, a single breeding program which estimates breeding values in both environments and has a breeding goal to simultaneously improve genetic gain in both environmental traits is most effective (Mulder et al., 2006). The calculated correlations in the current analysis meet this criteria, with the exception of fertility. Incorporating reproductive traits as $EBV_{GxEW}$ and $EBV_{GxES}$ into the standard selection index to evaluate the birds based on performance in both seasons could therefore increase the rate of genetic progress for the traits. Mulder et al. (2006) determined that for traits with correlations of less than 0.61, or with high levels of selection intensity, it can be more effective to run two separate breeding programs specific to each environment. This option, however, is unrealistic for turkey production systems because each evaluated animal can perform and contribute genetics to offspring performing in both production seasons.

Determining the relative selection importance for winter lay and summer lay traits, based on a breeding objective to improve overall performance levels, can be difficult when attempting to improve the rate of genetic gain using the selection index approach (Wood, 2009). One approach could involve equally weighting each seasonal trait. A second consideration could involve increasing the relative importance of the seasonal trait with lower performance levels in an effort to increase performance consistency throughout the year. As a result, there are two potential index-based ways to improve overall reproductive performance, either by improving both seasonal traits at the
same rate or by placing additional selection emphasis on the lower performance environment to also increase phenotypic consistency between seasons. Turkey breeding programs currently utilize BLUP to make selection decisions and this approach would identify birds with the most favourable performance across the year by taking into account summer and winter reproduction levels through relatives. The results from this study were therefore important to better understand the underlying genetic mechanisms that are influencing genetic improvement for egg production, fertility, and hatchability in a turkey breeding program.

Considering the impact of current turkey breeding programs, genetic selection has led to major improvements in growth characteristics in modern commercial birds (Havenstein et al., 2007b). This has been due to an industry focus primarily on improving meat yield and efficiency and less selection emphasis has been placed on reproductive ability due to its lower relative economic value compared to growth characteristics (Wood, 2009). Extensive research has been conducted on reproductive traits in broilers (Sharma et al., 1984; Tona et al., 2007) and as selection emphases and performance requirements are similar in broiler and turkey breeding programs, broiler variance component estimates and trait expression characteristics can be used as preliminary indicators of potential values in the turkey, where there have been fewer reported studies.

Heritability estimates for egg production in the turkey have ranged from 0.13 to 0.61 (McCartney et al., 1968; Nestor et al., 1996) and single trait selection for egg production in the turkey can result in significant increases in egg numbers within a small number of generations (Asmundson and Lloyd, 1935; Knox and Marsden, 1954). Low to moderate heritability estimates for fertility of 0.42, 0.18, and 0.34 have been estimated in
the turkey hen (Mccartney et al., 1968; Nestor et al., 1972; Dunnington et al., 1990). Similar to the fertility reproductive trait, reported heritability estimates for hatchability in the turkey of 0.16 and 0.17 are in the low range (Mccartney et al., 1968; Nestor et al., 1972). The moderate heritability estimate for egg production and low estimated values for fertility and hatchability in the turkey population in the current analysis are in agreement with previously published estimates.

The heritability, genotypic, and phenotypic variances were not consistent between seasons for egg number, fertility, and hatchability when modelled as two distinct traits. This indicates that seasonal environmental influences affect egg production, fertility, and hatchability genotypes to a different extent suggesting a GxE, which was supported by the genetic correlation below 1.0 for each trait expressed in different seasons (Table 2.4). Environmental sensitivity lowers the heritability of traits as the phenotypic expression is dispersed over different environments (De Jong, 1990). This trend was observed in the current analysis, as heritability estimates were higher from the bivariate model for fertility and hatchability in both lines. The increased heritability estimates can be attributed to increasing genetic variance, as shown in Table 2.1, Table 2.2, and Table 2.3, when each reproductive phenotype was considered as two seasonal traits. This indicates that the bivariate model can help to remove a portion of the confounding effect caused by some variability in the genetic control of performance across the two seasonal production environments.

A strong and negative correlation (-0.20) between fertility expressed in the summer and winter seasons was detected in the female line. Using an animal model to estimate variance components, the distribution of trait values was assumed to be normal.
Due to selection for reproductive traits in the female line, fertility performance is nearing the biological maximum of 100% with a high average value and low variance. This non-normal distribution of fertility in the female line in conjunction with a low range in trait values, resulted in a restricted ability of fertility to change in response to environmental fluctuations as values remain high under all conditions as shown in Figure 2.4. In contrast, the genetic correlation in the male line is more representative of environmental influences seen in other traits in this study. In this population, the phenotypic average is lower and the variance in phenotypic values is higher, allowing for greater freedom to alter the performance levels in response to climatic fluctuations. When the distributions of egg production and hatchability performance were plotted the phenotypic records were close to resembling a normal distribution, and the impact on non-normality was assumed to have a little impact on parameter estimations for these traits.

The genetic trends detected in this study are related to turkey reproductive physiology, and turkey populations are stimulated by environmental cues to come into season and lay. Critical day length (CDL) must be exceeded together with a sufficient contrast in light intensity, to simulate night and day, for egg production to occur (Siopes, 1994). A fluctuating trend in reproductive performance was evident in the studied turkey population that could not be explained by changes in photoperiod or intensity, as these were managed in light proof barns with all the light controlled. Barn management cannot completely eliminate turkey exposure to seasonal changes in temperature and humidity and as a consequence, the ambient environment is not consistent throughout the year. As a result, GxE interactions influenced by climate may be expressed in the turkey.
The preliminary evidence for GxE interactions is change in performance levels between environments and this has been evidenced in broilers where seasonal environmental differences effect reproductive performance. Changes in performance of varying magnitude as the ambient temperature and humidity fluctuate have resulted in a re-ranking of genotypes (Mathur and Horst, 1994; Yalcin et al., 1997). Evidence of the ambient environment creating a GxE was reported by Hartmann (1990), as the correlation between egg production expressed in different geographical locations was below unity. Egg production has been shown to decrease in response to heat stress in broilers (McDaniel et al., 1995). This trend was also reflected in a study of the variation in broiler egg production levels between seasons, with the lowest egg production levels expressed in the summer months (Torshizi et al., 2008). The environmental influence on broiler egg production supports the GxE detected in the current study of egg production in the turkey. Broiler fertility is lowest in the summer compared to other times of the year (Smyth and Leighton, 1953; Horn and Perenyi, 1974; Keirs, 1982). Similarly, hatchability of eggs drops in the heat of the summer season compared to cooler seasons (Horn and Perenyi, 1974; Tona et al., 2007). The impact of seasonal changes in light levels, humidity, and temperature on fertility and hatchability in broilers substantiates the GxE observed for these reproductive traits in the turkey.

GxE interactions may not be consistent across genetic groups and previous studies have determined that higher growth rate broiler chicken lines are more sensitive to environmental fluctuations (Settar et al., 1999). The amount of selective pressure on a trait could influence the animals’ ability to respond to changing environments and this is reflected in the variation in sensitivity of broiler growth rate to environmental
fluctuations, based on selective pressure. Similarly, a trend was seen in the present study for egg number and fertility. The female line, with higher selection pressure on reproductive traits, produced lower correlations between the summer and winter EBVs shown in Table 2.4. Increasing the selection pressure on a trait may increase susceptibility to changes in expression environment (Kolmodin et al., 2003). This indicates that performance traits in male line turkeys may be more sensitive to changes in performance environment, while greater sensitivity of reproductive traits could be expected in female line birds, based on the relative selection pressures in the breeding program.

The advantage of using a multiple trait model is the consideration of each environment as a distinct character state and the bivariate model provides a starting point for GxE interaction studies to which alternative models can be compared. Multiple trait models can thus enable the differences between seasonal environments to be accounted for directly. There are, however, alternative models to estimate environmental impact on trait expression, including random regression models, which can be considered to validate results from a multiple trait model.

Random regression models used to study environmental influence on performance detect a GxE as significant differences in reaction norms which indicate individual variability in environmental sensitivity (De Jong, 1990). This approach has been used to study changes in laying hen and turkey egg production performance throughout a single lay cycle (Anang et al., 2002; Kranis et al., 2007), although there are no reported studies on the effect of seasonal environment on total egg production for a lay cycle. Previous random regression analysis in the turkey showed that multiple-trait models have higher
heritability values, however the mean squared error of an egg production model is reduced using a random regression approach (Kranis et al., 2007). A random regression model can be used to help determine the characteristics of environmental sensitivity in the population, however the bivariate approach can be considered most useful to analyze the GxE interactions for consideration in a breeding program. As a result there was interest in using a random regression model on the data set used in this bivariate study to determine if both analyses yield the same conclusion, as reported in the present chapter of this thesis.

In conclusion, egg production, fertility, and hatchability could be considered as two separate seasonal traits in a turkey breeding program. Although commercial breeding operations attempt to maintain a constant internal environment, the turkey’s ability to respond to seasonal environmental factors is expressed in the GxE interaction. While selection based on BLUP may help account for seasonal variations in relative genetic merit for reproductive traits, it was important to understand the possible difference in genetic control regulating the traits throughout the year. An overall improvement in the genes that influence reproductive ability in both the summer and winter lay seasons would therefore increase the efficiency of genetic gain in reproductive traits, which is important given the antagonistic relationship between reproduction and growth.

Note: Minor revisions have been made to the original, published manuscript
Table 2.1 Heritability and variance component estimates of egg production as a single annual trait (Total), as a single trait within season (Winter lay and Summer lay) and based on a multiple trait model (Winter lay GxE and Summer lay GxE) for all turkeys and by season.

<table>
<thead>
<tr>
<th>Variable</th>
<th>$\sigma_p^2 \pm SE$</th>
<th>$\sigma_A^2 \pm SE$</th>
<th>$h^2 \pm SE$</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Female line</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total$^1$</td>
<td>141.3 ± 2.89</td>
<td>45.58 ± 4.72</td>
<td>0.32 ± 0.03</td>
</tr>
<tr>
<td>Winter lay$^2$</td>
<td>131.4 ± 3.94</td>
<td>34.77 ± 6.19</td>
<td>0.26 ± 0.04</td>
</tr>
<tr>
<td>Summer lay$^3$</td>
<td>145.2 ± 4.04</td>
<td>44.54 ± 6.67</td>
<td>0.31 ± 0.04</td>
</tr>
<tr>
<td>Winter lay$^5$ GxE</td>
<td>132.6 ± 4.01</td>
<td>37.49 ± 6.28</td>
<td>0.28 ± 0.04</td>
</tr>
<tr>
<td>Summer lay$^3$ GxE</td>
<td>146.9 ± 4.16</td>
<td>48.76 ± 6.92</td>
<td>0.33 ± 0.04</td>
</tr>
<tr>
<td><strong>Male line</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total$^1$</td>
<td>118.3 ± 1.74</td>
<td>38.35 ± 27.83</td>
<td>0.32 ± 0.02</td>
</tr>
<tr>
<td>Winter lay$^2$</td>
<td>121.5 ± 2.79</td>
<td>41.09 ± 4.81</td>
<td>0.34 ± 0.04</td>
</tr>
<tr>
<td>Summer lay$^3$</td>
<td>113.6 ± 2.25</td>
<td>32.19 ± 3.54</td>
<td>0.28 ± 0.03</td>
</tr>
<tr>
<td>Winter lay$^5$ GxE</td>
<td>122.4 ± 2.81</td>
<td>42.97 ± 4.73</td>
<td>0.35 ± 0.03</td>
</tr>
<tr>
<td>Summer lay$^3$ GxE</td>
<td>114.4 ± 2.27</td>
<td>33.68 ± 3.50</td>
<td>0.29 ± 0.03</td>
</tr>
</tbody>
</table>

1 Total annual egg production without genotype by environment effect = flock + b(age)
2 Winter egg production (out of season) defined turkeys laying between January and May
3 Summer (in season) defined turkeys laying between July and November
Table 2.2 Heritability and variance component estimates of fertility for all turkeys as a single annual trait (Total), as a single trait within season (Winter lay and Summer lay) and based on a multiple trait model (Winter lay GxE and Summer lay GxE) for all turkeys and by season.

<table>
<thead>
<tr>
<th>Variable</th>
<th>σ² + SE</th>
<th>σ² + SE</th>
<th>h² + SE</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Female Line</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total¹</td>
<td>296.3 ± 46.68</td>
<td>24.03 ± 5.07</td>
<td>0.08 ± 0.02</td>
</tr>
<tr>
<td>Winter lay²</td>
<td>341.7 ± 8.86</td>
<td>33.99 ± 6.19</td>
<td>0.10 ± 0.03</td>
</tr>
<tr>
<td>Summer lay³</td>
<td>270.9 ± 6.25</td>
<td>37.44 ± 8.47</td>
<td>0.14 ± 0.03</td>
</tr>
<tr>
<td>Winter lay² GxE</td>
<td>341.7 ± 8.87</td>
<td>34.09 ± 10.67</td>
<td>0.10 ± 0.03</td>
</tr>
<tr>
<td>Summer lay³ GxE</td>
<td>271.0 ± 6.26</td>
<td>37.83 ± 8.50</td>
<td>0.14 ± 0.03</td>
</tr>
<tr>
<td><strong>Male Line</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total¹</td>
<td>576.9 ± 6.59</td>
<td>48.43 ± 14.67</td>
<td>0.08 ± 0.01</td>
</tr>
<tr>
<td>Winter lay²</td>
<td>605.5 ± 11.49</td>
<td>66.75 ± 10.67</td>
<td>0.11 ± 0.02</td>
</tr>
<tr>
<td>Summer lay³</td>
<td>555.2 ± 8.90</td>
<td>53.03 ± 10.48</td>
<td>0.10 ± 0.02</td>
</tr>
<tr>
<td>Winter lay² GxE</td>
<td>605.7 ± 11.50</td>
<td>67.31 ± 14.68</td>
<td>0.11 ± 0.02</td>
</tr>
<tr>
<td>Summer lay³ GxE</td>
<td>556.2 ± 8.96</td>
<td>56.86 ± 10.76</td>
<td>0.10 ± 0.02</td>
</tr>
</tbody>
</table>

¹ Total annual fertility without genotype by environment effect = flock + b(age)
² Winter fertility (out of season) defined turkeys laying between January and May
³ Summer (in season) defined turkeys laying between July and November
Table 2.3 Heritability and variance component estimates of hatchability as a single annual trait (Total), as a single trait within season (Winter lay and Summer lay) and based on a multiple trait model (Winter lay GxE and Summer lay GxE) for all turkeys and by season.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Female Line</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$\sigma_P^2 \pm SE$</td>
<td>$\sigma_A^2 \pm SE$</td>
<td>$h^2 \pm SE$</td>
<td></td>
</tr>
<tr>
<td>Total(^1)</td>
<td>267.1 ± 4.24</td>
<td>24.44 ± 4.82</td>
<td>0.09 ± 0.02</td>
<td></td>
</tr>
<tr>
<td>Winter lay(^2)</td>
<td>307.9 ± 8.02</td>
<td>32.39 ± 9.86</td>
<td>0.11 ± 0.03</td>
<td></td>
</tr>
<tr>
<td>Summer lay(^3)</td>
<td>234.6 ± 5.39</td>
<td>30.95 ± 7.20</td>
<td>0.13 ± 0.03</td>
<td></td>
</tr>
<tr>
<td>Winter lay(^5) GxE</td>
<td>308.2 ± 8.02</td>
<td>32.05 ± 9.71</td>
<td>0.10 ± 0.03</td>
<td></td>
</tr>
<tr>
<td>Summer lay(^3) GxE</td>
<td>235.1 ± 5.41</td>
<td>32.05 ± 7.21</td>
<td>0.14 ± 0.03</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Variable</th>
<th>Male Line</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$\sigma_P^2 \pm SE$</td>
<td>$\sigma_A^2 \pm SE$</td>
<td>$h^2 \pm SE$</td>
<td></td>
</tr>
<tr>
<td>Total(^1)</td>
<td>582.5 ± 7.05</td>
<td>90.01 ± 9.87</td>
<td>0.15 ± 0.02</td>
<td></td>
</tr>
<tr>
<td>Winter lay(^2)</td>
<td>641.8 ± 12.60</td>
<td>108.6 ± 18.51</td>
<td>0.17 ± 0.03</td>
<td></td>
</tr>
<tr>
<td>Summer lay(^3)</td>
<td>535.9 ± 8.81</td>
<td>71.46 ± 11.79</td>
<td>0.13 ± 0.02</td>
<td></td>
</tr>
<tr>
<td>Winter lay(^5) GxE</td>
<td>664.0 ± 12.69</td>
<td>114.0 ± 18.63</td>
<td>0.18 ± 0.03</td>
<td></td>
</tr>
<tr>
<td>Summer lay(^3) GxE</td>
<td>537.6 ± 8.89</td>
<td>76.54 ± 12.01</td>
<td>0.14 ± 0.02</td>
<td></td>
</tr>
</tbody>
</table>

\(^1\)Total annual hatchability without genotype by environment effect = flock + \(b\)(age)
\(^2\)Winter hatchability(out of season) defined turkeys laying between January and May
\(^3\)Summer (in season) defined turkeys laying between July and November
Table 2.4 Correlation between winter lay and summer lay traits estimated from a multiple trait model.

<table>
<thead>
<tr>
<th>Line</th>
<th>Trait</th>
<th>r</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female Line</td>
<td>Egg number</td>
<td>0.76 ± 0.12</td>
</tr>
<tr>
<td></td>
<td>Fertility</td>
<td>-0.20 ± 0.26</td>
</tr>
<tr>
<td></td>
<td>Hatchability</td>
<td>0.75 ± 0.23</td>
</tr>
<tr>
<td>Male Line</td>
<td>Egg number</td>
<td>0.86 ± 0.08</td>
</tr>
<tr>
<td></td>
<td>Fertility</td>
<td>0.43 ± 0.19</td>
</tr>
<tr>
<td></td>
<td>Hatchability</td>
<td>0.68 ± 0.13</td>
</tr>
</tbody>
</table>
Figure 2.1 The effects of month of hatch on phenotypic performance of turkey egg production (a), fertility (b), and hatchability (c)
(a) Female Line

(b) Fertility EBV

(c) Hatchability EBV

Monthly Change in Egg Number EBV

Jan     Feb    Mar    Apr    May   Jun     Jul     Aug    Sep   Oct     Nov     Dec

Egg Number EBV

Male Line

Monthly Change in Egg Number EBV

Jan     Feb    Mar    Apr    May   Jun     Jul     Aug    Sep   Oct     Nov     Dec

Egg Number EBV
Figure 2.2 The effects of hatch month on egg production (a), fertility (b), and hatchability (c) estimated breeding values. Winter lay season is defined as January to May. Summer lay season is defined as July to November. Annual fluctuations in egg production EBVs is 1.21 percent days with egg produced in the female line and 0.45 percent days with egg produced in the male line. Annual fluctuation of fertility is 0.33% in the female line and 0.64% in the male line. Annual fluctuation in hatchability EBVs is 0.33% in the female line and 0.64% in the male line.
(a) Monthly Change in Egg Number EBV for Line 330

(b) Monthly Change in Fertility EBV for Line 330

(c) Monthly Change in Hatchability EBV for Line 330
Figure 2.3 The effects of hatch month on winter lay EBVs and summer lay EBVs for egg number (a), fertility (b), and hatchability (c). Annual fluctuations in the winter and summer lay egg production EBVs were 1.49 percent days with egg produced and 1.72 percent days with egg produced, respectively for the female line. Annual fluctuations in the winter and summer lay egg number EBVs were 1.29 percent days with egg produced and 1.16 percent days with egg produced, respectively for the male line. Annual fluctuations in fertility winter and summer lay EBVs were 0.72% and 0.64%, respectively for the female line. Annual fluctuations in fertility winter and summer lay EBVs were 1.08% and 1.27%, respectively for the male line. Annual fluctuations in the winter and summer lay EBVs were 0.71% and 0.59%, respectively for female line hatchability. Annual fluctuations in the winter and summer lay EBVs were 1.39% and 1.27%, respectively for the male line hatchability.
Figure 2.4 Cumulative density of phenotypic performance of fertility in the female line.
Chapter 3

Random regression analysis of seasonal effects on reproductive genetics in the turkey (Meleagris gallopavo)

L.A. Case\textsuperscript{a,*}, S.P. Miller\textsuperscript{a} and B.J. Wood\textsuperscript{a,b}

\textsuperscript{a} Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada;

\textsuperscript{b} Hybrid Turkeys, Suite C, 650 Riverbend Drive, Kitchener, ON, Canada

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3.1 Abstract

A random regression model was used to analyse egg production, fertility, and hatchability throughout the year in male and female line of turkeys in a longitudinal nature. The genetic correlation between reproductive traits measured in each month was estimated by fitting third order orthogonal polynomials to sire effects. Correlations below 0.8 indicated that there was a genotype by environment (GxE) interaction. Heritability values, estimated for each month, showed similar trends in both the male and female lines. The heritability of egg production tended to increase in the second half of the year. In contrast, the heritabilities of fertility and hatchability were higher in the first half of the year. For all traits, the genetic correlation between months that were temporally closer were higher than the correlation between months that were further apart throughout the year. Correlations also tended to be higher for egg production than for fertility or hatchability. A reaction norm model was then used to analyse if reproduction genotypes respond differently to temperature and day length gradients. These environmental factors were variable throughout the year and may be producing the observed GxE interactions.

3.2 Introduction

Genotype by environment (GxE) interactions have been detected for turkey egg production, fertility, and hatchability using a bivariate model (Case et al., 2010b). The
genetic correlation between production seasons was significantly less than 1, indicating that performance differed between the summer and winter seasons for similar genotypes. The rate of genetic progress in a breeding program is correlated to the ability to identify the best selection candidates within a production environment. This capability is reduced if production season influences the genetic control of reproductive traits.

The GxE indicates that a superior genotype is not consistent throughout the year and as a result animals re-rank for performance between environments (Falconer and Macay, 1996). GxE interactions can also lower heritability estimates as the GxE results in an additional variance component within the environmental variance (De Jong, 1990). This reduces the proportion of additive genetic variation because the impact of temporal and environmental factors are not considered.

Random regression (RR) models are advantageous to study GxE interactions as they assess genetic variation in phenotypic plasticity (De Jong, 1990). Random regression has been used to study egg production throughout a lay cycle in both broilers and turkeys (Anang et al., 2002; Kranis et al., 2007). The influence of season on total egg production, fertility, and hatchability, however, has not yet been studied in the turkey using a random regression approach. The objective of the present analysis was to determine if the GxE interaction for turkey reproductive traits is due to animal variation in response to annual changes in the environment. This was completed using a random regression model by treating months as independent variables. Reaction norms were also utilized to determine if day length or temperature gradients were responsible for the variation in environmental sensitivity.
3.3 Materials and Methods

3.3.1 Study Population and Management

The data set used in the current study was the same as the data used previously for the multiple-trait analysis of reproductive traits in the turkey (Case et al., 2010b). Populations were a pedigreed large white female and male line with a breeding objective balanced between commercial and reproductive traits. The female line included 430,975 birds, with 21,195 sires and 10,471 dams. There were 1,658 full sib families with an average number of 5.3 individuals per family and 1,032 half sib families with an average number of 9.2 turkeys per family ($n_{\text{max full sib}} = 31$, $n_{\text{min full sib}} = 2$, $n_{\text{max half sib}} = 64$, $n_{\text{min half sib}} = 2$). There were 423,159 turkeys in the male line, including 1,772 sire and 15,949 dams. This included 3,181 full sib families and 1,205 half sib families with an average number of 4.1 and 12.5 individuals, respectively ($n_{\text{max full sib}} = 23$, $n_{\text{min full sib}} = 2$, $n_{\text{max half sib}} = 74$, $n_{\text{min half sib}} = 2$). A total of 854,134 turkeys related to the animals with records were included in the pedigree file for the final analyses. A stronger selection emphasis was placed on reproductive traits in the female line compared with the male line. Traits were recorded between 1995 and 2007. There were 8,809 and 13,875 records for egg production, 8,787 and 15,735 records for fertility, and 8,765 and 15,631 records for hatchability for the female and male lines, respectively. The male to female ratio in the female and male lines was approximately 1 to 5 and 1 to 10, respectively. Artificial insemination was used for all matings, with 203 flocks across the 13 year period and a consistent number of hens starting lay throughout the year. Eggs were stored for between 4 and 14 days before incubation.
Rearing until 20 weeks of age was under a standard commercial production environment and feeding regime. After 20 weeks of age hens were placed onto a commercial parent stock bodyweight restriction diet. Light conditions were controlled in dark-out barns and lighting consisted of equal 12 hourly periods of light and dark with a light intensity of approximately 107 LUX. From 16 – 30 weeks birds were exposed to 6 hourly periods of dark and 18 hours of light with an intensity of approximately 88 LUX. Light intensities could be varied with flock requirement, temperament and other management factors. From 30 weeks of age the light conditions consisted of 16 hours of light with an intensity of approximately 107 LUX and 8 hour periods of dark.

Egg production was evaluated as percentage days with egg produced between 210 and 420 days of age. Fertility was measured 14 days after being set as the proportion of eggs that were candled fertile. Hatchability was calculated as the percentage of fertile eggs that produced a live poult.

### 3.3.2 Statistical Analysis

A random regression model to describe reproductive performance throughout the year was developed using Legendre polynomials as recommended by Kirkpatrick et al. (1990). Each month was treated as an independent variable and Legendre polynomials of order k were denoted as $\phi(m)$ with $m_i$ standardized to lie within the range of -1 and 1 using the formula

$$m_i = \frac{2(t_i - t_{min})}{(t_{max} - t_{min})} - 1$$

where $t_i$ represents the month being analyzed, $t_{min}$ represents the earliest month (January = 1) and $t_{max}$ represents the latest month (December = 12). The RR model used was:
\[ y_{abcdef} = FL_a + b(AGE)_b + b(YR)_c + b(MNTH)_d + \sum_{k=0}^{n} s_k \phi_k(m) + e_{abcdef} \]

where \( y \) is the trait value (egg production, fertility, or hatchability), FL is the fixed flock classification effect accounting for temporary environmental effects influencing a group of hens laying in the barn at the same time, \( b(AGE) \) a fixed regression on the age of a hen in days when the flock was photo-stimulated, \( b(YR) \) and \( b(MNTH) \) are fixed regressions on the hatch year and hatch month of the hen, respectively, the fifth term is a random regression of order \( n \) on sire, and \( e \) is the random residual variance, homogenous across time periods, which was consistent with other random regression models for reproductive traits in poultry (Kranis et al., 2007; Wole and Szwaczkowski, 2009). A summary of values associated with each fixed effect are presented in Table 3.1.

Based on previous reports, third order Legendre polynomials were sufficient to fit a genetic correlation structure including sire effects (Pool et al., 2000; Odegard et al., 2003; Carlen et al., 2009). As a result third and fourth order Legendre polynomials were tested to determine which model had the best fit, by comparing to models with higher order orthogonal polynomials. The degrees of freedom for each effect were calculated as \( \frac{1}{2} m(m + 1) \) and the log likelihood ratio test was used to compare models, where \( m \) equals the number of covariates for different orders of polynomials. Non-zero eigenvalues were also used to indicate significant variance in the population for a given order polynomial (Kirkpatrick et al., 1990).

The covariance (\( \hat{G} \)) between monthly genetic effects was calculated as \( \phi(m)K\phi^T(m) \) where \( K \) is a symmetrical variance-covariance matrix between RR coefficients, \( \phi \) is a matrix of the polynomial coefficients for each month, and \( T \) is the
transpose (Kirkpatrick et al., 1990). Covariances were used to determine the correlations between months. Correlations below unity (r=1) were indicative of a GxE interaction. All estimates were calculated using restricted maximum likelihood with ASREML (Gilmour et al., 2002). The procedure was repeated by using June as t_{\text{min}} and May as t_{\text{max}} to evaluate the impact of the months’ position in the defined time scale on heritability estimates.

A reaction norm model was used to determine if annual temperature and day length gradients have a significant differential impact on genotype. The reaction norm model was:

\[ y_{\text{abcdefg}} = FL_a + b(AGE)_b + b(YR)_c + b(MNTH)_d + \text{animal}_e + bX(sire)_f + e_{\text{abcdefg}} \]  

where the fixed effects of flock, age, hatch year and hatch month were the same factors described for the random regression model, and animal was the random additive genetic effect of each individual. The term bx(sire) is a linear random regression of the reproductive trait on the environmental gradient (X), either temperature or day length, nested within sire. The (co)variance of the random linear regression coefficient were assumed proportional to the genetic relationship matrix. Historical records for Toronto, Ontario were used to obtain the monthly average temperatures and day lengths for the analysis as this location is in close proximity to the turkey barns and had a complete set of records for the study period (National Research Council of Canada; Environment Canada, 2009). The log likelihood ratio test was used to determine if the regression coefficients described a significant proportion of variation for the reproductive traits.
3.4 Results

Third order Legendre polynomials were used in the random regression model. This model was most appropriate as the difference between the third and fourth order models were not significant and the eigenvalue of the quartic coefficient was near zero. The covariance and corresponding correlation matrices for the random regression coefficients are shown in Table 3.2. The majority of the variance was explained by the intercept and linear coefficients for all traits. This was supported by the high percentage of variation explained by the eigenvalues for these terms. The genetic correlations between monthly egg production, fertility, and hatchability traits are shown in Table 3.3, Table 3.4, and Table 3.5, respectively. Correlations between months that were closer temporally were generally higher. The correlations between all months tended to be higher for egg production than for fertility and hatchability. Correlations between months were generally positive, except for negative weak to moderate values between winter and summer months for hatchability in the female line.

Heritability estimates for monthly egg production, fertility, and hatchability analyzed using January as the starting point of the time gradient in the male and female line are shown in Figure 3.1a, Figure 3.2a, and Figure 3.3a, respectively. The results from the analysis using June as the first month in the time gradient are shown in Figure 3.1b, Figure 3.2b, and Figure 3.3b, respectively. Heritability for egg production ranges from 0.28 – 0.66 in the female line and from 0.25 – 0.41 in the male line. Heritability is higher and shows an increasing trend in the second half of the year. Heritability of fertility decreases through the summer and begins to increase through the winter months with estimates ranging from 0.05 – 0.22 in the female line and from 0.05 – 0.14 in the
male line. Heritability of hatchability is lowest in the summer with values ranging from 0.07 – 0.31 in the female line and from 0.08 – 0.24 in the male line. The general trends from both analyses were similar, however there were differences in the heritability estimates when the months were repositioned within the environmental scale.

The temperature ranges were -9°C – 24.3°C and the day length ranges were 10.1 – 16.6 hours. Results from the reaction norm analysis indicate that the response of the turkey to temperature and day length gradients were significantly variable for fertility in the male line, and for hatchability in both the male and female lines (Table 3.6). These results suggest that genotypes respond differently to fluctuating environmental conditions throughout the year.

3.5 Discussion

A RR model was used in the current analysis because of its ability to determine the genetic covariance between traits as a function of months of the year (De Jong, 1990). Repeated records on an individual across the time periods is required for RR modelling, however each hen has one cumulative, lifetime value for the analysed reproductive traits. Sire effects were therefore incorporated into the model as each sire has progeny laying throughout the year. As a consequence, repeated records for sires were used to estimate the RR trajectories and to determine if there was genetic variation in the curve parameters.

There was no significant difference between the third and fourth order polynomial models and these results were similar to other studies that had fit sire and animal effect RR models (Odegard et al., 2003; Carlen et al., 2009). The quartic coefficient also
explained a very low proportion of the genetic variance. Over-parameterization increases the computational time and can decrease the accuracy of the parameter estimation (Misztal et al., 2000). As a result, third order polynomials were most appropriate to model genetic effects for the traits throughout the year.

A multiple trait model has previously been used to investigate a GxE interaction for turkey egg production, fertility, and hatchability (Case et al., 2010b). Genetic correlations less than one indicated GxE interactions for all traits and the correlations between months shown in Table 3.1, Table 3.2, and Table 3.3 would support these findings. The bivariate model considered two production seasons (January – May and July – December). The RR results showed higher correlations within these defined seasons than between seasons. The highest correlations between months in the present study were estimated for egg production and this supports the higher correlation for egg production between seasons in the multiple trait bivariate model than for fertility or hatchability. The heritability estimates were very similar between lines in the multiple trait study and this is also in agreement with the current results which show comparable heritability ranges for the male and female lines. It is evident that GxE interactions could be studied with both bivariate or random regression models and the similarity of results between both types of analysis strengthen the conclusion that the environment significantly affects the genetic expression of turkey reproductive traits.

The heritability of egg production was highest, relative to the other reproductive traits, indicating that there is more additive genetic control of egg production. Literature results for the heritability of reproductive traits are variable, however estimates for egg production and fertility tend to be moderate while heritability of hatchability is in the
lower range (Buss, 1989). The genetic correlations between months for egg production also tended to be higher than for fertility or hatchability. As a result, a larger proportion of the genetic factors regulating the trait are constant throughout the year and a higher proportion of the genetic factors influencing egg production are common between months. This agrees with the higher genetic correlation between seasonal measures of egg production than fertility or hatchability measured by Case et al. (2010b). The heritabilities based on the RR model were higher than in the bivariate model (Case et al., 2010b). The increased heritabilities in the current study may be due to the analysis of traits at twelve monthly periods, instead of in two seasons. The use of a smaller time span to estimate the trajectories could enable better partitioning of the genetic effects from the fluctuating environment by reducing the environmental variance estimated for each monthly trait, compared to the larger environmental variance occurring during the measurement of a seasonal trait.

Estimates from the analysis, with January identified as the beginning of the temporal distribution, showed heritability values that tended to peak at the extremes of the yearly distribution. Neither the average or variance of the residuals increased in January nor December, indicating consistently good model fit throughout the entire year. The model was therefore describing the data and the heritability peaks in the early and late months were an artefact of the random regression model. To determine the impact of a month’s position in the environmental scale on heritability estimates, new values were calculated by identifying June and May as the beginning and end of the time variable, respectively. The trends in heritability were similar for both analyses, however there were detectable differences. This is particularly evident in Figure 3.2. The heritability
estimates increase at the beginning and end of the time scale and this occurs in January and December for the first analysis (Figure 3.2a) and in May and June for the second analysis (Figure 3.2b). Similar patterns of heritability estimates varying from trends at the beginning and end of the environmental distribution have been seen in other random regression analyses including the evaluation of poultry egg production throughout a lay cycle and milk production characteristics in cattle (Jamrozik and Schaeffer, 1997; Anang et al., 2002; Kranis et al., 2007; Wolc and Szwaczkowski, 2009). These estimates indicate that the defined environmental gradient can have an impact on the absolute values of heritability at the extremes of the distribution, but does not largely impact the ability of the model to predict how heritability changes with environment. This problem related to estimating heritability at the beginning and end of the distribution and the effect of repositioning elements in the environmental gradient warrants further investigation as the use of random regression models in animal breeding expands. The consistent model fit throughout the year in the present study indicated that homogenous variance was appropriate, however as random regressions continue to be explored in the poultry industry and for genotype by environment analysis, the use of a heterogeneous variance structure could be investigated in future studies.

The results from the reaction norm model indicated that genotypes regulating fertility and hatchability respond differently to changes in day length and temperature. Efforts are made to maintain a constant temperature in turkey barns and to control the hours turkeys are exposed to light. These results suggest, however, that the production barn environment is susceptible to change in response to exterior light and temperature and as a result reproductive performance is affected. The relationship between the
environmental variables and fertility in the female line was not significant. This is likely a result of the skewed distribution towards very high performance levels in the female line. Due to consistently high performance, levels cannot fluctuate in response to environmental variables. The significant result in the male line is therefore a better indication of how different genotypes controlling fertility respond to changes in day length and temperature.

There are both benefits and disadvantages to using results from multiple trait and random regression models in a breeding program. RRs can be used to model changes in genetic potential throughout the entire year on a continuous time scale. RR results, however, may not be as easily implemented into a breeding program. The multiple trait model allows the adaption of a selection index to include two seasonal traits, each of which can be assigned equal or different weighting factors to increase overall performance in a breeding objective. The weighting of regression coefficients in a breeding program would be more difficult, however, as more “traits” are involved and also because multiple trait EBVs are individual estimates while the EBVs from the random regression model are for the sire. RR results can, however, be used to aid in multiple trait selection. Monthly heritability estimates can indicate the best month within each season to evaluate genetic potential. Basing selection decisions on months with the highest heritability can increase the rate of genetic improvement provided the correlation of the selected month is high with the other months in the season, as seen in the present study. BLUP based selection, which is currently practiced in turkey breeding programs, could be considered the most efficient way to increase annual reproductive performance in the turkey hen, accounting for relative genetic merit across seasons through
information on relatives. The random regression model is therefore most useful for evaluating the longitudinal nature of traits and bivariate models can be more easily implemented into breeding programs.

In conclusion, the polynomials describing turkey egg production, fertility, and hatchability performance throughout the year were significantly variable between individuals. This resulted in correlations less than one when traits are expressed in different months of the year. Correlations decreased as the months became more dispersed throughout the year indicating a seasonal GxE interaction. The GxE may be a result of a turkey’s exposure to a fluctuating barn environment, such as changes in the external light and temperature. Random regression results can be most useful to determine the months when heritability peaks, within production seasons.

Note: Minor revisions have been made to the original, published manuscript
Table 3.1 Number of values (n) and summary of minimum number of observations, maximum number of observations, and mean number of observations per value of the fixed effects in the random regression and reaction norm models.

<table>
<thead>
<tr>
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<th>Max</th>
<th>Mean</th>
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<tr>
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<td>89</td>
<td>54</td>
</tr>
<tr>
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<td>3609</td>
<td>1016</td>
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<tr>
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</tr>
<tr>
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<td>625</td>
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<tr>
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<td></td>
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<tr>
<td>Flock</td>
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<td>Hatch Year</td>
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<td>530</td>
<td>1377</td>
<td>1082</td>
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Table 3.2 Estimates of random regression coefficients (diagonal) and covariances (lower triangle) and correlations (upper triangle) between coefficients (0: intercept, 1: linear, 2: quadratic, 3: cubic) of the 3\textsuperscript{rd} order Legendre polynomials together with the eigenfunction which indicated the proportion of variance explained by each coefficient

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$^1$ Percent of variance explained by eigenfunction
Table 3.3 Monthly genetic correlations for egg production in the female line (below the diagonal) and the male line (above the diagonal) estimated using a random regression model.

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Table 3.4 Monthly genetic correlations for fertility in the female line (below the diagonal) and the male line (above the diagonal) estimated using a random regression model.

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Table 3.5 Monthly genetic correlations for hatchability in the female line (below the diagonal) and the male line (above the diagonal) estimated using a random regression model.

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Table 3.6 Effect of increasing external temperature and day length on egg production, fertility, and hatchability in a male and female turkey line.

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* Significant based on a log likelihood ratio test with a critical value of 3.8 ($\delta^2 < 0.05$)
Figure 3.1 Heritability of egg production estimated for each month using a random regression model in the male and female line with January (a) and June (b) defined as the first month in the analysis.
Figure 3.2 Heritability of fertility estimated for each month using a random regression model in the male and female line with January (a) and June (b) defined as the first month in the analysis.
Figure 3.3 Heritability of hatchability estimated for each month using a random regression model in the male and female line with January (a) and June (b) defined as the first month in the analysis.
Chapter 4

The genetic parameters of feed efficiency and its component traits in the turkey (*Meleagris gallopavo*)

4.1 Abstract

The genetic parameters of residual feed intake (RFI) and feed conversion ratio (FCR) can be incorporated into a breeding program to select for feed efficiency. Alternatively, the direct measures can be used to analyze the underlying variation in traits that impact overall efficiency. These constituent traits can then be appropriately weighted in an index to achieve genetic gain. To investigate feed efficiency in the turkey, feed intake and weight gain were measured on male primary breeder line turkeys housed in individual feeding cages from 15 – 19 weeks of age. The raw feed conversion ratio (rFCR), a derived feed conversion trait (dFCR), and RFI all showed moderate heritability values of 0.16, 0.25, and 0.24, respectively. Feed intake, body weight, and weight gain were also moderately heritable (0.21, 0.35, and 0.18, respectively). Weight gain was negatively correlated to the feed conversion ratio traits and was not genetically correlated...
to RFI. Body weight had small and positive genetic correlations to RFI (0.09) and rFCR (0.12) but was not genetically correlated to dFCR. Feed intake was positively correlated to RFI (0.62) and dFCR (0.28) genetically, however there was no genetic correlation between feed intake and raw feed conversion ratio. These estimates of heritability and the genetic correlations can be used in the development of an index to improve feed efficiency and reduce the cost of production.

4.2 Introduction

Feed represents two thirds of the total costs in a poultry production system and feed requirements are an important consideration in the turkey industry. Furthermore, as genetic progress is made in body weight traits, feed consumption could be expected to increase as the larger birds require more feed. Consequently, improving feed efficiency by identifying animals that require the same amount of feed as their contemporaries but have higher body weight or weight gain is valuable. This is feasible in a breeding program and genetic selection, combined with management, has improved feed conversion ratio (FCR) by approximately 20% since 1966 (Havenstein et al., 2007b).

Feed efficiency is often assessed as either FCR or residual feed intake (RFI). The ratio of feed intake to weight gain, or FCR, provides an indication of a bird’s ability to convert the energy in feed to body weight, however selection based on a ratio is not ideal. The RFI trait attempts to isolate a measure of biological efficiency independent of production and is estimated as the difference between actual feed intake and a predicted feed intake based on body weight and production (Koch et al., 1963). The RFI and FCR traits have moderate heritability values in broilers (Van Bebber and Mercer, 1994;
Aggrey et al., 2010), however published parameters for feed efficiency traits in the turkey are not widespread.

Reliable genetic parameters are essential for selection index design and variance components of feed efficiency traits are required to determine the expected gains in efficiency, as well as correlated responses to selection that will occur in other traits in a selection index. As a result, accurate estimates of genetic parameters will enable turkey breeders to determine the impact that selection for feed efficiency will have overall on a breeding program. The objective of the present study was to determine the heritability of RFI and FCR in the turkey and to determine the heritability and genetic correlations between a selection of production traits.

4.3 Materials and Methods

4.3.1 Study Population and Management

Data collected on toms from a male primary breeder turkey line (n = 16,412) over a 10-year period were used. Pedigree information extended back a minimum of 5 generations and included 28,464 relatives of the birds with records. Rearing until 14 weeks of age was under a standard commercial production environment and feeding regime. At 14 weeks of age, the toms were placed in individual cages (0.60 meters wide, 0.85 meters long, 0.82 meters high) to acclimatize and the turkeys remained in the same cages throughout the feeding trial. The feeding trial was conducted from 15-19 weeks of age, as this is time that feed efficiency is currently assessed in pure line turkeys. Feed intake (FI) and body weight were measured at the start of the trial (15 weeks of age) and at the end of the trial (19 weeks of age). During this period toms were fed a standard
commercial diet and had ad libitum access to feed and water from individual feeders and shared drinkers within each cage.

4.3.2 Data Analysis

Average daily gain (ADG) was calculated as

\[ ADG = \frac{\text{weight at end of trial (kg) - weight at start of trial (kg)}}{\text{days on trial}} \]

and mean metabolic weight (MMW) was calculated as

\[ MMW = \left( \frac{\text{weight at end of trial (kg) + weight at start of trial (kg)}}{2} \right)^{0.75} \]

Raw feed conversion ratio (rFCR) was calculated as feed intake (FI) divided by weight gain. The derived feed conversion trait (dFCR) was calculated by adjusting rFCR using a regression approach to remove the effects of body weight and performance, which was considered live weight gain. The exact formula used to calculate dFCR is proprietary to the primary turkey breeding company that managed the birds in the present study. Means and standard deviations for the traits that were measured are shown in Table 4.1.

Expected feed intake was calculated using two different regressions (M1 and M2) as:

M1: \[ FI = \mu + b_1\text{MMW} + b_2\text{WG} + \text{hatch} + e \]

M2: \[ FI = \mu + b_3\text{BW} + b_2\text{WG} + \text{hatch} + e \]

where \( FI \) represents feed intake, \( \mu \) is the intercept, \( b_1, b_2, \) and \( b_3 \) represent the regression coefficients on mean metabolic weight, weight gain, and body weight at the start of the trial (BW), respectively, hatch was a fixed contemporary group effect adjusting for the common environment influencing a group of birds hatched on the same date and managed in the same contemporary group. Hatch also accounted for sex and line as these
factors were common for all birds within a flock. The residual effect was represented by $e$. The R-squared value of M2 was higher than the value for M1 and consequently coefficients from M2 were used to calculate RFI as:

$$RFI = FI - (\hat{\mu} + \hat{b}_1BW + \hat{b}_2WG)$$

Data exceeding 3 standard deviations from the mean were removed as outliers for each trait and the remaining 15,831 individuals with records for all traits were used for the genetic analysis.

### 4.3.3 Genetic Analysis

Heritabilities, phenotypic, and genetic correlations were estimated using ASReml (Gilmour et al., 2002). The model for all traits was:

$$Trait = hatch + animal + e$$

where $Trait$ represents RFI, rFCR, dFCR, FI, BW, or ADG, $hatch$ was the same fixed contemporary group effect used in the RFI models, $animal$ represents the random additive genetic effect, and $e$ is the residual random effect. The random effects were assumed to be normally distributed with mean of zero and a (co)variance structure equal to:

$$V \left( \begin{array}{c} a \\ e \end{array} \right) = \begin{pmatrix} A\sigma^2_a & 0 \\ 0 & I\sigma^2_e \end{pmatrix}$$

where $A$ represents the additive genetic relationship matrix and $I$ is an identity matrix. Phenotypic correlations and genetic correlations were estimated pair wise in bivariate models and the reported heritabilities were averages from across the bivariate models.
4.4 Results

The R-squared value of M2 (0.79) was higher than the value for M1 (0.75) and as a result, body weight at the start of the trial explained a larger proportion of the variation in feed intake than metabolic mid-weight. For this reason, the regression coefficients from M2 were used to calculate RFI. The R-squared value indicates that RFI may account for up to 21% of the remaining variation in feed intake after adjusting for body weight, weight gain, and hatch.

Heritabilities, phenotypic, and genetic correlations are shown in Table 4.2. All traits showed a moderate heritability. The genetic correlations between feed intake, body weight, and average daily gain were all positive and in the moderate to high range (0.28-0.67). There were also high positive correlations between the measures of feed efficiency (RFI, dFCR, and rFCR) ranging from 0.65 to 0.77. The genetic correlation between feed intake and both RFI (0.62) and dFCR (0.28) was positive, however the correlation between feed intake and rFCR was approximately zero. The ADG trait was negatively correlated dFCR (-0.24) and rFCR (-0.67) and was not genetically correlated to RFI. There were weak positive correlations between body weight and both RFI (0.09) and rFCR (0.12), but body weight was not genetically correlated to dFCR.

4.5 Discussion

The feed efficiency traits (dFCR, rFCR and RFI) that were analysed could all be considered for in a selection program and the magnitude of heritability indicated that selection could effectively improve each trait. The heritabilities of RFI, body weight, and
feed intake agree with previous moderate estimates in broiler chickens and turkeys (Van Bebber and Mercer, 1994; Nestor et al., 2000; Gaya et al., 2006). The heritability of rFCR was intermediate between results in these studies (0.12 - 0.16) and higher values from a recent broiler study, which ranged from 0.41 – 0.49 (Aggrey et al., 2010).

Genetically, the rFCR and dFCR traits were negatively correlated to ADG and this relationship between FCR and weight gain also exists in the chicken and beef cattle with genetic correlations of -0.50 and -0.52, respectively (Van Bebber and Mercer, 1994; Schenkel et al., 2004). These correlations can be expected due to the relationship between the FCR ratio and its component trait, ADG. Both RFI and dFCR were adjusted for body weight, and, as expected, the phenotypic and genetic correlations between these traits and bodyweight were low. Near-zero correlations between RFI and body weight at the start of a trial have also been estimated in meat-type chickens (Van Bebber and Mercer, 1994).

In a broiler study, RFI was calculated using a regression on MMW in place of body weight and positive genetic correlations (0.29 – 0.49) between MMW and RFI were estimated (Aggrey et al., 2010). These results indicate that, in meat-type poultry with a very high and non-linear growth rate, the effect of increasing size on the mid-trial MMW measurement may confound the independence of RFI from this body size trait. Consequently, body weight at the start of a trial may be a more beneficial trait to use, relative to MMW mid-trial, in the calculation of RFI in meat-type poultry to remove the genetic correlation between feed efficiency and body size. This would allow the analysis of the metabolic, nutritional, and physiological factors that contribute to RFI independently of the nutritional needs required to maintain body size and for gain weight.
Future work on feed efficiency in the turkey could also consider evaluating the birds at different ages. This would allow the determination of how relationships between efficiency and production traits change over the growing period in turkeys as genetic parameters at different ages are not consistent in broilers (Aggrey et al., 2010).

RFI showed high genetic correlations to the feed conversion traits, which was expected given their intrinsic relationship and also based on results from other species (Schenkel et al., 2004; Hoque et al., 2007). The very high correlation between RFI and dFCR can be attributed to the similar methodology for calculating the two measures of efficiency. Positive genetic correlations estimated between feed intake and both RFI and dFCR were favorable as increased efficiency was associated with a decrease in feed intake. This relationship was stronger between feed intake and RFI than between feed intake and dFCR. Alternatively, the genetic correlation between feed intake and rFCR was near zero indicating that improvement in one trait would not impact the other. This correlation was unexpected based on the inherent relationship between the traits and positive correlations in beef and swine, however a near-zero correlation was also estimated in a broiler study (Van Bebber and Mercer, 1994; Schenkel et al., 2004; Hoque et al., 2007). Studies in broilers have also found that selection for FCR has a negligible impact on feed intake and zero genetic correlation was estimated between feed intake and FCR in lines selected for feed efficiency (Pym and Nicholls, 1979). Consequently, results suggest that RFI may be more correlated to feed intake and more independent of performance traits than either rFCR or dFCR.

Ideally, feed efficiency measures would be independent of production and this was shown for RFI. In this way, selection for feed efficiency would not have an impact
on other economically important traits. There was, however, a moderate genetic correlation between ADG and dFCR. If the genetic regression between ADG and dFCR was equal to the phenotypic regression the traits would be genetically independent (Van Der Werf, 2004), however the correlation estimated between the traits indicates that this is not occurring in the turkey population. As a result, selection on dFCR may have an impact on the genetic progress of weight gain. Additionally, not considered here were the production traits related to body composition such as breast meat yield. These traits should also be considered prior to implementation into a breeding program as important genetic relationships with body conformation traits, like back fat, muscle area, and meat yield have been observed in other species (Schenkel et al., 2004; Gilbert et al., 2007).

Previous research demonstrated that a linear selection index can be more efficient than selection on a ratio trait like FCR (Gunsett, 1984; Campo and Rodriguez, 1990). A direct measure of feed efficiency can be omitted from an index, without decreasing the accuracy, if it is developed with appropriate weights on the component traits (feed intake, body weight, and growth) (Van Der Werf, 2004). RFI may be advantageous, however, because it can be considered independently, unlike feed intake, which is difficult to interpret as a standalone trait independent of growth rate and body size. As a result, genetic improvement for efficiency can be accomplished by including a feed efficiency trait in a selection index or through its component traits, with the appropriate parameters as presented here.

These results provide the required genetic parameters of feed efficiency in the turkey for consideration in the development of a breeding program. The heritabilities and genetic correlations can be used to calculate selection index weights. The results can also
be utilized to determine expected gains, as well as correlated responses that will result from selection. The moderate heritability of feed efficiency traits and the genetic correlations to feed intake, weight gain, and body weight indicate that selection can improve feed efficiency. The direct measures of dFCR, rFCR and RFI can be best utilized to study the traits that impact overall efficiency. A breeding program can then use this information to incorporate the efficiency constituent traits into an index to achieve genetic progress. This will, ultimately, reduce the relative cost of production and improve profit performance in the turkey industry.
Table 4.1 Means and standard deviations of raw feed conversion ratio (rFCR), a derived feed conversion trait (dFCR) cumulative feed intake (FI), body weight at 15 weeks (BW) and weight gain (ADG) during a 4 week feeding trial

<table>
<thead>
<tr>
<th>Traits</th>
<th>Units</th>
<th>Mean</th>
<th>Standard Deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>rFCR</td>
<td>kg/kg</td>
<td>2.96</td>
<td>0.46</td>
</tr>
<tr>
<td>dFCR</td>
<td>kg/kg</td>
<td>2.95</td>
<td>0.39</td>
</tr>
<tr>
<td>FI</td>
<td>kg</td>
<td>18.56</td>
<td>3.50</td>
</tr>
<tr>
<td>BW</td>
<td>kg</td>
<td>13.58</td>
<td>1.46</td>
</tr>
<tr>
<td>ADG</td>
<td>kg</td>
<td>0.23</td>
<td>0.06</td>
</tr>
</tbody>
</table>
Table 4.2 Heritabilities (on diagonal), phenotypic (above diagonal) and genetic (below diagonal) correlations, plus or minus standard errors, between residual feed intake (RFI), raw feed conversion ration (rFCR), derived feed conversion ratio (dFCR), cumulative feed intake (FI), body weight at 15 weeks (BW) and weight gain (ADG) during a 4 week feeding trial in turkeys

<table>
<thead>
<tr>
<th>Traits</th>
<th>RFI</th>
<th>rFCR</th>
<th>dFCR</th>
<th>FI</th>
<th>BW</th>
<th>ADG</th>
</tr>
</thead>
<tbody>
<tr>
<td>RFI</td>
<td>0.21±0.02</td>
<td>0.49±0.01</td>
<td>0.94±0.00</td>
<td>0.66±0.01</td>
<td>0.00±0.01</td>
<td>0.06±0.01</td>
</tr>
<tr>
<td>rFCR</td>
<td>0.65±0.05</td>
<td><strong>0.16±0.02</strong></td>
<td>0.50±0.01</td>
<td>-0.13±0.01</td>
<td>0.10±0.01</td>
<td>-0.74±0.00</td>
</tr>
<tr>
<td>dFCR</td>
<td>0.77±0.02</td>
<td>0.68±0.04</td>
<td><strong>0.25±0.02</strong></td>
<td>0.55±0.01</td>
<td>-0.04±0.01</td>
<td>-0.01±0.01</td>
</tr>
<tr>
<td>FI</td>
<td>0.62±0.04</td>
<td>0.06±0.07</td>
<td>0.28±0.06</td>
<td><strong>0.21±0.02</strong></td>
<td>0.41±0.01</td>
<td>0.55±0.01</td>
</tr>
<tr>
<td>BW</td>
<td>0.09±0.06</td>
<td>0.12±0.07</td>
<td>-0.07±0.06</td>
<td>0.67±0.04</td>
<td><strong>0.35±0.02</strong></td>
<td>0.17±0.01</td>
</tr>
<tr>
<td>ADG</td>
<td>-0.04±0.07</td>
<td>-0.67±0.04</td>
<td>-0.24±0.07</td>
<td>0.28±0.06</td>
<td>0.41±0.06</td>
<td><strong>0.18±0.02</strong></td>
</tr>
</tbody>
</table>
Chapter 5

Investigation of body surface temperature measured with infrared imaging and its correlation to feed efficiency in the turkey (*Meleagris gallopavo*)

5.1 Abstract

As feed intake is an expensive trait to measure in a breeding program, this study investigated whether body surface temperature was correlated to feed efficiency in the turkey. Infrared images were captured on male turkeys in individual feeding cages at approximately 19-weeks of age. Body surface temperature was measured on the eye, head, distal metatarsus, and neck of the birds with temperatures ranging from 34°C to 40°C. Body weight, feed intake, and weight gain data were collected and feed efficiency was measured as residual feed intake (RFI), raw feed conversion ratio (rFCR), and a derived feed conversion trait (dFCR). Distal metatarsus temperature showed moderate correlations to body weight (0.15), average daily gain (0.27), and feed intake (0.24). Surface temperature at the other measured areas was not as strongly correlated with these
production traits. The feed efficiency traits showed low correlations to eye temperature ranging from -0.03 to -0.13 and surface temperature at the other measured body areas was not correlated to feed efficiency. Surface temperature traits explain only a small proportion of variation in feed intake and increased the R-squared value of a model including body weight and weight gain by 0.0036. While the collection of infrared images was efficient and required minimal contact with the caged birds, the low correlations indicate that the technology, as used in this study, has limited advantages for increasing the accuracy of selection for feed efficiency.

5.2 Introduction

Feed represents the highest single cost for turkey production and as a result feed efficiency is an important trait in any selection index. Measurement of feed intake is required to calculate feed efficiency and birds are often housed in individual cages to collect these records. As a result of the high cost of collecting the data, feed intake is often only measured on a limited number of selection candidates. The current measurement of feed intake on caged birds may also not be an accurate representation of feeding behaviours in the group-housed commercial turkeys. Consequently, alternative measures of feed efficiency warrant investigation.

A proportion of the feed energy ingested by turkeys is used for metabolic processes and these result in the generation of heat (Whittow, 2000; Rivera-Torres et al., 2010). Exchange of this generated heat occurs across the skin surface and specific vascular arrangements under the skin surface, called arteriovenous anastomoses, allow heat dissipation particularly in the unfeathered areas of the body (Whittow, 2000).
Consequently, variation in surface temperature, as an indicator of the heat produced as a by-product of metabolism, may be correlated to efficient feed utilization.

In cattle, infrared imaging of the eye, cheek, and foot showed that efficient animals had a lower surface temperature in those locations compared to cattle that were less feed efficient (Montanholi et al., 2009). These results indicated that body surface temperature was correlated to feed efficiency in cattle, and therefore a relationship between these traits in the turkey may also be present. Accordingly, the objective of the present study was to capture infrared images at different sites on the turkey to determine if body surface temperatures were correlated to feed efficiency.

5.3 Materials and Methods

5.3.1 Study Population and Management

The populations used in this study were large white toms (n = 1,566) from both male and female primary breeder selection lines. The female line breeding objective had a greater emphasis on reproductive traits compared to the male lines which had a heavier focus on commercial production traits. Birds were placed in individual feeding cages (0.60 meters wide, 0.85 meters long, 0.82 meters high) at 14 weeks of age and had a one-week acclimatization period. Feed intake and weights measured at the start of the feeding trail (15 weeks of age) and end of the feeding trial (19 weeks of age) were used to calculate total feed intake and weight gain. Average daily gain (ADG) was calculated as total weight gain divided by days on trial. Birds were fed a standard commercial diet and had ad libitum access to individual feeders and shared water drinkers within each cage.
throughout the measurement period. All infrared images were recorded in the final week of the measurement period when the turkeys were approximately 19 weeks of age.

Separate images of the head and neck (Figure 5.1), feet (Figure 5.2), and back (Figure 5.3) were captured using an infrared camera (ThermaCam™ SC2000; FLIR Systems, Inc., Wilsonville USA) at a distance of approximately a 0.5 – 1.0 meter from the birds. Cage lids were lifted and images of the head and neck area as well as the back were taken from a standing position. The image of the feet was captured at ground level. The camera converted body surface radiation (\( \lambda = 8-12 \, \mu \text{m} \)) into a thermal pattern and was capable of detecting temperature differentials of 0.1°C. The camera was calibrated at the beginning of each session by measuring and inputting values for the ambient temperature in the barn. The camera required an emissivity value to be set and 0.98 was used as this value is recommended for biological tissues (Steketee, 1973).

ThermaCAM Researcher Pro 2.8 SR-1 software (FLIR Systems AB, Danderyd, Sweden) was used to measure body surface temperature and Figures 5.1, 5.2, and 5.3 show the areas where temperatures were measured. To make the sites of temperature assessment as consistent as possible, average temperature of the back (\( T_{\text{back}} \)), across the distal metatarsus (\( T_{\text{DM}} \)), and side profile of the head (\( T_{\text{head}} \)) were used for the analysis. The coolest temperature within the eye region was used (\( T_{\text{eye}} \)) and this was assumed to be a point where the eye was not partially covered by the eyelid. The turkeys had an area of elevated temperature spanning from the auditory canal to the middle of the neck and the average temperature of this zone was also recorded (\( T_{\text{neck}} \)). Temperatures exceeding 3 standard deviations of the mean were removed as outliers for each body surface area.
The birds remained in the cages for image capture and contact with birds was kept to a minimum to reduce any stress-induced change in body surface temperature.

5.3.2 Statistical Analysis

Raw feed conversion ratio (rFCR) was calculated as feed intake divided by weight gain. A derived feed efficiency trait was also calculated (dFCR) and used a regression to remove the effect of body weight and ADG. The exact formula used to calculate dFCR values is proprietary to the primary breeding company that managed the turkeys in the present study. To calculate RFI, expected feed intake was calculated as

\[ FI = \mu + b_1 BW + b_2 WG + line + group + e \]

where \( FI \) was feed intake, \( \mu \) was the intercept, \( b_1 \) and \( b_2 \) were the partial regression coefficients on 15-week body weight (\( BW \)) and weight gain (\( WG \)), respectively, \( line \) was a fixed effect which accounted for a turkey’s pure line, and \( group \) was a contemporary group effect including all birds with images recorded during the same 1-hour time interval within a session. The group effect was included to account for any changes in the barn environment that may influence surface temperature including fluctuating ambient temperature and ventilation. Residual feed intake (RFI) was the \( e \) term. All other traits were adjusted for the fixed effects of line and group. Adjusted observations were used to estimate phenotypic correlations after removing data that exceeded three standard deviation of the mean as outliers.

To determine additional proportion of variation in feed intake explained by the infrared traits partial regression on \( T_{head}, T_{eye}, T_{neck}, \) and \( T_{DM} \) were added to the feed intake model and \( R^2 \) values were compared. Animals with RFI values in the 5\textsuperscript{th} and 95\textsuperscript{th} percentiles were then assigned to the low and high RFI groups, respectively. Two-tailed
t-tests were used to determine if the mean $T_{\text{head}}$, $T_{\text{eye}}$, $T_{\text{neck}}$, and $T_{\text{DM}}$ were significantly different between these efficiency groups.

5.4 Results

Means and variances of performance and infrared traits are shown in Table 5.1 with the average temperature of the non-feather covered areas being between 34°C and 40°C. The neck was the warmest area of the body, followed by the head, distal metatarsus, and eye, respectively. Phenotypic correlations and standard errors of prediction between surface temperature traits and the production and efficiency traits are shown in Error! Reference source not found.2. Due to feather cover, imaging of the back was unsuccessful with a low average temperature (23°C) and as a result, back temperature was not considered in the analysis. The distribution of the residuals of the $T_{\text{head}}$, $T_{\text{eye}}$, $T_{\text{DM}}$, and $T_{\text{neck}}$ traits approximated a normal distribution as shown in Figure 5.4.

The correlations between temperature traits and efficiency traits were low (-0.13 - 0.00) and the correlations to the production traits were in the low to moderate range (-0.00 - 0.27) as shown in Error! Reference source not found.2. Distal metatarsus temperature had the strongest correlation to BW, ADG, and feed intake (0.15, 0.27, and 0.24, respectively). This indicates that warmer surface temperatures were associated with larger size, faster growth, and increased feed consumption. Surface temperature of the neck also showed low positive correlations to these traits with values of 0.07, 0.09, and 0.09, respectively. Head temperature had a correlation of 0.02 and 0.02 to bodyweight
and feed intake, respectively, and eye temperature also showed a low correlation to bodyweight (0.10).

In Error! Reference source not found.2, similar trends in the production traits can be seen with low correlations between temperature and feed efficiency traits. Eye temperature was negatively correlated to rFCR (-0.03), dFCR (-0.11), and RFI (-0.13). Surface temperatures of the head, neck, and distal metatarsus were not correlated to the feed efficiency traits.

Surface temperature of the head, eye, and neck explained a small portion of the variation in FI ranging from 0.18% - 0.46% as shown in Table 5.3 and the relationship between feed intake and the surface temperature traits is plotted in Figure 5.5. When head, eye and neck were all included in the model the combined infrared traits increased the R-squared value by 0.0036 and therefore explained an additional 0.36% variation in feed intake.

The relationship between the surface temperature traits and RFI is plotted in Figure 5.6. The mean RFI value of the high and low RFI groups was 1,440.6 and -1,341.4, respectively and the difference in the mean of the surface temperature residuals between the high and low efficiency groups for each body site is shown in Table 5.4. Based on a two-tailed t-test, there was no significant difference in surface temperature at any measured site at a significance level of p < 0.05. A two-tailed t-test was chosen as the phenotypic correlations suggested that efficiency was not consistently associated with either higher or lower surface temperature at different areas of the body.

Due to the lack of connectedness between birds in each line and the weak relationship between efficiency traits and the surface temperature traits, the genetic
correlations were small with large standard errors. As the genetic correlations were all non-significant the results have not been reported.

### 5.5 Discussion

Infrared technology was of interest as a method to improve selection for feed efficiency in a turkey breeding program as an alternative to individual feed intake measurements, which are expensive to collect. Surface temperatures of the head, eye, distal metatarsus, and neck were both practically measureable and showed variation. As these traits are novel to the turkey population, the distribution of the traits was of interest and it was determined that surface temperature measured at different sites in the body followed a normal distribution.

Surface temperature of the distal metatarsus was moderately correlated to the production traits, however adjusting feed intake for body size and growth eliminated the correlation between the efficiency traits and temperature at this site. Low correlations indicated that surface temperature of the eye may be associated with feed efficiency, though the relationship was not strong. Biologically, a higher surface temperature in more efficient turkeys could be due to a correlation between metabolic rate and heat production in birds (Whittow, 2000). Studies in other species have shown that eye temperature, measured with infrared imaging, is correlated to core body temperature (Dunbar et al., 2009; Johnson et al., 2011). As a result, efficient turkeys may have a higher metabolism and the excess heat produced could be visible as increased surface temperature of the eye. The low correlation, however, indicated that there are many other non-metabolic factors contributing to surface temperature and these could include activity
level, differences in natural resting body temperature, or the influence of unidentified environmental factors.

Surface temperature had a small impact on the $R^2$ of the models used to predict feed intake. The low proportion of variation in feed intake explained by surface temperature is similar to the finding in cattle where rear temperature did not impact the $R^2$ value of a RFI model and foot temperature had a small impact, increasing $R^2$ by 0.05 (Montanholi et al., 2009). While alternatives to linear modeling approaches could be considered, the relationship between the surface temperature traits and feed intake in the turkey does not show a distinct trend that would be indicative of a significant non-linear relationship (Figure 5.5).

The collection of infrared images was efficient and consequently it would be feasible to use within a breeding program if the correlations to feed efficiency were significant, however this was not the case. When taking the images, the goal was to minimize contact and to obtain comparable images from each bird. A challenge was the high levels of bird movement as the birds were flighty within the cages while the images were taken. This resulted in variable positioning of the turkeys within the images and consequently image analysis became important to achieve consistency. In the future, development of a methodology to capture images of turkeys in a larger flock situation could be considered. This may be a more effective implementation of the imaging technology if the birds remain calmer and move less in their flock setting than in feeding cages. Using an infrared camera that can simultaneously take live and infrared images would also help to ensure consistent analysis.
The 5% of turkeys with the highest RFI values and 5% of turkeys with the lowest RFI values were compared to determine if surface temperature was significantly different between these efficiency groups. Results indicated that there was no significant difference in body surface temperature, at any of the areas studied, between the most efficient and least efficient birds. Figure 5.6 illustrates that there is no strong correlation between RFI and surface temperature traits and supports these findings.

These results indicate that there is limited advantage to including surface temperature in models to predict feed intake in the turkey or as a correlated trait to select for feed efficiency. Temperature traits, measured with infrared imaging, explained little variation in feed intake beyond that explained by body weight and growth rate and there is no relationship between surface temperature and the efficiency extremes. Consequently, the value of these traits in a breeding program would be negligible.

The surface temperature traits were more strongly correlated to production traits than feed efficiency. Feed efficiency is genetically correlated to feed intake, ADG, and bodyweight in the turkey and broilers (Van Bebber and Mercer, 1994; Gaya et al., 2006; Aggrey et al., 2010; Case et al., 2010a) and studies have suggested that genetic gains in feed efficiency can be accomplished by using appropriate weights on these traits in a selection index (Gunsett, 1984; Campo and Rodriguez, 1990; Van Der Werf, 2004). As bodyweight, ADG, and feed intake can be measured directly, there is little advantage to measuring distal metatarsus temperature as a correlated trait in a turkey breeding program.

To utilize infrared technology for the indirect selection of feed efficiency, a further study involving a large population of related turkeys would be required to
determine the heritabilities and genetic correlations. The low phenotypic correlations in the present study, however, indicate that the relationships were not strong and the anticipated results of a larger study are difficult to justify as the potential benefits may not warrant the costs.

Feed intake records, and hence individual feed efficiency estimates, are not available for the majority of turkeys in a selection program. Ideally, infrared traits could be collected on all birds including those that do not participate in a feeding trial and the infrared traits could then be used to indirectly select for feed efficiency. However, the low correlations to the direct measures of feed efficiency as well as FI, BW, and ADG indicate that the advantages to a breeding program would not outweigh the financial and labour costs.

Infrared images can be captured quickly and it would be possible to take infrared pictures of all selection candidates, including those that are not in a feeding trial. The phenotypic correlations estimated in the present study indicate that temperature traits were a weak indicator of feed efficiency. Investigation of the genetic variance parameters would indicate if the traits can be used to increase the accuracy of a selection index, however a further study required to estimate these parameters would not be recommended as preliminary phenotypic results indicate that genetic relationships might not be strong.
Table 5.1 Means and standard deviations for 15-week body weight (BW), average daily gain (ADG), feed intake (FI), raw feed conversion ratio (rFCR), derived feed conversion ratio (dFCR), and temperature of the head (T_{head}), eye (T_{eye}), distal metatarsus (T_{DM}), and neck (T_{neck}) measured during a 4-week feeding trial.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Units</th>
<th>Mean</th>
<th>Standard Deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>BW</td>
<td>kg</td>
<td>13.27</td>
<td>2.03</td>
</tr>
<tr>
<td>ADG</td>
<td>kg/day</td>
<td>0.20</td>
<td>0.05</td>
</tr>
<tr>
<td>FI</td>
<td>kg</td>
<td>14.37</td>
<td>2.65</td>
</tr>
<tr>
<td>rFCR</td>
<td>kg/kg</td>
<td>0.39</td>
<td>0.05</td>
</tr>
<tr>
<td>dFCR</td>
<td>kg/kg</td>
<td>2.54</td>
<td>0.22</td>
</tr>
<tr>
<td>T_{head}</td>
<td>ºC</td>
<td>37.17</td>
<td>0.47</td>
</tr>
<tr>
<td>T_{eye}</td>
<td>ºC</td>
<td>34.26</td>
<td>0.82</td>
</tr>
<tr>
<td>T_{DM}</td>
<td>ºC</td>
<td>35.02</td>
<td>2.06</td>
</tr>
<tr>
<td>T_{neck}</td>
<td>ºC</td>
<td>38.17</td>
<td>0.47</td>
</tr>
<tr>
<td>T_{back}</td>
<td>ºC</td>
<td>23.28</td>
<td>3.33</td>
</tr>
</tbody>
</table>
Table 5.2 Phenotypic correlations, with standard errors (in brackets), between 15-week body weight (BW), average daily gain (ADG), feed intake (FI), raw feed conversion ratio (rFCR), derived feed conversion ratio (dFCR), residual feed intake (RFI), and temperature of the head (T_{head}), eye (T_{eye}), distal metatarsus (T_{DM}), and neck (T_{neck}) measured during a 4-week feeding trial.

<table>
<thead>
<tr>
<th></th>
<th>T_{head}</th>
<th>T_{eye}</th>
<th>T_{DM}</th>
<th>T_{neck}</th>
</tr>
</thead>
<tbody>
<tr>
<td>BW</td>
<td>0.02 (0.03)</td>
<td>0.10 (0.03)</td>
<td>0.15 (0.03)</td>
<td>0.07 (0.03)</td>
</tr>
<tr>
<td>ADG</td>
<td>0.00 (0.03)</td>
<td>-0.02 (0.03)</td>
<td>0.27 (0.02)</td>
<td>0.09 (0.03)</td>
</tr>
<tr>
<td>FI</td>
<td>0.02 (0.03)</td>
<td>-0.03 (0.03)</td>
<td>0.24 (0.02)</td>
<td>0.09 (0.03)</td>
</tr>
<tr>
<td>rFCR</td>
<td>0.03 (0.03)</td>
<td>-0.03 (0.03)</td>
<td>-0.04 (0.03)</td>
<td>0.02 (0.03)</td>
</tr>
<tr>
<td>dFCR</td>
<td>-0.01 (0.03)</td>
<td>-0.11 (0.03)</td>
<td>-0.02 (0.03)</td>
<td>0.01 (0.03)</td>
</tr>
<tr>
<td>RFI</td>
<td>-0.02 (0.03)</td>
<td>-0.13 (0.03)</td>
<td>-0.03 (0.03)</td>
<td>0.00 (0.03)</td>
</tr>
</tbody>
</table>
Table 5.3 Proportion of variance ($R^2$) in feed intake (FI) explained by models including 15-week body weight (BW), weight gain (WG), and temperature of the head ($T_{\text{head}}$), eye ($T_{\text{eye}}$), distal medius ($T_{\text{DM}}$), and neck ($T_{\text{neck}}$) and increase in $R^2$ from the base model (Increase) measured during a 4-week feeding trial.

<table>
<thead>
<tr>
<th>Model</th>
<th>$R^2$</th>
<th>Increase</th>
</tr>
</thead>
<tbody>
<tr>
<td>$FI = \mu + \text{Line} + \text{Group} + b_1 BW_i + b_2 WG_i$</td>
<td>0.8206</td>
<td></td>
</tr>
<tr>
<td>$FI = \mu + \text{Line} + \text{Group} b_1 BW_i + b_2 WG_i + b_3 T_{\text{head}}$</td>
<td>0.8252</td>
<td>0.0046</td>
</tr>
<tr>
<td>$FI = \mu + \text{Line} + \text{Group} b_1 BW_i + b_2 WG_i + b_4 T_{\text{eye}}$</td>
<td>0.8224*</td>
<td>0.0018</td>
</tr>
<tr>
<td>$FI = \mu + \text{Line} + \text{Group} b_1 BW_i + b_2 WG_i + b_5 T_{\text{neck}}$</td>
<td>0.8235</td>
<td>0.0029</td>
</tr>
<tr>
<td>$FI = \mu + \text{Line} + \text{Group} b_1 BW_i + b_2 WG_i + b_6 T_{\text{DM}}$</td>
<td>0.8203</td>
<td></td>
</tr>
<tr>
<td>$FI = \mu + \text{Line} + \text{Group} b_1 BW_i + b_2 WG_i + b_3 T_{\text{head}} + b_4 T_{\text{eye}} + b_5 T_{\text{neck}}$</td>
<td>0.8242*</td>
<td>0.0036</td>
</tr>
</tbody>
</table>

$^1$ $\mu$ represents the mean, $\text{Line}$ is a fixed effect accounting for pure line, $\text{Group}$ is a fixed contemporary group effect for all birds with images recorded in the same hour within an imaging session, and $b_1$, $b_2$, $b_3$, $b_4$, $b_5$, and $b_6$ represent regression coefficients on body weight (BW), weight gain (WG), and temperature of the head ($T_{\text{head}}$), eye ($T_{\text{eye}}$), distal medius ($T_{\text{DM}}$), and neck ($T_{\text{neck}}$), respectively.

*$p < 0.001$ for $T_{\text{Eye}}$
Table 5.4 Difference in mean surface temperature residuals, after adjusting for line and group, between high and low RFI groups with associated p-values a two-tailed t-tests

<table>
<thead>
<tr>
<th>Trait(^1)</th>
<th>Mean Difference</th>
<th>P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>T(_{\text{head}})</td>
<td>-0.02</td>
<td>0.78</td>
</tr>
<tr>
<td>T(_{\text{eye}})</td>
<td>-0.24</td>
<td>0.07</td>
</tr>
<tr>
<td>T(_{\text{DM}})</td>
<td>-0.26</td>
<td>0.37</td>
</tr>
<tr>
<td>T(_{\text{neck}})</td>
<td>0.08</td>
<td>0.25</td>
</tr>
</tbody>
</table>

\(^1\)T\(_{\text{head}}\), T\(_{\text{eye}}\), T\(_{\text{DM}}\), and T\(_{\text{neck}}\) represent surface temperature of the head, eye, distal metatarsus, and neck, respectively
Figure 5.1 Infrared image of the turkey head and neck showing areas of average temperature measurement
Figure 5.2 Infrared image of the turkey distal metatarsus showing areas of average temperature measurement
Figure 5.3 Infrared image of the turkey back showing areas of average temperature measurement
Figure 5.4 Distribution of surface temperature of the head ($T_{\text{head}}$), eye ($T_{\text{eye}}$), distal metatarsus ($T_{\text{DM}}$), and neck ($T_{\text{neck}}$) residuals after adjusting for the fixed effects of line and measurement group
Figure 5.5 Relationship between feed intake and surface temperature residuals at the head ($T_{\text{head}}$), eye ($T_{\text{eye}}$), distal metatarsus ($T_{\text{DM}}$), and neck ($T_{\text{neck}}$) after adjusting for the fixed effects of line and measurement group.
Figure 5.6 Relationship between residual feed intake and surface temperature residuals at the head ($T_{\text{head}}$), eye ($T_{\text{eye}}$), distal metatarsus ($T_{\text{DM}}$), and neck ($T_{\text{neck}}$) after adjusting for the fixed effects of line and measurement group.
Chapter 6

Factors affecting breast meat yield in turkeys

L.A. Case¹*, S.P. Miller¹ and B.J. Wood¹, ²

¹ Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada;

² Hybrid Turkeys, Suite C, 650 Riverbend Drive, Kitchener, ON, Canada

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6.1 Summary

There is a global demand for turkey products and there is a high value attributed to breast meat. Breast meat can be considered the most important component of the carcass and consequently it is important to investigate factors that influence breast meat yield (BMY). The BMY trait is influenced by both genetics and the environment at all stages from pre-hatch until the end of the commercial growing period. Additive genetic effects appear to be the primary genetic contributor to BMY, as there is minimal evidence for heterosis or maternal inheritance. The genetic potential for BMY is also affected by sex, strain, and selection pressure within a pure line and this affects both the muscle morphology and the yield. For a turkey to fulfil its full genetic potential for BMY, optimal turkey husbandry and management is required. Nutrition is an important component of production efficiency and turkeys may be able to tolerate a reduction in dietary protein levels without a negative response in BMY, provided that the levels of all other nutrients are sufficient to meet metabolic needs. Housing conditions, such as barn temperature and lighting, also influence production efficiency. Cooler temperatures increase both weight gain and BMY, relative to a warmer rearing environment. Further, a light cycling program with a daily set light and dark-out schedule is associated with higher BMY values compared to frequently alternating light and dark periods throughout the day in an intermittent lighting regime. Due to the influence of both genetics and the environment on BMY, maximisation of yield requires optimum management by all
segments of the turkey production industry from the primary breeder through to the commercial grower.

6.2 Introduction

Turkey production is both an important and profitable agricultural industry and the investigation of factors that affect profitability is warranted, especially for a consumer-valued product such as turkey breast meat. Increasing the proportion of breast meat contributes to higher yields from the carcass and increases overall profitability as breast meat has the highest economic value relative to other carcass components and makes a large contribution to the gross margin. Consequently, breeding and management practices that optimise the trait should be identified and implemented. Sex, strain, and selection pressure affect final carcass yields. This inherited genetic potential interacts with environmental factors including nutrition, light, and temperature to determine the proportion of breast meat on the carcass. Breast meat accretion is influenced at all stages of production, including breeder, hatchery, and grow-out operations. This necessitates careful planning of management practices throughout all segments of the turkey industry in order for a turkey to fulfill it’s full genetic potential. As a result, all segments of the turkey industry must be conscious of the impact their management decisions can have on the final breast meat yield.

6.3 Defining breast meat yield

Breast meat yield is most commonly defined as the proportion of breast meat relative to the weight of the processed carcass or as the weight of the breast relative to
slaughter weight. The *M. pectoralis superficialis* (fillet) and the *M. pectoralis profundus* (tender) are the contributing muscles to breast meat and are considered in these definitions. However, the method of carcass dissection and muscle isolation is variable between processing plants and BMY analysis is often only relevant when comparing measurements taken at the same processing plant. As a result, standard procedure for breast meat separation would be beneficial. This would enable a straight-forward comparison between carcass yield studies based on the evaluation of equivalent cuts. To this end, a review was published to illustrate a method for turkey carcass dissection (Hahn and Spindler, 2002). A regulated dissection procedure would ensure that the weight of the two breast muscles and carcass weight, which are required to calculate BMY, are comparable across studies.

### 6.4 Allometric growth

The relative body composition of a turkey changes throughout the growing phase because the body components do not increase in size at a uniform rate (Peng et al., 1985; Brenoe and Kolstad, 2000). This allometric growth results in a disproportionate increase in the size of the breast at later stages of the growth trajectory. The observed increase in the proportion of breast meat is primarily due to an accelerated increase in the depth of the breast, as the relative length and width remain fairly constant with increasing body size (Swatland, 1979; 1989a). *M. pectoralis superficialis* growth is primarily responsible for the relationship between breast and body size as this muscle has a stronger and more consistent relationship with both body weight and age across strains and sexes (Barbour and Lilburn, 1995; Brake et al., 1995). A positive linear correlation between BMY and
body weight reflects these phenotypic observations (Summers et al., 1989; Brake et al., 1995).

Similar to the allometric growth between body compartments, different muscles within the breast grow at different rates. The proportion of the *M. pectoralis superficialis* is increased in growth selected lines (Wilson et al., 1990; Lilburn and Nestor, 1991). This suggests that selection to increase body size has a stronger impact on the growth rate of the *M. pectoralis superficialis* relative to the *M. pectoralis profundus*. The allometric growth of the turkey, therefore, results in unequal expansion of the breast relative to other body components and growth rates are also variable between the breast muscles. Consequently, the overall growth characteristics result in a linear increase in BMY as body size increases.

**6.5 Muscle Development**

As a turkey’s muscles develop, the increase in size can be attributed to an increase in both the number (hyperplasia) and the size (hypertrophy) of the muscle fibres. The relative influence of these two factors changes between the growing phases with hyperplasic and hypertrophic growth predominating pre-hatch and post-hatch, respectively. The significance of post-hatch hypertrophy is indicated by the increase in protein and DNA content of the muscle during the growing phase (Kang et al., 1985; Swatland, 1989b; Mozdziak et al., 1994; Velleman, 2007). Muscle development is consequently not a static process and the factors controlling breast growth shift throughout development from early hyperplasia to later hypertrophy.
The early stage of post-hatch hypertrophy is characterized by high satellite cell mitotic activity and a high rate of protein deposition, and this initial phase is followed by an increase in the cytoplasm to nucleus ratio of the fibres (Kang et al., 1985; Mozdziak et al., 1994; Moore et al., 2005). This pattern indicates that hypertrophy occurs by first contributing new genetic material to the muscle fibres, and these new nuclei enable the expansion of muscle fibre size. The initial supply of new DNA is critical and restricting satellite cell proliferation can decrease a muscle’s capacity for growth, which can reduce the size of the mature muscles (Mozdziak et al., 1997; Mozdziak et al., 2000). The outcome of the hypertrophic growth is an increase in fibre width and in the size of the extracellular space, while decreasing the fibre density as the bird ages (Velleman et al., 2003b). It is evident that hypertrophic growth is a dynamic process and new genetic material must first be generated to provide the DNA required for the fibres to expand in size.

The muscle growth processes interact differently with the growth trajectories of each sex (Shaklee et al., 1952; Chapuis et al., 1996). The linear relationship between BMY and body weight varies and this is shown by the different intercept and regression coefficient terms for toms and hens (Brake et al., 1995). These developmental differences are apparent physiologically where toms show an increased fibre diameter, increased number of muscle fibres, and increased rate of satellite cell differentiation compared to hens (Swatland, 1989a; Velleman et al., 2000). Cumulatively, these studies indicate that male and female birds have different growth physiology related to both hypertrophy and hyperplasia.
6.6 Inheritance

Additive genetic factors affect BMY as a trait independent of the relationship between absolute breast weight and body size (Velleman et al., 2003b; Velleman and Nestor, 2004). There are limited heritability estimates in the literature, but the few display moderate to high heritabilities (BMY $h^2 = 0.32$, breast width $h^2 = 0.30$) (Nestor et al., 1988; Le Bihan-Duval et al., 2003). This would indicate that selection based on BMY would result in relatively rapid genetic progress given a breeding objective developed with yield as an important component.

The patterns of inheritance and impact of selection on BMY have been studied by comparing lines that have been developed with different selection emphases on BMY. This has been done by contrasting experimental strains, developed by selecting for body weight alone, to commercial lines which are characteristically selected for both growth rate and BMY (Velleman et al., 2003b; Velleman and Nestor, 2004). Differences in BMY between lines can consequently be used to determine the impact of different selection emphases on characteristics of the breast muscles and to provide an indication of the level of genetic gain that can be achieved by including BMY in a breeding objective.

Phenotypic variation in BMY is related to changes in muscle morphology. These physiological differences can be attributed directly to increasing BMY and also due to increases in growth rate. The increased body size in both growth selected and commercial lines has been associated with a decrease in the width of the perimysial and endomysial spaces relative to random bred control lines (Velleman et al., 2003b; Velleman and Nestor, 2004). The proliferative capacity of satellite cells also increases with selection for
growth and the increased amount of genetic material is associated with an increase in the number and size of the muscle fibres. Larger muscles are favoured by focusing selection pressure on BMY in commercial breeding objectives as seen by an increase in fibre width and a decrease in fibre density (Swatland, 1989a; Wilson et al., 1990; Cherel et al., 1994; Merly et al., 1998; Velleman et al., 2000). These divergent patterns of morphology are established early in development as differences in the extracellular space and fibre width are apparent in growth selected and commercial lines, respectively, in the embryo at 25 days of incubation (Velleman et al., 2002). As a result of a selection emphasis on growth, the characteristics of the extracellular space are altered and increased selection pressure on BMY is associated with a change in the morphology of the muscle fibre.

In contrast to additive genetic variation, heterosis and maternal effects do not appear to have a significant effect on BMY. Line crosses do not consistently show heterotic effects, only being detected for a specific cross within one study (Velleman and Nestor, 2004). Similarly, in a maternal effects study objective measurements were not significant when contrasts were made between F2 crosses and did not support differences detected in visual scores of muscle morphology (Velleman et al., 2003a; Velleman and Nestor, 2004). These studies would indicate that additive genetic factors are the primary genetic contributor to variance in breast morphology, while maternal and heterotic effects have a lower impact on phenotypic differences.

### 6.7 Effect of strain

Muscle morphology and breast yields differ between genetic strains indicating a divergence in additive genetic factors between genetic groups. There are primarily two
genetic pools maintained in the turkey industry; Aviagen Turkeys and Hybrid Turkeys, with a number of small niche breeders supplying the balance of the world parent stock market (Wood et al., 2006). Pure lines derived from nucleus breeding populations are crossed to create commercial strains and these genetic groups, as well as selection pressure within the crossed lines, results in varying BMY potential between strains (Macneil and Buss, 1968; Blair et al., 1989; Lilburn and Nestor, 1991; Brake et al., 1995). As a result, the coefficients describing the linear relationship between BMY and body weight are specific to each strain (Brake et al., 1995).

Variation in breast growth between strains supports the distinct genetic parameters and relationships with body weight. Before 12 weeks of age, strain effects are most significant on the proportion of M. pectoralis superficialis (Barbour and Lilburn, 1996). The effect of strain shifts throughout the growing period to significantly effect M. pectoralis profundus yield at later ages (Lilburn et al., 1992; Lilburn and Emmerson, 1993; Barbour and Lilburn, 1995; Roberson et al., 2003). It is apparent that the independent development of genetic resource pools has created turkey strains with differences in both the genetic potential for BMY as well as pattern of muscle development.

6.8 Hatchery effects

Management of the hatchery environment is important as hyperplasia occurs primarily in the embryo and an increase in the number of muscle fibres is associated with larger mature muscle size. Growth and commercially selected lines show significant variation in the number and size of muscle fibres pre-hatch by 20 days of incubation.
(Velleman et al., 2002). The effect of incubation environment was tested by increasing incubation temperature for short periods between 0 and 12 days of incubation (Maltby et al., 2004). The result was an increase in the number of muscle fibres as well as density of nuclei, and this early increase in hyperplasia and hypertrophic mechanisms could contribute to a larger final muscle size in the birds at slaughter. The positive effect of increased temperature, however, was not apparent when temperature was increased after 24 days of incubation (Christensen et al., 2007). While incubation temperature manipulation can impact BMY, varying oxygen levels has not been shown to have an effect on breast muscle development (Christensen et al., 2007). This would indicate that temperature control throughout the early incubation period may contribute to higher BMY by stimulating both muscle hyperplasia and hypertrophy while varying oxygen levels would have no effect.

Nutrition is a key environmental factor post-hatch and the early feeding regime must be carefully managed for a poult to fulfill it’s genetic potential. Short and long term increases in the proportion of breast meat can be achieved by feeding poults immediately post-hatch (Noy and Sklan, 1998; 1999). In contrast, post-hatch starvation reduces the proportion of the M. pectoralis superficialis and overall BMY when birds are compared to those given nutrients (Mozdziak et al., 2002; Moore, 2005). A decrease in satellite cell mitotic activity in the first 4 days post-hatch as well as a smaller fibre diameter and nuclear density were also observed in the starved birds. The association of smaller muscle fibres, lower DNA content, and reduced early satellite cell proliferation with decreased final muscle size indicates that post-hatch starvation could negatively impact final BMY. An alternative to feeding poults post-hatch is in-ovo delivery of nutrients to the embryo
(Moore, 2005; Foye et al., 2006; Deoliveira, 2007). Results were not supportive of a beneficial relationship with BMY as, regardless of the composition or delivery method, injection of nutrients into the egg did not have an impact on the rate of satellite cell proliferation or BMY. Providing nutrients to poulets immediately post-hatch should, consequently, be considered as an effective way to reduce the negative effect that post-hatch starvation may have on BMY.

6.9 Nutrition

Nutrition throughout the growing phase has an effect on BMY and a feeding program that produces the most profitable carcass while minimizing feed costs is required. To identify ways to increase production efficiency, a large number of studies have investigated the effect of diet on BMY. Research has primarily focused on the impact of total feed levels, dietary protein and energy content, and amino acid levels. Study results are summarised in Table 6.1.

Feed costs could be reduced by limiting the total quantity or nutrient content of feed. The effect of dietary restriction, however, relative to more expensive feeding regimes on carcass yields must be considered. As would be expected, severe feed restriction negatively impacts BMY (Crouch et al., 2002). On the contrary, dietary protein can be restricted by up to 10%, relative to NRC recommendations, without negatively impacting BMY (Blair et al., 1989; Clarke et al., 1993; Barbour and Lilburn, 1996; Kidd et al., 1997; Waibel et al., 2000). The negative impact of protein restrictions in excess of 10% on final yield values is reduced when the diet limitation occurs before 6 weeks of age (Oju et al., 1988; Ferket and Sell, 1989). This suggests that the time and
length of the restriction period must also be considered. Feeding a diet supplemented to contain a 20% increase in protein, above NRC recommendations, after a protein restriction of greater than 10% can also help reduce the negative effect (Hester et al., 1990). Potential for compensatory growth may therefore be higher in younger turkeys and may also be favoured by diets that contain excess protein after the restriction period. These studies indicate that there is potential for the protein content of turkey feed to be reduced to 90%, if all other nutrients are formulated to meet or exceed NRC recommendations, without negatively impacting BMY.

Reducing the total amino acid content, or a combination of essential amino acids (Lys, Met+Cys, Thr, Trp, Arg, His, Leu, Ile, Phe, and Val), has a negative impact on BMY (Waldroup et al., 1993; Waldroup et al., 1998; Lemme et al., 2006). The effect of amino acid reduction becomes stronger later in the growing phase and with longer restriction periods (Lemme et al., 2006). This supports the increase in sensitivity to dietary restriction with age.

The effect of variation in dietary concentration of specific essential amino acids depends on the amino acid considered. Increasing threonine levels in a diet that meets basic protein requirements can improve the trait, however supplemented threonine does not have a positive effect on BMY when birds are fed a protein deficient diet (Kidd et al., 1997; Lehmann et al., 1997; Waibel et al., 2000). Varying methionine levels has also shown to be ineffective, however there is a positive dietary effect when betaine is added with the methionine (Noll, 2002). This is a result of the interaction between betaine and both methionine and the lipid metabolic pathway. Alternatively, increasing lysine levels in turkey feed had a positive impact on BMY and this occurs independently of the
relative proportion of dietary arginine (Lilburn and Emmerson, 1993; Lehmann et al., 1996; Kidd and Kerr, 1998; Veldkamp et al., 2003). Cumulatively, these studies show that limitation of certain amino acids, including methionine and threonine, is possible without affecting BMY, however there are positive correlations between BMY and total amino acid and lysine levels.

The addition of fat as an energy source has been used to improve growth performance, however increasing the dietary fat concentration has not significantly affected BMY (Salmon, 1974; Sell et al., 1985; Halvorson et al., 1991; Sell, 1993; Sell et al., 1994). If the level of protein to energy (fat) in the feed is not maintained, BMY can be reduced (Salmon, 1983). Increasing dietary fat levels, consequently, is not a viable option to reduce feed costs, as the relative level of protein must also be increased to maintain performance levels.

Antibiotics and feed additives have been considered as a means to improve growth performance. Results have shown a positive benefit of virginiamycin and ractopamine on both feed efficiency and body weight (Waibel et al., 1991; Ferket et al., 2002; Elanco, 2008; Cervantes, 2009). While the increase in body weight caused by virginiamycin is not associated with an increase in BMY, cellular studies have indicated that ractopamine can increase the number, protein, and DNA content of muscle cells in the turkey (Shappell et al., 2000; Parks et al., 2005). These cellular responses may have a positive effect on breast growth, however there is limited research on the effect of ractopamine on BMY and conclusions cannot be made. As a result, a reduction in dietary protein provides the most potential for reducing feed costs without impacting BMY.
Caution should be taken to ensure the dietary amino acid and lysine levels are formulated to meet requirements if the concentration of other nutrients is altered.

6.10 Growing Environment

Natural climatic fluctuations and controlled growing environments have been used to investigate the impact of rearing environment on BMY. Breast meat yield is negatively impacted by heat and increased environmental temperatures decrease BMY (Rose and Michie, 1987; Noll et al., 2001; Noll, 2002; Veldkamp et al., 2005). Rearing environments with higher temperatures during light periods and lower temperatures during dark-out produce intermediate BMY relative to a consistent hot or cool environment (Halvorson et al., 1991). Altering the dietary electrolyte balance and nutrient levels has been attempted to reduce the negative impact of heat, however these manipulations were not effective (Veldkamp et al., 2000a; Veldkamp et al., 2000b).

Light cycling programs involve a fixed-length light period followed by a fixed-length dark-out each day. Alternatively, intermittent lighting involves exposing the birds to more frequent alternating light and dark periods during a 24 hour day. Light cycling has been shown to increase BMY and the effect has been significant if the light periods are substantially longer than the periods of dark (18L:6D) (Halvorson et al., 1991; Clarke et al., 1993). When light cycling is practiced, gradually decreasing the light exposure results in higher BMY when compared to gradually increasing light hours (Peng et al., 1985; Lilburn et al., 1992). The effect seems to be most strongly correlated to the development of the M. pectroalis superficialis (Lilburn et al., 1992). Maintaining lower rearing temperatures as well as light cycling should thus be utilized to optimize BMY.
These positive correlations are most likely due to the reduced biological stress and stimulation of bird activity that can be created by these management practices.

6.11 Conclusions

The processes regulating muscle growth are dynamic, and hyperplasia and hypertrophy both contribute to breast development. The physiological characteristics of the breast muscle, as well as total yields from the carcass, are under the influence of additive genetic factors and genetic potential can vary by sex and strain. This genetic component makes trait improvement possible by applying selection pressure to breast meat yield in a breeding program. Management of the rearing environment, including nutrition, lighting, and temperature, all must be carefully considered for turkeys to fulfill their genetic potential. As a result of the combined impact of both genetics and environment on breast meat yield, all industry levels from the primary breeder to the commercial grower must consider the influence that they can have on final proportion of breast meat.
<table>
<thead>
<tr>
<th>Source</th>
<th>Significant Treatment 1,2</th>
<th>Effect on BMY 3</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Feed restriction</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(Crouch et al., 2002)</td>
<td>Feed restriction sufficient to reduce BW by 45%, 3-16 weeks</td>
<td>Proportion <em>p. superficialis</em> reduced</td>
</tr>
<tr>
<td><strong>Protein restriction</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(Barbour and Lilburn, 1996)</td>
<td>13% protein restriction + 20% lysine restriction, 0-8wk</td>
<td>BMY reduced</td>
</tr>
<tr>
<td>(Blair et al., 1989)</td>
<td>12% protein restriction, 8-24wk</td>
<td>BMY reduced</td>
</tr>
<tr>
<td>(Clarke et al., 1993)</td>
<td>&gt;20% protein restriction, 2-8wk</td>
<td>BMY reduced</td>
</tr>
<tr>
<td>(Ferket and Sell, 1989)</td>
<td>40% protein restriction, 1-6wk</td>
<td>BMY reduced</td>
</tr>
<tr>
<td>(Hester et al., 1990)</td>
<td>26% protein and amino acid restriction, 6-12wk 20% increase in protein and amino acid levels, 12-20wk</td>
<td>BMY reduced, supplementation after 12wk restored BMY</td>
</tr>
<tr>
<td>(Kidd et al., 1997)</td>
<td>&gt;84% protein restriction, 0-18wk</td>
<td>BMY reduced</td>
</tr>
<tr>
<td>(Lemme et al., 2004)</td>
<td>20% protein restriction, 3-22wk</td>
<td>BMY reduced</td>
</tr>
<tr>
<td>(Oju et al., 1988)</td>
<td>25% reduction in protein + 34% reduction in methionine and lysine, 0-6wk</td>
<td>BMY consistently reduced in toms until 16 wk and in hens until 6wk</td>
</tr>
<tr>
<td>(Waibel et al., 2000)</td>
<td>&gt;15% reduction in protein</td>
<td>BMY reduced</td>
</tr>
<tr>
<td><strong>Amino acid levels</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(Kidd et al., 1997)</td>
<td>0.2% threonine addition to low protein diet, 0-18wk</td>
<td>No effect</td>
</tr>
<tr>
<td>(Kidd and Kerr, 1998)</td>
<td>20% increase in Arg:Lys</td>
<td>No effect</td>
</tr>
<tr>
<td>(Lehmann et al., 1996)</td>
<td>0.35% lysine addition to diet, 16-20wk</td>
<td>BMY increased</td>
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<tr>
<td>(Lehmann et al., 1997)</td>
<td>0.15% threonine addition to diet</td>
<td>No effect</td>
</tr>
<tr>
<td>(Lemme et al., 2004)</td>
<td>10% protein, Arg, Val, Ile, and Leu restriction, 3-22wk</td>
<td>BMY reduced</td>
</tr>
<tr>
<td>(Lemme et al., 2004)</td>
<td>20% increase in essential aa, 1-13 wk 10% decrease in essential aa, 14-22wk</td>
<td>BMY increased when aa levels increased early in growing phase BMY reduced when aa levels reduced late in growing phase</td>
</tr>
<tr>
<td>(Lilburn and Emmerson, 1993)</td>
<td>Increase in lysine and sulfur aa, 0-12wk</td>
<td>BMY increased 12wk, proportion <em>p. superficialis</em> improved 20wk, proportion <em>p. profundus</em> improved</td>
</tr>
<tr>
<td>(Noll, 2002)</td>
<td>30% increase in methionine 0.1% betaine addition</td>
<td>No effect of methionine BMY increased by betaine</td>
</tr>
<tr>
<td>(Veldkamp et al., 2003)</td>
<td>25% reduction in lysine</td>
<td>BMY reduced</td>
</tr>
<tr>
<td>(Waibel et al., 2000)</td>
<td>Threonine supplementation to low protein diet</td>
<td>No effect</td>
</tr>
<tr>
<td>(Waldroup et al., 2000)</td>
<td>25% reduction in amino acids</td>
<td>BMY reduced 1,4</td>
</tr>
<tr>
<td>Year</td>
<td>Description</td>
<td>Effect</td>
</tr>
<tr>
<td>------------</td>
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</tr>
<tr>
<td>1993</td>
<td>(Waldroup et al., 1998)</td>
<td>BMY reduced¹</td>
</tr>
<tr>
<td>1993</td>
<td>25% reduction in amino acids</td>
<td></td>
</tr>
<tr>
<td>Energy level</td>
<td>(Halvorson et al., 1991)</td>
<td>No effect²</td>
</tr>
<tr>
<td>1993</td>
<td>1-8% increase energy with age</td>
<td></td>
</tr>
<tr>
<td>1993</td>
<td>(Salmon, 1974)</td>
<td>No effect</td>
</tr>
<tr>
<td>1993</td>
<td>12.9% increase in energy</td>
<td></td>
</tr>
<tr>
<td>1993</td>
<td>(Salmon, 1983)</td>
<td>BMY reduced</td>
</tr>
<tr>
<td>1993</td>
<td>18% increase in fat, relative to protein</td>
<td></td>
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<tr>
<td>1993</td>
<td>(Sell et al., 1985)</td>
<td>No effect</td>
</tr>
<tr>
<td>1993</td>
<td>8% increase in energy</td>
<td></td>
</tr>
<tr>
<td>1993</td>
<td>(Sell, 1993)</td>
<td>No effect</td>
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<tr>
<td>1993</td>
<td>2% or 8% increase during different feeding stages</td>
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</tr>
<tr>
<td>1993</td>
<td>(Sell et al., 1994)</td>
<td>No effect</td>
</tr>
<tr>
<td>1993</td>
<td>2% or 8% increase during different feeding stages</td>
<td></td>
</tr>
</tbody>
</table>

¹ Evaluated at 5% significance level
² If time period unspecified, treatment was administered from 0wk to slaughter
³ Effect on BMY at slaughter, unless otherwise specified
⁴ Negative effect on BMY stronger for 0-6wk and 6-12wk restriction, relative to 0-3wk restriction
⁵ Genotype by environment interaction: additional energy increased BMY in birds raised at low temperature (7°C)
Chapter 7

The investigation of ultrasound technology to measure breast muscle depth as a correlated trait to breast meat yield in the turkey (*Meleagris gallopavo*)

7.1 Abstract

Ultrasound measurements of muscle depth were analyzed to determine if these objective trait measurements could be used to increase the rate of genetic gain in breast meat yield. Two measurements of breast depth, one taken horizontally across both breast lobes and one parallel to the keel, were captured using ultrasound. The heritabilities of the muscle depth traits ranged from 0.35 – 0.70. These values were higher than the heritabilities of conformation score that ranged from 0.25 – 0.47 within sex and line. The ultrasound traits also showed high genetic correlations to breast meat yield, ranging from 0.43 - 0.75, indicating that selection for BMY using the depth traits as a correlated
information source would result in an improvement in breast meat yield. Including the ultrasound traits in a linear regression model predicting breast meat yield increased the proportion of variation explained by the models by 0.08 – 0.17, relative to using conformation score as the only \textit{in vivo} estimate. The ultrasound measures of muscle depth can also increase the accuracy of a selection index for breast meat yield by 0.02 – 0.16 and could increase the rate of genetic gain in breast meat yield by up to 25\%, based on results from a simulated turkey breeding program. As a result, ultrasound technology has the potential to improve the rate of genetic gain in breast meat yield in a breeding program.

7.2 Introduction

Due to consumer preference for white meat, the value of the turkey breast is relatively high compared to other components of the carcass. This has made breast meat yield (BMY) an important trait to consider in breeding objectives as increases in the proportion of breast muscle on the carcass can have a significant financial impact when the carcass is processed. As a result, it is desirable to determine if alternative measures of BMY could be measured and included in a selection index to increase the accuracy of selection and accelerate genetic gains (Emmerson, 2003).

Ultrasound measurements of muscle depth can be recorded on the live bird and may be used as a selection criterion for breast meat yield. Relative to conformation scoring, the precision of estimating BMY \textit{in vivo} can be increased by using ultrasound to generate continuous muscle depth measurements and preliminary studies in turkeys, broilers, and ducks support the use of ultrasound in the poultry industry (Gillis et al.,
Ultrasound has been used in phenotypic studies to measure muscle depth as an estimator of meat yields in the live turkey (Wilkiewicz-Wawro et al., 2003) and evidence in cattle has shown that the technology can be advantageous for selection to increase the accuracy of live animal prediction of carcass quality traits (Herring and Kemp, 2001).

Ultrasound images are generated by the reflection of ultrasonic waves off tissues of varying density and the images can be used to estimate tissue depth (Houghton and Turlington, 1992). Measurements of muscle depth may be useful for BMY selection in poultry as estimates of breast muscle weight are more strongly correlated to breast thickness than length or width of the breast muscles in broilers (Scheuermann et al., 2003). Further, the genetic correlation between breast muscle weight predicted using ultrasound muscle thickness and carcass values are high, ranging from 0.64 to 0.69 in broilers and there is also a phenotypic relationship in the turkey (Gaya et al., 2006; Wilkiewicz-Wawro et al., 2003).

Ultrasound technology has also been used to estimate muscle area in the beef and swine industries as an alternative to the traditional approach of progeny and sibling testing (Herring and Kemp, 2001). A review of ultrasound imaging to predict longissimus muscle area in beef cattle reported an average heritability of 0.32, with more recent estimates ranging from 0.37 – 0.61, and high genetic correlations to the carcass muscle area of 0.54 – 0.80 (Herring and Kemp, 2001; Crews and Kemp, 2002; Crews et al., 2004). Ultrasound measurements of longissimus muscle area can also be used to predict lean carcass percentage in beef cattle with genetic correlations ranging from 0.48–0.59 (Bergen et al., 2006). Similar values are also seen in the pig, where estimates of
ultrasound heritability are 0.46 with correlations to lean muscle area 0.87 (Lo et al., 1992).

Evidence in other livestock species indicates that ultrasound traits measured on the live animal are correlated to carcass values and that selection based on ultrasound-measured muscle traits can be used to achieve genetic gains in the carcass traits. The objective of the present study was to use conformation score and ultrasound technology to estimate breast muscle depth in the turkey and to determine their correlations to percentage breast meat yield. The study also aimed to evaluate how ultrasound measures of breast depth can be used to improve genetic progress in breast meat yield, relative to conformation scoring, using a revised selection index that includes in vivo estimates of the trait as well as carcass data from a sibling testing program.

7.3 Materials and Methods

7.3.1 Study Population and Management

Large white turkeys from a male (n_toms = 530, n_hens = 703) and a female (n_toms = 597, n_hens = 902) primary breeder line were used in this study. The breeding objective had a heavier emphasis on reproductive traits in the female line while commercial performance traits had a greater emphasis in the male line. The birds were raised under standard commercial rearing conditions and feeding programs. Body weight (BW), breast conformation score (Conf), and ultrasound measurements were taken at approximately 14 weeks and 20 weeks of age in the male line toms and hens, respectively. The measurements were taken at approximately 15 weeks and 14 weeks, respectively, in the female line toms and hens. The birds were sent for slaughter the same week that the live-
animal measures were recorded. At processing, yield of breast meat (BY) was evaluated as the weight of the boneless, skinless breast muscle (fillet and tender) and percentage breast meat yield (BMY) was then calculated as breast yield divided by body weight (Table 7.1).

### 7.3.2 Trait Measurement

Birds were hung upside-down on a hanging scale and weighed. A trained selector felt the shape of the breast muscle to assign a conformation score from 1 – 6, which is industry-standard procedure. The same scorer assessed all the birds within a contemporary group. While suspended, breast muscle depth was also recorded on each bird at two sites, as shown in Figure 7.1, using an ultrasound machine (Aloka SSD-500, Tokyo, Japan) equipped with a 172mm probe (model 5044; 172 mm; 3.5 MHz; Corometrics Medical System, Wallingfort, CT, U.S.A.) and a stand-off block developed to mirror the curvature of a turkey breast (Designer Genes Technologies Inc., AR, USA). Ultrasound images were analyzed using the AUSKey program (Animal Ultrasound Services, Ithaca, NY, USA). One image was captured along the right side of the breast with the top of the probe positioned above the furcula (wishbone) and running parallel to the keel. The first breast depth measurement (D1) was recorded from this image as depth from the skin surface to the ribcage using the furcula junction as a landmark (Figure 7.2). A second image was taken 90° to the first with the stand-off centered in the middle of the chest, where the corucoid bones meet the keel, and spanning both breast lobes. The second muscle depth trait (D2), measured from this image, was the average depth from the skin surface to the apex of the ribcage recorded on both sides of the body (Figure 7.3). Vegetable oil was used as a contact agent between the stand-off and probe as well as
between the stand-off and skin. Feathers were not removed but were separated from the scanning site to maximize contact between the stand-off and skin surface.

7.3.3 Genetic Analysis

Pedigree information extending back a minimum of 5 generations was available for all birds. Variance components were estimated within sex and line using ASReml (Gilmour et al., 2002). The model was

\[ y = \mu + Flock + a + e \]

where \( y \) was the recorded trait (body weight, absolute breast yield, BMY, conformation score, D1, or D2), and \( \mu \) was the average trait value for all animals. \( Flock \) was a fixed contemporary group effect. \( Flock \) also accounted for the conformation scorer effect as all birds within a flock were assessed by the same conformation scorer in a single measurement session. The random additive genetic effect and the random residual effect were represented by \( a \) and \( e \), respectively. The additive genetic and residual effects were assumed normally distributed with mean of zero and (co)variance structure equal to:

\[
V\left(\begin{array}{c}
a \\
e
\end{array}\right) = \left(\begin{array}{cc}
A\sigma_a^2 & 0 \\
0 & 1\sigma_e^2
\end{array}\right)
\]

where \( A \) represents the additive genetic relationship matrix and \( I \) was an identity matrix. Bivariate models, with the same effects as the single trait models, were used pair-wise for all traits to estimate genetic and residual covariances. These estimates were then used for the calculation of genetic correlations shown in Tables 7.2 and 7.3 and heritabilities were calculated as the average of estimates from across the bivariate models.
7.3.4 Index Accuracy

To analyze the benefits of using the ultrasound traits in a selection program, the variation in BMY explained by models including body weight (BW), conformation score (Conf), and the breast depth measurements (D1 and D2) were compared (Table 7.4). The models were

\[ y = \mu + Flock + b_1BW + b_2Conf + e \]  \hspace{1cm} [1]

\[ y = \mu + Flock + b_1BW + b_3D1 + e \]  \hspace{1cm} [2]

\[ y = \mu + Flock + b_1BW + b_4D2 + e \]  \hspace{1cm} [3]

\[ y = \mu + Flock + b_1BW + b_3D1 + b_4D2 + e \]  \hspace{1cm} [4]

\[ y = \mu + Flock + b_1BW + b_2Conf + b_3D1 + b_4D2 + e \]  \hspace{1cm} [5]

where \( y \) was BMY, \( \mu \) was the intercept, \( Flock \) was the same fixed effect used in the genetic models, and \( b_1, b_2, b_3 \) and \( b_4 \) represent the regression coefficients on body weight, conformation score, D1, and D2, respectively.

Selection indexes for BMY were also developed to determine the increase in accuracy resulting from selection based on the ultrasound traits. The indexes were defined as

\[ I = b'x \]

where \( b \) was a matrix of selection index weights and \( x \) was the phenotypic information from all sources. All indexes included body weight and conformation score on the individual, sire, dam, 3 full sibs, and 10 half sibs. Indexes modeled to determine the impact of adding ultrasound information as well as cut-up information on siblings and the simulated indexes are shown in Table 7.5. The accuracy of the indexes (\( r \)) were
calculated, based on the information available on the selection candidate and its relatives, in the MTINDEX program (van der Werf, 2010) as

\[
r = \sqrt{\frac{b' G v'}{v' C v'}}
\]

where \( G \) was a genetic (co)variance matrix between observations in the index and in the breeding objective and contained the line and sex specific values estimated in the genetic analysis component of this study. The breeding objective contained only the BMY trait and as a result \( v \), a vector of economic weights, contained a weight of 1 for BMY and similarly \( C \), the genetic (co)variance matrix among traits in the breeding objective, contained a value of 1 as BMY was the only trait considered.

### 7.3.5 Simulated Response to Selection

The advantage of using ultrasound technology to measure breast muscle depth at different stages of selection in a turkey breeding program was estimated using the SelAction program (Rutten et al., 2002). SelAction uses deterministic simulation and accounts for the reduction in variance due to selection (Bulmer, 1971). The program also adjusted selection intensity for the correlation between index values of family members as well as finite population size (Meuwissen, 1991). Two-stage selection schemes were simulated with discrete generations. Multiple-trait pseudo BLUP (Villanueva et al., 1993) was used to predict genetic gain in a hierarchal mating structure with dams nested within sires for half sib family structure and random mating of selected animals.

In the simulated population 10 toms were randomly mated to 50 hens (Figure 7.4). Each hen produced 40 poults with a sex ratio of 1:1 generating a total of 1,000 toms and 1,000 hens (20 x 50 = 1,000). To evaluate BMY, 50 birds of each sex were
designated for carcass testing spread equally across each family. A pre-selection stage was simulated using body weight and conformation score on all selection candidates as the *in vivo* selection criteria. In the second stage of selection, ultrasound measures of D1 and D2 were measured on the proportion of individuals kept after pre-selection \((p_1)\). At the second stage, carcass BMY information was also available on the siblings that were sent for processing. The proportion of turkeys kept as breeder parents \((p_2)\) after the second round of selection was calculated to maintain a consistent selection intensity of 5% in hens and 1% in toms, which is an assumed idealized situation in which there is no loss due to mortality. The 5:1 mating ratio was more representative of a female primary breeding line and all female line birds had the D1 and D2 traits measured at selection age in this study. As a result, the phenotypic variance and genetic parameters from female line toms were used and the simulation was repeated using the female line hen parameters to determine the trends in response to selection (Table 7.1 and Table 7.3).

To evaluate the impact that the ultrasound traits would have on selection for BMY a simplified breeding objective was assumed as

\[
H = EBV_{BMY}
\]

where \(EBV_{BMY}\) is the true economic value for BMY and as a result, for the purpose of this study, all selection emphasis was focused on improving the BMY trait.

The proportion of individuals measured after pre-selection \((p_1)\) was increased from 0% to 100% to determine the benefits of measuring the ultrasound traits on a varying number of selection candidates. As \(p_1\) increased, the number of selection candidates available for ultrasound measurement increased and the change in response to selection was calculated. Consequently, a \(p_1\) of 0% simulated the use of conformation
score as the only *in vivo* BMY measurement and a $p_i$ of 100% simulated the measurement of D1 and D2 on all selection candidates.

### 7.4 Results

Means and standard deviations of the measured traits are shown in Table 7.1. Body weights, absolute and percentage breast meat yields, and ultrasound depths were higher in the male line compared to the female line. Toms from the male line had lower conformation scores and hens from the male line had higher conformation scores than same sex birds in the female line. The female line toms and hens also showed higher variation for percentage breast meat yield and lower variation for D1. When comparing same sex birds between lines, variation in D2 was higher in male line toms and female line hens.

All of the measured traits had moderate to high heritabilities (Table 2 and Table 3). Body weight, absolute breast yield, and percentage breast meat yield had heritabilities of comparable magnitude in both sexes in the female line and hens from the male line, with slightly lower estimates in male line toms which were measured at a younger age and earlier selection stage than other groups of birds. The heritability of conformation score was similar in the toms (0.40) and hens (0.34) in the male line. The heritability of conformation score was higher in female line hens (0.46) than in toms (0.26). Heritabilities of the D1 (0.59) and D2 (0.70) traits were highest in the female line hens with similar estimates in the other groups of birds ranging from 0.35-0.51.

Phenotypic and genetic correlations for the male and female lines are shown in Tables 7.2 and 7.3, respectively. In both lines, body weight was highly correlated to
absolute breast yield (0.80 – 0.88), and less correlated to percentage breast meat yield (0.03 – 0.35). The genetic correlations between body weight and the depth traits were similarly high in all groups (0.51 – 0.69). The correlation between body weight and conformation was highest in toms from the female line (0.82) and ranged from 0.54 – 0.64 in the other groups. The absolute breast yield and BMY traits were highly correlated in toms and hens from both lines, as were the two measurements of ultrasound muscle depth. Conformation was more strongly correlated to D1 than D2. The correlation between conformation score and absolute breast yield was higher than the correlation between conformation score and BMY and the same trend was seen for the ultrasound depth traits. In hens from the male line, BMY was more strongly correlated to D1 (0.68) than conformation score (0.60). In female line toms D2 was more strongly correlated to BMY (0.75) than conformation score (0.61). Female line hens showed similar genetic correlations between BMY and the ultrasound and muscle depth traits. In male line toms, BMY was more genetically correlated to conformation score (0.85) than D1 (0.63) or D2 (0.51).

Any model to predict breast meat yield that included the ultrasound depth traits explained a larger proportion of variation than models that included conformation score as the only live bird measurement as shown in Table 7.4. In male line toms and hens, as well as female line hens, models incorporating D1 had higher $R^2$ values than models including D2. The D2 trait explained a larger proportion of variation than D1 in female line toms. Models that included both measures of muscle depth increased $R^2$ values by 0.05 - 0.09, relative to an index including conformation score. Including both depth traits in addition to conformation score explained an additional 8% - 17% of the variation in
breast meat yield. The ultrasound traits had the largest impact on toms from the female line.

The accuracy of an index to select for BMY was higher when individual records for ultrasound traits were simulated relative to selection based on conformation score alone, with and without the consideration of sibling testing (Table 7.5). The impact of the D1 and D2 traits was similar in hens from both the male and female line. The increase in accuracy was higher using D1 in male line toms and D2 in female line toms. Using both measures of muscle depth in addition to conformation score increased the accuracy of an index by 0.02 – 0.23, relative to using conformation score alone as shown by comparing indexes 1 and 7. Selection based on all three in vivo estimates of breast meat yield increased the accuracy of the indexes including sibling testing by 0.02 – 0.16, representing an increase of up to 30%, shown by comparing indexes 2 and 8. The increases in accuracy by adding the ultrasound traits were lower in male line toms than other groups of birds at the time periods measured due to the high correlation between BMY and conformation score in that group of birds. The impact of sibling testing was higher for an index including conformation score alone, with increases of 0.01-0.08 as shown when comparing indexes 1 and 2, than for indexes including the ultrasound traits (increases of 0.01-0.04 when indexes 7 and 8 are compared).

Response to selection in breast meat yield increased from 1.13% to 1.44% and from 1.64% to 1.98% using the tom and hen parameters, respectively, when conformation score was the only live bird measurement of BMY taken compared to when D1 and D2 were measured on all selection candidates. The increase of 0.3% BMY in both toms and hens represents approximately a 25% improvement in response to selection. This was
based on the assumed population parameters and a breeding objective focused solely on improving the breast meat yield trait. The change in response to selection as the proportion of birds kept after pre-screening increases from 0% - 100% is shown in Figure 7.5. The rate of increase was rapid until approximately 40% of animals had D1 and D2 records, using both the tom and hen parameters, and after this point the response to selection increased at a much slower rate.

7.5 Discussion

The increased precision and accuracy of ultrasound measures of breast muscle depth make selection based on these traits advantageous to improve BMY, relative to conformation scoring. Using an ultrasound measurement of breast depth would increase the accuracy of an index selecting for breast meat yield, and the effect would persist both with and without a sibling testing program. This increase in accuracy would ultimately be reflected by an increase in response to selection. As an advantage to industry implementation, ultrasound traits can be recorded quickly and non-invasively indicating that the technology.

Heritability estimates of ultrasound-measured breast depth have not been published in the turkey and values were slightly higher than estimates in broilers, which range from 0.28 – 0.29 (Gaya et al., 2006). Ultrasound traits were also more heritable than conformation score for toms and hens from both turkey lines. As a result, the potential to achieve genetic gain in breast meat yield may be greater by including the muscle depth traits as selection criteria relative to conformation score alone.
The strong correlation between body weight and absolute breast yield and the lower correlation between body weight and percentage breast meat yield estimated in the turkey population has also been shown in broilers (Le Bihan-Duval et al., 1999). The correlation between body weight and breast meat yield was lower, with a proportionally higher standard error, in male line hens. The male line hens were measured at a later age than the other groups of birds and the difference in genetic correlation may be a result of these turkeys being at a different stage along the growth curve. This trend of a lower genetic correlation between BW and BMY as age increases has also been seen in a recent turkey study (Aslam, 2011). These correlations indicate that selection for weight alone would not be the most optimal method to increase the percentage of meat on a carcass in meat type poultry. This emphasizes the importance of identifying a live trait that is both heritable and genetically correlated to BMY.

The genetic correlations between the ultrasound traits and breast muscle weight in the present study are slightly lower than estimates in broilers, which ranged from 0.64 – 0.69 (Gaya et al., 2006). Genetic correlations for ultrasound traits have not been reported in the turkey, however preliminary studies have shown a phenotypic relationship between ultrasound measurements of breast muscle depth and meat yields (Wilkiewicz-Wawro et al., 2003). Genetically, D1 was more strongly correlated to BMY compared to conformation score for hens from the male line. The D2 trait was more strongly correlated to BMY in female line toms and all three in vivo estimates showed similar correlations to BMY in the female line hens. Breast muscle conformation is variable between sexes and lines and this may have produced the variation in correlations between muscle depth measurements and BMY. Growth of the breast muscle occurs as increasing
muscle depth later in the growth trajectory (Swatland, 1979; 1989a). The male line toms were measured earliest in their growing phase and showed a higher correlation between conformation score and BMY compared to the other groups of birds. This indicates that conformation score may be a better indicator of meat yields earlier in growth when width and length of the muscle are stronger indicators of yield than depth, which may become a larger factor at predicting BMY as the birds continue to reach finishing weights.

The heritabilities of absolute and percentage breast meat yields were very similar to estimates in broiler chickens (Le Bihan-Duval et al., 1999; Le Bihan-Duval et al., 2001). The heritabilities of body weight in the present study tended to be slightly higher than previous results in meat type poultry, which range from 0.31 – 0.45 (Le Bihan-Duval et al., 1999; Nestor et al., 2000; Le Bihan-Duval et al., 2001; Aggrey et al., 2010). The birds used in the present study were separated from the population after a phenotypic selection within a flock. As a result, the birds with ultrasound measurements may have showed a lower phenotypic variance than would be expected in the entire population and this may have elevated the heritability estimates.

The heritability values were generally lower for the male line toms than the other groups of birds. Growth curves in the turkey are line and sex specific (Maruyama et al., 1998) and, for the population used in the present study, the female line birds matured at an earlier age than turkeys in the male line. Breast muscle development is also correlated to allometric growth in the turkey and results in accelerated breast tissue development at later stages in growth (Peng et al., 1985; Brenoe and Kolstad, 2000). As a result, the male line toms were measured at an earlier stage of growth and development. Future investigation of ultrasound should consider measuring male line toms at 20 weeks of age.
when the turkeys are at a later stage of maturity. This may increase the heritability to values that would be comparable to male line hens and female line birds. It would also be of value to measure male line hens at 15 weeks of age, as male line birds typically undergo two-stage selection and breeding programs could make use of distinct parameters for each selection stage.

Ultrasound technology has been used in broilers to estimate total breast muscle area (Oviedo-Rondon et al., 2007). Multiple regression on body weight and ultrasound muscle area explained 97% of the variation in breast muscle weight. Due to the larger size of the turkey breast, it was not possible to capture the entirety of the breast muscle in a single image with the available probe and stand-off. As a result, it was necessary to use muscle depth measurements as an estimator of BMY in the turkey. Breast meat yield is more highly correlated to breast depth (0.66) than breast width (0.39) or length (0.23) in broilers and higher breast meat yields are associated with a larger maximum meat depth, relative to breast width, in the turkey (Swatland, 1980; Scheuermann et al., 2003). This supports the use of ultrasound to estimate breast depth. In agreement, preliminary phenotypic results in have shown moderate correlations between ultrasound measures of breast muscle depth and meat yields in turkeys (Wilkiewicz-Wawro et al., 2003). For industry implementation, the depth traits were efficient to analyze with imaging software and the rate of analysis may be faster for muscle depth traits, relative to tracing an entire muscle.

Models that explain a larger proportion of variation in breast meat yield are better predictors of the carcass trait and, as a result, are more efficient for selection. Of the ultrasound traits, D1 and D2 were comparable predictors of breast meat yield in female
line birds and in hens from the male line, while D1 explained a larger proportion of variation in male line toms. This was expected based on the estimated genetic parameters as the depth traits with higher correlations produced indexes with higher accuracies within sex and line. For all groups of birds, it was better to include both measures of breast muscle depth and the proportion of variation explained was largest when all three \textit{in vivo} estimates of breast meat yield were included in the regression.

In agreement with the linear models, including both ultrasound traits increased the accuracy of a selection index. The largest increase in accuracy occurred when the ultrasound traits were included in addition to conformation score, with and without the inclusions of sibling carcass records. Measurement of BMY from siblings is important to provide a direct measure of the trait for selection, however the impact of adding sibling information was not as large as the use of ultrasound traits. With a sibling testing program implemented, the ultrasound traits can increase the accuracy of an index by up to 30\% and the technology, therefore, has the potential to have a strong positive impact on selection for BMY.

The simulated increases in accuracy when the ultrasound traits were measured on selection candidates were reflected by an increase in genetic progress. There is the potential to increase response to selection for BMY by up to 25\% by including the ultrasound breast depth traits as selection criterion for the carcass trait. These results along with results from the regression equations and selection indexes indicate that ultrasound would be very advantageous to use as a compliment to conformation scoring and sibling testing in a breeding program to improve BMY.
The implementation of ultrasound technology into a breeding program should be considered. The breeding program would be required to make an initial investment for an ultrasound machine and there would be continual labour costs associated with taking the depth measurements and analyzing the images. The results from the breeding program simulation indicate that pre-selecting turkeys based on conformation score and measuring the ultrasound depth traits on the top 40% of selection candidates results in near-optimal gains. As a result, the breeding program would work optimally with a pre-selection based on conformation score and the measurement of ultrasound traits on the top 40% of the birds. This would be the most efficient implementation of the technology, in terms of time and labour costs, and near-maximal advantages would be achieved.

For selection in the turkey breeding industry, determining the heritability and covariance of traits at both 15 weeks and 22 weeks of age in male line birds could be beneficial. This would enable the development of a selection program utilizing the parameters of the population at both stages of selection to optimize selection. Determining how the heritability and genetic correlation of ultrasound traits are affected as the bird ages and body composition changes could also be valuable. The success of utilizing ultrasound traits to select for BMY in these preliminary simulations indicate that there is a large potential for ultrasound traits to improve the rate of genetic gain for BMY in the turkey. As a result, these additional parameters can be investigated as the technology is further applied by turkey breeding companies.

Together with body weight, BMY is the single most important production trait in the turkey industry. As a result, increasing carcass BMY is extremely important in a breeding program and the trait is an important parameter in breeding objectives. This
study has shown that ultrasound measures of breast depth are highly heritable and correlated to carcass BMY. Ultrasound breast depth traits thus have the opportunity to increase the rate of genetic gain in breast meat yield in the turkey. Turkey breeding companies should consider implementing ultrasound technology to improve the genetic progress obtainable in BMY. This would result in birds with a larger proportion of consumer-desired white meat and would also positively benefit the profitability of the turkey production industry.
Table 7.1 Phenotypic mean and standard deviation ($\sigma_p$) of body weight (BW), absolute breast yield (BY), percentage breast meat yield (BMY), conformation score (Conf), depth measured parallel to the keel (D1), and average depth measured across both lobes of the breast muscle (D2) in a male and female turkey line

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<td>14.23</td>
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<tr>
<td>BY (kg)</td>
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<td>3.74</td>
<td>0.32</td>
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<tr>
<td>BMY (%)</td>
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<td>1.14</td>
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<td>0.97</td>
<td>4.18</td>
<td>0.91</td>
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<td>D2 (cm)</td>
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<tr>
<td>BW (kg)</td>
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<td>0.86</td>
<td>6.54</td>
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<tr>
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<tr>
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<td>3.94</td>
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<tr>
<td>D1 (cm)</td>
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<td>4.33</td>
<td>0.34</td>
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<tr>
<td>D2 (cm)</td>
<td>4.79</td>
<td>0.46</td>
<td>4.62</td>
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Table 7.2 Heritability (on diagonal) of body weight (BW), absolute breast yield (BY), percentage breast meat yield (BMY), conformation score (Conf), depth 1 (D1), and depth 2 (D2) with phenotypic (above diagonal) and genetic (below diagonal) correlations in a male turkey line with standard error in brackets

<table>
<thead>
<tr>
<th></th>
<th>BW</th>
<th>BY</th>
<th>BMY</th>
<th>Conf</th>
<th>D1</th>
<th>D2</th>
</tr>
</thead>
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<tr>
<td><strong>Toms</strong></td>
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</tr>
<tr>
<td>BW</td>
<td>0.45 (0.12)</td>
<td>0.85 (0.01)</td>
<td>0.25 (0.05)</td>
<td>0.44 (0.04)</td>
<td>0.65 (0.03)</td>
<td>0.65 (0.03)</td>
</tr>
<tr>
<td>BY</td>
<td>0.88 (0.05)</td>
<td><strong>0.49 (0.12)</strong></td>
<td>0.69 (0.03)</td>
<td>0.58 (0.03)</td>
<td>0.73 (0.03)</td>
<td>0.69 (0.03)</td>
</tr>
<tr>
<td>BMY</td>
<td>0.35 (0.21)</td>
<td>0.70 (0.12)</td>
<td><strong>0.43 (0.12)</strong></td>
<td>0.49 (0.04)</td>
<td>0.51 (0.04)</td>
<td>0.42 (0.04)</td>
</tr>
<tr>
<td>Conf</td>
<td>0.59 (0.17)</td>
<td>0.86 (0.10)</td>
<td>0.83 (0.10)</td>
<td><strong>0.40 (0.11)</strong></td>
<td>0.58 (0.02)</td>
<td>0.39 (0.03)</td>
</tr>
<tr>
<td>D1</td>
<td>0.54 (0.14)</td>
<td>0.67 (0.11)</td>
<td>0.63 (0.14)</td>
<td>0.85 (0.08)</td>
<td><strong>0.50 (0.12)</strong></td>
<td>0.59 (0.03)</td>
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<tr>
<td>D2</td>
<td>0.62 (0.15)</td>
<td>0.70 (0.13)</td>
<td>0.51 (0.20)</td>
<td>0.41 (0.23)</td>
<td>0.54 (0.17)</td>
<td><strong>0.30 (0.11)</strong></td>
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<td><strong>Hens</strong></td>
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<tr>
<td>BW</td>
<td>0.75 (0.10)</td>
<td>0.77 (0.02)</td>
<td>0.11 (0.05)</td>
<td>0.47 (0.04)</td>
<td>0.45 (0.04)</td>
<td>0.53 (0.04)</td>
</tr>
<tr>
<td>BY</td>
<td>0.80 (0.06)</td>
<td><strong>0.59 (0.11)</strong></td>
<td>0.71 (0.03)</td>
<td>0.63 (0.03)</td>
<td>0.63 (0.03)</td>
<td>0.66 (0.03)</td>
</tr>
<tr>
<td>BMY</td>
<td>0.03 (0.15)</td>
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<td><strong>0.59 (0.11)</strong></td>
<td>0.48 (0.04)</td>
<td>0.49 (0.04)</td>
<td>0.43 (0.04)</td>
</tr>
<tr>
<td>Conf</td>
<td>0.54 (0.13)</td>
<td>0.74 (0.09)</td>
<td>0.60 (0.13)</td>
<td><strong>0.34 (0.09)</strong></td>
<td>0.56 (0.03)</td>
<td>0.45 (0.04)</td>
</tr>
<tr>
<td>D1</td>
<td>0.56 (0.12)</td>
<td>0.83 (0.07)</td>
<td>0.68 (0.11)</td>
<td>0.81 (0.10)</td>
<td><strong>0.41 (0.10)</strong></td>
<td>0.56 (0.03)</td>
</tr>
<tr>
<td>D2</td>
<td>0.59 (0.11)</td>
<td>0.79 (0.08)</td>
<td>0.51 (0.13)</td>
<td>0.60 (0.15)</td>
<td>0.78 (0.09)</td>
<td><strong>0.50 (010)</strong></td>
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</table>
Table 7.3 Heritability (on diagonal) of body weight (BW), absolute breast yield (BY), percentage breast meat yield (BMY), conformation score (Conf), depth 1 (D1), and depth 2 (D2) with phenotypic (above diagonal) and genetic (below diagonal) correlations in a female turkey line with standard error in brackets

<table>
<thead>
<tr>
<th></th>
<th>BW</th>
<th>BY</th>
<th>BMY</th>
<th>Conf</th>
<th>D1</th>
<th>D2</th>
</tr>
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<tbody>
<tr>
<td><strong>Toms</strong></td>
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</tr>
<tr>
<td>BW</td>
<td>0.68 (0.11)</td>
<td>0.80 (0.02)</td>
<td>0.12 (0.05)</td>
<td>0.56 (0.03)</td>
<td>0.46 (0.04)</td>
<td>0.41 (0.04)</td>
</tr>
<tr>
<td>BY</td>
<td>0.82 (0.05)</td>
<td>0.64 (0.11)</td>
<td>0.68 (0.03)</td>
<td>0.67 (0.03)</td>
<td>0.60 (0.03)</td>
<td>0.57 (0.03)</td>
</tr>
<tr>
<td>BMY</td>
<td>0.15 (0.16)</td>
<td>0.66 (0.09)</td>
<td>0.61 (0.11)</td>
<td>0.46 (0.04)</td>
<td>0.46 (0.04)</td>
<td>0.47 (0.04)</td>
</tr>
<tr>
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<td>0.61 (0.16)</td>
<td>0.26 (0.09)</td>
<td>0.51 (0.03)</td>
<td>0.34 (0.04)</td>
</tr>
<tr>
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<td>0.75 (0.10)</td>
<td>0.69 (0.16)</td>
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<td><strong>Hens</strong></td>
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<tr>
<td>BW</td>
<td>0.71 (0.09)</td>
<td>0.81 (0.02)</td>
<td>0.15 (0.05)</td>
<td>0.47 (0.04)</td>
<td>0.60 (0.03)</td>
<td>0.48 (0.04)</td>
</tr>
<tr>
<td>BY</td>
<td>0.83 (0.04)</td>
<td>0.69 (0.09)</td>
<td>0.70 (0.03)</td>
<td>0.60 (0.03)</td>
<td>0.73 (0.02)</td>
<td>0.64 (0.03)</td>
</tr>
<tr>
<td>BMY</td>
<td>0.16 (0.03)</td>
<td>0.70 (0.07)</td>
<td>0.61 (0.09)</td>
<td>0.43 (0.04)</td>
<td>0.49 (0.03)</td>
<td>0.70 (0.04)</td>
</tr>
<tr>
<td>Conf</td>
<td>0.64 (0.10)</td>
<td>0.88 (0.05)</td>
<td>0.78 (0.09)</td>
<td>0.46 (0.10)</td>
<td>0.63 (0.03)</td>
<td>0.45 (0.04)</td>
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<td>0.77 (0.06)</td>
<td>0.70 (0.08)</td>
<td>0.64 (0.10)</td>
<td>0.54 (0.17)</td>
<td>0.70 (0.09)</td>
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Table 7.4 Proportion of variation explained ($R^2$) in breast meat yield (BMY) by linear models including a fixed flock effect (Flock), body weight (BW), conformation score (Conf), breast depth measured parallel to the keel (D1) and breast depth measured horizontally across the check (D2)

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<th>Toms</th>
<th>Hens</th>
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<td>$BMY=Flock+b_1BW+b_2Conf$</td>
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<td>0.27</td>
<td>0.36</td>
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<tr>
<td>$BMY=Flock+b_1BW+b_3D1$</td>
<td></td>
<td>0.29</td>
<td>0.36</td>
</tr>
<tr>
<td>$BMY=Flock+b_1BW+b_4D2$</td>
<td></td>
<td>0.20</td>
<td>0.34</td>
</tr>
<tr>
<td>$BMY=Flock+b_1BW+b_3D1+b_4D2$</td>
<td></td>
<td>0.32</td>
<td>0.42</td>
</tr>
<tr>
<td>$BMY=Flock+b_1BW+b_3Conf+b_3D1+b_4D2$</td>
<td></td>
<td>0.38</td>
<td>0.48</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Model</th>
<th>Female Line</th>
<th>Toms</th>
<th>Hens</th>
</tr>
</thead>
<tbody>
<tr>
<td>$BMY=Flock+b_1BW+Conf$</td>
<td></td>
<td>0.35</td>
<td>0.63</td>
</tr>
<tr>
<td>$BMY=Flock+b_1BW+b_3D1$</td>
<td></td>
<td>0.32</td>
<td>0.65</td>
</tr>
<tr>
<td>$BMY=Flock+b_1BW+b_4D2$</td>
<td></td>
<td>0.35</td>
<td>0.64</td>
</tr>
<tr>
<td>$BMY=Flock+b_1BW+b_3D1+b_4D2$</td>
<td></td>
<td>0.44</td>
<td>0.68</td>
</tr>
<tr>
<td>$BMY=Flock+b_1BW+Conf+b_3D1+b_4D2$</td>
<td></td>
<td>0.52</td>
<td>0.71</td>
</tr>
</tbody>
</table>

$^1\mu$ is the intercept and $b_1$, $b_2$, $b_3$ and $b_4$ represent the regression coefficients on body weight, conformation score, D1, and D2, respectively.
Table 7.5 Accuracy of an index\textsuperscript{1,2} to select for breast meat yield including individual (I) records for conformation score (Conf), breast depth measured parallel to the keel (D1), breast depth measured horizontally across the chest (D2), and breast meat yield (BMY) measured from the carcass on 1 full sib and 2 half sibs (S)

<table>
<thead>
<tr>
<th>Information Source</th>
<th>Male Line</th>
<th>Female Line</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Conf</td>
<td>D1</td>
</tr>
<tr>
<td>1</td>
<td>I</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>I</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>I</td>
<td>I</td>
</tr>
<tr>
<td>4</td>
<td>I</td>
<td>I</td>
</tr>
<tr>
<td>5</td>
<td>I</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>I</td>
<td>I</td>
</tr>
<tr>
<td>7</td>
<td>I</td>
<td>I</td>
</tr>
<tr>
<td>8</td>
<td>I</td>
<td>I</td>
</tr>
</tbody>
</table>

\textsuperscript{1}All indexes included body weight on the individual as well as body weight, conformation score of the sire, dam, 3 full sibs and 10 half sibs

\textsuperscript{2}The indexes (I) were equal to $I = b^t x$, where $b^t$ is a vector of selection index weights and $x$ is a vector of the information sources
Figure 7.1 Ultrasound scan sites measured on the live bird parallel to the keel (D1) and horizontally across both breast lobes (D2)
Figure 7.2 Two ultrasound images showing measurement of the first breast muscle depth trait (D1) as depth from the skin surface to the ribcage, using the furcula junction as a landmark.
Figure 7.3 Two ultrasound images showing measurement of the second breast muscle depth trait (D2) trait as the average depth from the skin surface to the apex of the ribcage recorded on both sides of the body (i.e. \((D_{21} + D_{22})/2\))
Figure 7.4 Population structure of the simulated turkey breeding program where body weight and conformation score are measured on all turkeys at pre-selection and $p_1$ % are kept for the recording of ultrasound traits to select for breast meat yield.
Figure 7.5 The change in response to selection for BMY as the proportion of candidates kept after pre-selection ($p_1$), and therefore with measurements of breast meat yield depth, increases in a simulated turkey breeding program using the performance and variance parameters estimated on female line toms (Toms) and hens (Hens).
Chapter 8

Determination of the optimum slaughter weight to maximize gross profit in a turkey production system

L. A. Case¹, S. P. Miller¹, and B. J. Wood¹,²

¹ Department of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada N1G 2W1; and

² Hybrid Turkeys, Suite C, 650 Riverbend Drive, Kitchener, Ontario, Canada N2K 3S2.

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8.1 Abstract

A deterministic model was used to optimize turkey slaughter weight based on a profit equation that described the commercial grower and processing divisions of an integrated company. The objective was to determine optimum slaughter weights for toms and hens, using both a heavy and super heavy strain, to maximize gross margin of the system. Sensitivity of optimum slaughter weight in response to feed cost and breast meat price was also considered. Higher margins could be achieved with toms and super heavy strain birds. This indicated that larger birds, from a heavier weight strain or toms within a strain, could be more efficient and profitable given the assumed production values. Results were based on the assumed market conditions and changes in costs or turkey component values (i.e. breast meat) could result in a shift in the optimal turkey strain to use. Increased feed cost results in a lower optimum slaughter weight and decreased margin. Optimum slaughter weight and profit increased with higher breast meat values. Increasing the profit of an integrated company can be accomplished by targeting slaughter to an optimum weight.

8.2 Introduction

Gross margin is maximized when the difference between costs and returns is highest in the production system. For an integrated turkey company, which is the common situation in the USA and Europe, costs are incurred in growing and processing birds and returns are generated with the sale of processed carcass. This ratio is dynamic
and varies throughout the growing phase as biological parameters such as feed conversion, bodyweight, and carcass yields change. During growth, age related increases in both the deposition of breast muscle and feed conversion are translated into increased carcass value and input feed costs, respectively (Moran, 1977; Peng et al., 1985; Swatland, 1989b). Together with these growth parameters, other factors that change with time and slaughter weight include mortality, condemnation level, and processing costs. A production (or profit) equation can incorporate these values to determine the most profitable slaughter weight based on relative costs and returns.

The objective of this study was to estimate the slaughter weight that will maximize the profit of an integrated production system for both a heavy and super heavy strain, using a deterministic production model while considering the sensitivity of input costs and market values.

8.3 Materials and Methods

A modified turkey production model was developed based on a previous economic model (Wood, 2009). This model considered integrated production with the margin calculated based on a unit of live turkey weight delivered to the processing plant. In the current study, changes in costs and returns from the commercial grower and processing divisions were modeled through the growth period by changing time and body weight dependent variables. A deterministic modeling approach was implemented to match the structure of the system and to reveal the correlation between input parameters, where the implications of a change in one input variable is reflected by changes in other values.
A sex-specific fixed poult cost was assumed. The cost of toms and hens was $1.40 and $0.65, respectively, for the heavy strain and $1.50 and $0.75, respectively, for the super heavy strain. Margin was calculated considering input costs required for growth from poult to slaughter balanced by the returns from a carcass at processing (Figure 8.1). At various carcass weights, different parameters for breast meat yield (BMY) were used. This is because the turkey has an allometric growth pattern resulting in an increased rate of breast meat deposition at later ages (Summers et al., 1989).

8.3.1 Model Development

The commercial grower segment is affected by slaughter weight as changing weight alters the requirements for feed, housing, and labour. The processing segment is affected as slaughter weight is correlated to the returns from the sale of processed turkey (Figure 8.1). As a result, these two divisions were considered for the optimization analysis. Feed input costs at the commercial level were influenced by the price of feed and feed conversion. The variable cost of housing and labour was based on bird size. Commercial density was set to a fixed value to ensure that a higher density did not decrease performance as bird size increased (Table 8.2). The increase in bird size associated with growth to a later age and weight resulted in fewer birds in the production system. Consequently, unit cost per bird increased as fixed and variable costs were spread across fewer turkeys. Costs were further affected by mortality and condemnation level, as these birds add to costs but do not contribute to returns. Increasing mortality also increases overall poult cost, as more are needed to be placed to deliver the same live weight to the processing plant. After processing, financial returns were influenced by both carcass yield and the market value of the carcass.
Function coefficients to describe the relationship of body weight and feed intake with time were estimated for both strains based on commercial performance goals (Hybrid Hybrid Turkeys, 2009). Data were summarized into weekly averages for body weight and cumulative feed conversion. Turkey body weight changes as a function of time \((t)\) and was modelled with a Gompertz function:

\[
Body \, Weight = ae^{\frac{b}{1+ct}} \tag{1}
\]

where \(a\) is the asymptotic maximum weight, \(b\) is used to equate \(ae^{-b}\) to weight at time \(t = 0\), and \(c\) is the rate of exponential decay of growth rate (Buffington et al., 1973).

Cumulative feed intake for each week was calculated as the product of body weight and cumulative feed conversion (kg feed/kg bodyweight). A second order polynomial function was used to describe the change in the cumulative feed intake values over time:

\[
Cumulative \, Feed \, Intake = a + bt + ct^2 \tag{2}
\]

Change in total mortality throughout the growing period was also represented by a quadratic equation:

\[
Mortality = a + bt + ct^2 \tag{3}
\]

where \(a\), \(b\) and \(c\) are the intercept, linear and quadratic coefficients, respectively, for the polynomial functions (equations [2] and [3]) and \(t\) was time (one-hundredth of a day).

Total condemnation levels, processing costs, and BMY change as a function of body weight and were represented by linear relationships

\[
y = a + bx \tag{4}
\]

where \(y\) is the parameter value, \(x\) is a vector of body weights, \(a\) is the intercept term and \(b\) is the linear coefficient. Regression coefficient values for condemnation levels and
processing costs were derived from integrated company data reports (Agristats, 2009). Intercept values were calculated based on known processing costs and condemnation levels for a given body weight at a slaughter age of 20 weeks and 16 weeks in toms and hens, respectively (Agristats, 2009). Any negative predicted condemnation levels occurring very early in production were set equal to zero. Parameters to describe the linear change in BMY as body weight increases were estimated from Agristats (2009) data. Function [4] represents the increase in condemnation level (%), decrease in processing cost ($/kg), and increase in BMY (%) as body weight increases. The market value of the carcass included meat, skin, and trimming yields. However, as the allometric growth pattern for the breast is primarily due to muscle development (Swatland, 1979; 1989a) total breast yield was calculated by adding constant skin and trimming yield values as a percentage of the carcass weight, to the meat yield at a specific weight. Fixed costs used to calculate margin and production variables are shown in Figure 8.1 and Figure 8.2, respectively.

Gross margin was calculated by simulating the change in body weight, feed intake, and mortality as a function of time using equations [1], [2], and [3], respectively (Figure 8.3). This was repeated for time increments (one-hundredth of a day) over a 26 week period for toms and a 20 week period for hens. Condemnation level, processing costs, and BMY were changed over the growing period as functions of body weight using equation [4]. Each iteration of the model resulted in the calculation of a final margin associated with a bodyweight and other performance parameters specific to that given weight. Length of the modelled growing period extend beyond what is common practice, however this enabled the visualization of the peak in margin. The slaughter weight that
resulted in the highest margin during the modelled period was considered the optimum slaughter weight.

### 8.3.2 Sensitivity Analysis

Heavy strain performance data was utilized to determine the sensitivity of optimum values to changing market conditions. Change in optimum slaughter weight was determined for two 10% increments above and below base values for feed cost and breast meat value, as shown in Figure 8.1. Optimum slaughter weights were calculated using the previous method for each feed cost or breast meat value.

### 8.4 Results

Function parameters for body weight and feed intake are presented in Table 8.3 and modelled values are plotted in Figure 8.2. Optimum slaughter age, weight, and margin for toms and hens from each strain are shown in Table 8.4. Larger birds have a higher optimum slaughter weight and maximum margin. This is shown by higher values for the super heavy strain birds relative to the heavy strain, as well as higher values for toms compared to hens within strain, which can be seen in Figure 8.3.

Optimum slaughter weight is sensitive to changing feed prices and the relationship is approximately linear, with the margin decreasing as feed price increases (Figure 8.4). This was associated with a decrease in optimum slaughter weight. The margin at the optimum slaughter weight was negative for all feed prices above $0.29 and $0.28 in toms and hens, respectively. Conversely, as the value of breast meat increases, the optimum slaughter weight increases as shown in Figure 8.5 and the relationship
between breast meat value and optimum margin also showed an approximately linear trend.

## 8.5 Discussion

The ratio of input costs to returns changes through the growing period, producing a peak in the margin curve and this represents the most profitable average weight to slaughter a turkey flock. Depending on strain, the margin curve peaks at between 20.4 and 21.4 weeks in toms and 14.0 and 14.3 weeks in hens, and beyond this time profits decrease. Margin is highly dependent on body weight, carcass composition, and feed intake as reflected by their high relative economic value in previously developed breeding objectives (Pasternak et al., 1985; Wood, 2009). Accordingly, rising profit levels can primarily be attributed to increasing carcass yield and increased proportion of breast meat, which are both correlated to body weight. The rate of rise in returns is highest early in the growth trajectory and is associated with the time when growth rate is highest. The rapid growth rate, however, is not sustained and begins to slow (Figure 8.2). Feed efficiency decreases throughout the growing period and birds become less efficient at utilizing feed consumed to gain weight (Figure 8.2). This represents steadily increasing costs but is counterbalanced by the increase in BMY, which has a high value compared to other carcass components. The optimum slaughter weight therefore represents the time when the benefits of increasing bird size and BMY no longer outweigh the rising costs of production.

As a result of the sexual dimorphism and strain variability for growth pattern (Buffington et al., 1973; Sengul and Kiraz, 2005), sex and strain, specific growth
trajectories were used. This was incorporated into the model as different Gompertz function parameters for change in body weight. The higher $a$ and $c$ values for toms represent a higher maximum weight and a faster rate of decline in growth rate, respectively. Similarly, the super heavy strain had higher $a$ values while the deceleration of growth rate, or $c$ value, was similar between strains. Due to variability in the growth trajectories and allometric growth patterns, the optimum slaughter weight is achieved later for toms and super heavy strain birds.

Although the results indicated that super heavy strain birds were the more profitable strain, the selection of the optimum strain could alter with changes in the market. For example, an increase in feed cost lowers the optimum slaughter weight (Figure 8.4). As the optimum margin is achieved by growing smaller birds the heavy strain becomes more favourable, relative to the super heavy strain. This is because the smaller strain matures at a lighter slaughter weight, which is more profitable.

Input variables greatly influence margin and as a result an analysis of the response to changes in market variables was required (Figure 8.4 and Figure 8.5). Due to the strong correlation between the feed cost and gross margin as feed becomes more expensive older birds, with decelerating feed efficiency, represent higher input costs. As a result, gross margin peaks a lower weight. Accordingly, if the price of feed exceeds a critical threshold level a positive margin will not be possible. The maximum cost of feed to achieve a positive margin was $290/tonne for toms and $280/tonne for hens. At these feed costs, performance levels would have to improve or the value of the carcass increase to support profitable production. Alternatively, higher breast values result in increasing
profit at later ages, due to increasing proportion of breast meat with size, and the optimum slaughter weight becomes heavier.

   The broad shape at the peak of the margin curves provides an indication of the robustness of gross margin to changes in slaughter weight, as a small increase or decrease near the optimum is not reflected by a substantial decrease in profit. Consequently, the ideal weight is fairly stable as market variables change. As a result there is a range of slaughter weights that have near optimal profit returns.

   To maximize profitability the target market, performance levels, operational costs, and retail values must be considered. The results presented from the model were specific to the strains used in the analysis as well as the assumed market variables. The methodology, however, can be applied to other scenarios by adjusting performance goals and market variables to any study population, the Canadian quota system, or different commercial goals. This could include, but is not limited to, the incorporation of whole carcass values and specifically sized cut-outs. For example, hens are often marketed at lighter weights as a whole-bird product. However, if the value of breast meat is high, hens could be grown to a heavier slaughter weight and the carcass further processed. Once the optimum weight has been determined, it can be targeted to maximize profitability.

   In the developed model, the described relationships between age or body weight and their dependent traits are appropriate at later ages surrounding the peak in the profit curve. The assumed prediction equations are robust within the bounds of the normal slaughter ages for turkeys. As a consequence, extending predictions away from the time
period surrounding the profit peaks may produce misleading results where data used to
describe critical production relationships are limited.

In conclusion, gross margin for an integrated company could be maximized by
slaughtering toms and hens at a strain specific optimum body weight. This optimum
value represents the most profitable balance of inputs, including feed costs, and returns,
including body weight and breast yield. Optimum slaughter weight values are sensitive to
market variables and they increase with rising breast value and decrease as feed becomes
more expensive. The model can be used to determine optimum slaughter weight based
on the input costs and return values within a given market and also based on strain
specific production goals. As a result, the developed model is versatile and can be used
to maximize gross margin based on unique production objectives, consumer demands,
and market conditions.

Note: Minor revisions have been made to the original, published manuscript
Table 8.1 Performance levels of turkeys in the commercial grower and processor production stages input into the deterministic production model to calculate gross integrated company margin.

<table>
<thead>
<tr>
<th>Description</th>
<th>Units</th>
<th>Heavy Strain</th>
<th>Super heavy strain</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Toms</td>
<td>Hens</td>
</tr>
<tr>
<td>Commercial density</td>
<td>kg/m²</td>
<td>53.52</td>
<td>43.79</td>
</tr>
<tr>
<td>Turn around between flocks</td>
<td>days</td>
<td>14</td>
<td>14</td>
</tr>
<tr>
<td>Breast skin yield</td>
<td>%</td>
<td>2.25</td>
<td>2.91</td>
</tr>
<tr>
<td>Breast white trim yield</td>
<td>%</td>
<td>1.67</td>
<td>1.41</td>
</tr>
<tr>
<td>Thigh yield</td>
<td>%</td>
<td>12.0</td>
<td>11.60</td>
</tr>
<tr>
<td>Wing yield</td>
<td>%</td>
<td>8.73</td>
<td>7.69</td>
</tr>
<tr>
<td>Drum yield</td>
<td>%</td>
<td>9.49</td>
<td>9.70</td>
</tr>
<tr>
<td>Rack yield</td>
<td>%</td>
<td>16.89</td>
<td>17.74</td>
</tr>
<tr>
<td>Giblets yield</td>
<td>%</td>
<td>3.89</td>
<td>3.75</td>
</tr>
</tbody>
</table>
Table 8.2 Fixed input costs for the commercial grower and processor input into the deterministic production model to calculate gross integrated company margin.

<table>
<thead>
<tr>
<th>Description</th>
<th>Units</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Commercial housing cost to slaughter</td>
<td>$/m²/yr</td>
<td>13.98</td>
</tr>
<tr>
<td>Commercial labour cost to slaughter</td>
<td>$/m²/yr</td>
<td>6.99</td>
</tr>
<tr>
<td>Commercial feed price</td>
<td>$/kg</td>
<td>0.18</td>
</tr>
<tr>
<td>Commercial haulage cost to plant</td>
<td>$/kg</td>
<td>0.04</td>
</tr>
<tr>
<td>Breast Value</td>
<td>$/kg</td>
<td>3.32</td>
</tr>
<tr>
<td>Thigh Value</td>
<td>$/kg</td>
<td>1.66</td>
</tr>
<tr>
<td>Wing Value</td>
<td>$/kg</td>
<td>0.99</td>
</tr>
<tr>
<td>Drum Value</td>
<td>$/kg</td>
<td>0.99</td>
</tr>
<tr>
<td>Rack Value</td>
<td>$/kg</td>
<td>0.22</td>
</tr>
<tr>
<td>Giblet Value</td>
<td>$/kg</td>
<td>0.22</td>
</tr>
</tbody>
</table>
Table 8.3 Functions parameters ($y$) describing time dependent ($t$) and body weight ($x$) dependent parameters used in the deterministic production model to calculate integrated gross company margin.

<table>
<thead>
<tr>
<th>Model Parameter</th>
<th>Variable</th>
<th>Heavy Strain</th>
<th>Super Heavy Strain</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Toms</td>
<td>Hens</td>
</tr>
<tr>
<td>Body Weight (kg)$^1$</td>
<td>$a$</td>
<td>29.02</td>
<td>14.20</td>
</tr>
<tr>
<td></td>
<td>$b$</td>
<td>4.867</td>
<td>4.917</td>
</tr>
<tr>
<td></td>
<td>$c$</td>
<td>-0.018</td>
<td>-0.024</td>
</tr>
<tr>
<td>Feed Intake (kg)$^2$</td>
<td>$a$</td>
<td>-0.258</td>
<td>-1.02</td>
</tr>
<tr>
<td></td>
<td>$b$</td>
<td>2.73 x 10^{-4}</td>
<td>0.061</td>
</tr>
<tr>
<td></td>
<td>$c$</td>
<td>2.56 x 10^{-3}</td>
<td>1.43 x 10^{-3}</td>
</tr>
<tr>
<td>Breast Meat Yield (%)$^3$</td>
<td>$a$</td>
<td>12.40</td>
<td>16.51</td>
</tr>
<tr>
<td></td>
<td>$b$</td>
<td>0.55</td>
<td>0.49</td>
</tr>
<tr>
<td>Mortality (%)$^2$</td>
<td>$a$</td>
<td>2.44</td>
<td>2.22</td>
</tr>
<tr>
<td></td>
<td>$b$</td>
<td>6.85 x 10^{-3}</td>
<td>0.022</td>
</tr>
<tr>
<td></td>
<td>$c$</td>
<td>3.70 x 10^{-4}</td>
<td>1.83 x 10^{-3}</td>
</tr>
<tr>
<td>Total Condemnation (%)$^4$</td>
<td>$a$</td>
<td>-4.96</td>
<td>-2.42</td>
</tr>
<tr>
<td></td>
<td>$b$</td>
<td>0.4</td>
<td>0.4</td>
</tr>
<tr>
<td>Processing Costs ($/kg)$^5$</td>
<td>$a$</td>
<td>0.65</td>
<td>0.54</td>
</tr>
<tr>
<td></td>
<td>$b$</td>
<td>-0.022</td>
<td>-0.022</td>
</tr>
</tbody>
</table>

$^1y = ae^{-bt}$

$^2y = a + bt + ct^2$

$^3y = a + bx$
Table 8.4 Comparison of optimum slaughter age, optimum slaughter weight, and margin at the optimum slaughter weight for the heavy and super heavy strain toms and hens.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Optimum Slaughter Age (days)</th>
<th>Slaughter Weight (kg)</th>
<th>Margin ($/kg)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Toms</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Heavy strain</td>
<td>143</td>
<td>19.81</td>
<td>0.29</td>
</tr>
<tr>
<td>Super heavy strain</td>
<td>150</td>
<td>22.54</td>
<td>0.33</td>
</tr>
<tr>
<td><strong>Hens</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Heavy strain</td>
<td>98</td>
<td>8.87</td>
<td>0.22</td>
</tr>
<tr>
<td>Super heavy strain</td>
<td>100</td>
<td>9.89</td>
<td>0.25</td>
</tr>
</tbody>
</table>
Figure 8.1 Structural divisions within the turkey production industry, with grey segments representing divisions included in the slaughter weight optimization model. Input costs and financial returns are outlined, as well as biological and market variables that influence these parameters.
Figure 8.2 Change in body weight (kg) and cumulative feed intake (kg) over a 26 week growing period in toms (a) and 20 week growing period in hens (b).
Figure 8.3 Change in gross margin ($/kg live weight delivered to processing plant) of an integrated turkey production company as body weight increases during a 26 and 20 week growing period in toms and hens, respectively.
Figure 8.4 Response of optimum slaughter weight of the heavy strain to a 20% change in feed price ($/kg) above and below the defined base value toms (a) and hens (b)
Figure 8.5 Response of optimum slaughter weight to a 20% change in the value of breast meat ($/kg) above and below the defined base value in toms (a) and hens (b)
Chapter 9

General Conclusions

Commercial turkey breeding is focused on achieving genetic gains and providing genetically superior birds to the industry to improve performance levels. Body weight and growth traits remain a priority of breeding programs and this is also balanced with selection to improve reproductive traits, feed efficiency, and turkey characteristics that are appealing to consumers. This thesis was able to identify modeling methodologies, population parameters, and novel selection criteria that can be used to increase gains in a turkey breeding objective related to these economically important traits.

9.1 Reproduction

Methods to improve the efficiency of selection for reproductive performance in the turkey are important due to the antagonistic relationship between reproduction and growth traits. Biologically, turkeys are seasonal breeders and the intensified turkey production industry has developed methods to stimulate the hen to produce eggs year-round. The genetic correlations between each reproductive trait in the winter and summer seasons was less than 1, as identified in the first study, indicating that the phenotypes are
controlled by some unique genes or differential emphasis on an overlapping set of genes in different seasons. These GxE interactions indicate that a seasonal genetic component remains for the regulation of egg production, fertility, and hatchability in the turkey.

To improve the effectiveness of selection for reproductive traits in the turkey hen, breeding companies could be aware of distinct seasonal traits for egg production, fertility, and hatchability in a breeding program. Amplifying the frequency of the favourable genotypes for both summer and winter production should help disentangle the confounding effect that single trait selection would have for the reproductive traits. As a result, response in the breeding objective could be accelerated. An increase in reproductive performance would have a positive effect on the industry as a whole by improving reproductive efficiency of hens required to meet increasing production needs.

The genotype by environment interaction detected for reproductive traits in the turkey may be of interest to sheep and goat breeders. These species are also seasonal reproducers and have been stimulated to lamb and kid throughout the entire year in intense production systems. In this thesis, it was determined that the seasonal biology of turkey reproduction is influencing genetic regulation of the traits and a similar mechanism may also be occurring in the ewe and doe. As a result, genotype by environment interactions for reproductive traits warrant investigation in ewes and does. If identified, breeders could increase the rate of gains for reproductive traits by adapting selection indexes and this would have a positive impact on the livestock production industry.

The results generated from the random regression modeling of reproductive traits in the turkey supported the conclusions of the multiple trait studies. Study two provided
evidence that genotypes controlling egg production, fertility, and hatchability respond
differently to seasonal changes throughout the year. Differences in day length and
temperature in the summer and winter may be contributing the genotype by environment
interactions. This was important to identify from a management perspective.

Producers attempt to maintain an internal environment that is productive for all
turkey flocks throughout the year given environmental variation outside of the barns. To
maintain a consistent ambient temperature heating of the barns is required in the colder
seasons and fan-based cooling is utilized in the warm summer months. These results
indicate, however, that turkeys are responding to these changes in barn environment.
Since the reproductive genotypes of turkeys are sensitive to these necessary management
practices, the genetic parameters for the distinct seasonal traits from the multiple trait
study are valuable and could be considered in selection index design.

The approach to random regression modelling in the second study also
investigated a novel shifting of the time gradient. This has not been possible for the
current uses of random regression models in animal breeding, which are used to describe
traits of a longitudinal nature or with repeated records over an animal’s lifetime. These
traits require the minimum of the time gradient to be defined as the first expression of the
trait early in life and the maximum of the gradient is the final expression. Test day
records in dairy cattle or weights in meat-production species are examples of such traits.

Random regression models are known to skew parameter estimates at the
extremes of the time gradient. In this thesis, the time gradient was shifted and the same
parameters were re-estimated providing a unique look at the behaviour of random
regression. The results indicated that the exact values of parameters estimated at the
beginning and end of the time gradient were impacted, however the values still follow the same increasing or decreasing trend. Consequently, modeling in the second study of this thesis was able to help understand the behaviour of random regressions.

There will soon be further opportunity to continue investigating the impact that shifting a time gradient has on the estimation of genetic parameters in the turkey using random regression models. Technologies are being developed to record feeding behaviour information on individual turkeys throughout the day. Random regression models could be used, for example, to determine if feed intake in the morning is a unique trait from feed intake at other times of the day or if there is a seasonal based GxE interaction for feed behaviour traits. Hour of the day or months of the year could thus be utilized as a time gradient. These could be shifted in a similar method used with months in the present thesis. This would allow further study of the impact that position along a time gradient has on parameter estimates in a random regression model.

9.2 Feed Efficiency

The results from the GxE interaction studies can be used to increase the efficiency of selection for reproductive traits, which is important given the negative relationship between reproduction and growth. Similarly, the genetic parameters estimated in the third study can be used to develop accurate selection index weights to improve feed efficiency. This will help limit the rise in feed intake associated with higher performance levels for body weight and growth. The genetic parameters of feed efficiency traits in turkey are very limited in the literature and parameters for RFI had not yet been published. Consequently, the results are of interest to the scientific community who can
now compare the parameters of feed efficiency in meat-type poultry, with a very high growth rate, to other livestock species.

The heritabilities of RFI and feed conversion indicate that feed efficiency is a distinct biological trait in the turkey. The genetic correlations of RFI verify that it can be evaluated independently of weight and growth performance, unlike FCR traits. The genetic relationships calculated in the current thesis are also required to develop appropriate weights on traits genetically associated with efficiency that are presently included as selection criterion to determine correlated responses to selection.

To determine if novel traits correlated to feed efficiency could be considered as selection criterion, infrared imaging was investigated to identify if there was a relationship between surface temperature traits and feed efficiency, however the traits were not correlated. The results from the fourth study indicate that infrared measures of surface temperature were not a good indicator of feed efficiency. The weak relationship between feed efficiency and surface temperature indicate that any metabolic differences contributing to feed efficiency have a minimal impact on variation in turkey heat production detected as body surface temperature.

While infrared may not be beneficial to implement for feed efficiency selection, breeding companies are currently investigating methods to collect an increased amount of individual feed intake data and an increased amount of information could be of great value. Breeders will be able to investigate different traits that may be correlated to RFI and the increased number of records for feed intake will increase the power to detect relationships between traits. For example metabolite levels, circulating growth factors in the blood, or feeding frequency traits could be investigated for their correlation to RFI.
As novel traits are considered, the genetic parameters for efficiency and production traits calculated in the present thesis will continue to be useful for predicting correlated responses to selection.

9.3 Breast Meat Yield

Although results showed that infrared technology would not be advantageous to select for feed efficiency, the fifth study of this thesis indicated that ultrasound imaging has a great potential to increase the accuracy of a selection index as well as the response to selection for breast meat yield. Measurements of breast muscle depth were moderately heritable and highly correlated to carcass breast meat yield. Consequently, selection for muscle depth traits would result in genetic progress in breast meat yield due to correlated responses in the breast meat yield carcass trait. This is becoming a larger focus for turkey breeders and breast meat yield has become an important factor in breeding objectives due to consumer preference for white meat. As a result, breast muscle depth traits should be measured in a turkey breeding program and the genetic parameters estimated in this thesis can be used to determine selection index weights.

The advantages of measuring breast muscle depth, as an alternative to traditional conformation scoring, may increase as the market shifts toward further-processed meat products. The practice of conformation scoring was introduced due to its positive correlation to breast meat yield and to ensure the shape of the breast muscle would be appealing to consumers. In turkey markets that do not sell entire cuts, the overall yield of white meat is far more important than the shape of the breast muscle, which is difficult to evaluate in a single ultrasound image due to the size of the muscle area relative to the
length of available probes. As a result, there is an opportunity to weight objective measures of breast muscle depth more heavily, relative to conformation scoring, in selection indexes for pure lines that will be incorporated into further-processed meat products.

9.4 Production System Modelling

The increased rate of genetic gain in reproductive traits, feed efficiency, and breast meat yield accomplished at the primary breeder level will be reflected by improved performance of the pure lines birds as well as the multiplier and commercial turkeys. As a result, the improved efficiency of selection index design, through modeling or the use of technology to introduce novel traits, has an impact on downstream industry segments. To capitalize on the genetic gains individual producers should optimize flock management.

The modified production model developed in the present thesis can be used to visualize the change in ideal slaughter age required to maximize profits for a turkey flock. While the optimum value is dependent on input prices and the value of carcass products, this information can be specified in the model to meet the needs of individual producers. Parameters can also be adjusted for the growth and development of each strain of bird, making the model a dynamic tool. Further, as genetic progress changes the parameters that describe growth, feed intake, and meat yields the model can be updated.
9.5 Overall Conclusions

As a whole, the studies investigated here can be utilized to improve the efficiency of the turkey industry and can also be considered by other livestock breeding programs. With a focus on body weight, it is essential for selection indexes to also effectively achieve gains in other traits of economic importance. The genetic parameters presented in this thesis can be used to model egg production, fertility, and hatchability as distinct seasonal traits in a selection index, which will be reflected by increased performance levels through the entire year. The heritability feed efficiency traits and their correlation to production traits can also be used by turkey breeders to select for efficiency and control the rising cost of feed as growth rates increase. To meet market demands for white meat, turkey breeding companies can begin measuring breast muscle depth with ultrasound technology. This selection criterion will increase the rate of genetic gain for breast meat yield in a breeding objective. Approximately 6 billion kilograms of eviscerated meat are produced annually by the world’s top ten turkey-producing countries and, using the average breast meat yields and values considered in Chapters 7 and 8 (an increase in BMY of 0.3%, and a breast meat value of $3.32/kg), this represents a potential increase in gross returns of almost $60 million per year in these countries alone. These improvements at the primary breeder level will have an impact on all downstream segments of the turkey production industry. The decisions made by individual producers, however, are also important to maximize the benefits of the genetic gains. The developed slaughter weight optimization model is thus a valuable tool to improve efficiency at the final stages of production.
Overall, the efficiency of a turkey breeding program can be improved by considering the modeling methods, novel selection criterion, and management tools investigated. Breeders can also make use of the calculated genetic parameters for seasonal reproductive traits, efficiency measures, and muscle depths in selection index design. As a further advantage, the results from this thesis will help the animal breeding industry become aware of important traits and genetic aspects related to the turkey, which are under-reported relative to other livestock species.
Chapter 10

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