

A review of strategies to improve feed efficiency and reduce environmental footprint in poultry

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Summary

The aim of this review is to discuss possible strategies to improve feed efficiency (FE) in broilers and to reduce the environmental impact of poultry meat production. Despite over 30-years of selection, FE traits have sufficient heritability to expect further improvement. A number of different genomic regions potentially affecting FE indicates the highly polygenic character of those traits, which requires a more sophisticated application of genomic information rather than exclusively searching for candidate genes. Further genetic improvement should be examined jointly with feeding strategies, i.e. precision feeding and individual digestibility, and new approaches such as microbiome studies.

Keywords: chicken, digestibility, feeding, genetic improvement, selection.

Introduction

According to the FAO/OECD prognosis for the year 2020, poultry meat will be the most produced in the world reaching nearly 140 million (mln) tons. This indicates an increase of nearly 21% compared to 116 mln tons of meat produced in 2016. In addition, costs of feed are not stable, which reinforces the importance of feed efficiency improvement. The sustainability of poultry production is more important than ever with the increasing knowledge of environmental footprint of agriculture. This is especially visible in regions with very dense production, where emissions from poultry production includes: ammonia, phosphorus, nitrogen, carbon dioxide, and methane. Thus there is a need for breeding strategies to improve feed efficiency and reduce the environmental impact of poultry meat production.

The aim of this review is to discuss possible strategies to improve feed efficiency in broilers and to reduce the environmental impact of poultry meat production.

Measures of feed efficiency traits and their heritability

Feed efficiency (FE) is dependent on the relationship between feed intake – input – and growth (or body weight gain) – output – of an animal, and has been described by several traits: feed conversion ratio (FCR), residual feed intake (RFI) and coefficient of digestibility (CDU; Table 1). The RFI is often compared to FCR and a high genetic correlation has been shown between those traits 0.74 – 0.93 (e.g. Pakdel et al. 2005; Melo et al. 2006; N'dri et al. 2006). The

approach used for calculation of FCR and RFI does not directly account for an individual's ability to digest specific nutrients, whereas CDU represents the proportion of the particular nutrient (protein, lipid, starch, dry matter) that is actually digested and absorbed. The problematic aspect of all FE traits is very labor intensive phenotypic data collection. Despite that, after 30 years of selection towards improved growth rate and feed efficiency, body weight (BW) of broilers at day 35 changed from 1.40 kg to 2.44 kg, whereas feed intake only increased from 3.22 kg to 3.66 kg of feed (Siegel 2014). Furthermore, the heritability coefficients presented in Table 2 illustrate that despite intensive selection to improve FE traits, there is still potential to exploit the genetic variation in those traits and to further improve them by selection.

Selection strategies for feed efficiency

A high number of offspring information in broilers used in classical approaches of selection can nearly double the genetic improvement per generation compared to the same strategies applied to cattle (Jonas and de Koning 2015). However, the biggest shift in poultry breeding was brought by DNA based technologies and the first release of the chicken genome sequence (Hiller et al. 2004), which enabled opportunities to understand the underlying genetic architecture and biology of modern day chicken.

Classical selection approach

The FCR has been directly included in commercial breeding programs for decades and on average a change of 1.2% per generation was reported (Wall et al. 2010), which led to an improvement in this trait from an average of 2.30 kg/kg in year 1985 to 1.50 kg/kg in year 2010 (Siegel 2014). This increase in efficiency was possible mainly due to genetic improvement of growth rate and feed intake with the benefits of high energy diets (Siegel 2014).

To still achieve appropriate rate of breeding progress in FE traits resulting in much decreased waste levels and feed needed for growth, it is necessary to look not only at the overall feed efficiency, but also on genes that affect the utilization of different nutrients (Reyer et al. 2015). Zhang et al. (2003) conducted a study on phytate phosphorus utilization and their reduction, however, no clear recommendations for breeding programs were made. Recent studies on broiler lines selected for high and low apparent metabolized energy corrected for 0 N retention (Mignon-Grasteau et al. 2004), showed nearly 50% lower excretion of N and nearly 40% decreased excretion of P in line with high apparent metabolized energy (Mignon-Grasteau et al. 2010; de Verdal et al. 2011). A follow up study by de Verdal et al. (2013) focusing on genetic aspects of those results indicated that with selection for digestibility it is possible to reduce the environmental footprint of poultry breeding. Based on successful selection experiments CDU has been applied to commercial breeding programs.

Slow growing chicken

When selecting for improved RFI a certain tradeoff needs to be kept in mind. Since the meat production system prefers fast growing animals, the improvement in RFI results in an increase in productivity leading to a decrease in feed intake based on genetic correlations between the two traits. A suggested alternative to maintain a desired level of RFI would be slower growing

animals consuming less feed (Berry and Crowley 2012). A concept of slow growing chicken is becoming a hot topic in poultry breeding in some markets relating at least in part to improving animal welfare. The advocates see this approach as the next step in organic farming and argue for higher quality and protein levels in slow grown broilers (e.g. Fanatico et al. 2007). The opponents of this approach bring up the astonishing numbers of additional ~8 billion chickens (double the current situation), that would be needed if broilers grow with the same speed as in the 1950s (e.g. Van Eennemaan 2017). The slow-grow approach is further discussed as being not beneficial in terms of reducing the environmental footprint of poultry production. The FE traits are not as well controlled in those animals as in the fast-growing broilers and the slow-grow would demand higher water and land usage to feed the animals.

Strategies based on genomic information

The QTLs for FE traits were so far reported on 24 out of 39 chicken chromosomes including the sex chromosome Z. The first studies were performed by de Koning et al. (2003 and 2004) and revealed the regions associated with FCR and RFI. Since then, a number of studies detected new genomic regions associated with all FE traits (e.g. Parsanejad et al. 2004; Reyer et al. 2015; Shah et al. 2016) with the most recent in CDU (Mignon-Grasteau et al. 2015b). As reviewed by Sell-Kubiak et al. (2017), the QTLs detected so far explained from 0.005 to 0.22 of a fraction of phenotypic variance of FE traits. Unfortunately, very few QTLs overlapped between the studies (Sell-Kubiak et al. 2017). For example some QTLs for FCR detected by Mignon-Grasteau et al. (2015b) are located at the same position as QTLs for CDU of starch in Tran et al. (2014). However, those two studies used animals coming from the same experiment selecting animals for high and low digestive efficiency. Overlaps in the position of detected QTLs can also be seen in a single study (e.g. Tran et al. 2014; Mignon-Grasteau et al. 2015b), but not between them. This suggests that many of detected QTLs for FE traits are breed and experiment specific. Moreover, the high number of possible candidate genes for those QTLs involved in various biological processes suggests that FE traits are highly polygenic and have a complex genetic background. In breeding practice, application of many genomic regions with small effects into a selection schemes might be difficult or even not feasible. An alternative is genomic selection (Fulton 2012). Even though, only one study has presented the application of genomic prediction for FCR in chicken (González-Recio et al. 2009), and reported an astonishing improvement of 4-times the accuracy of selection compared with the classical pedigree information, in breeding companies those strategies are already being implemented for various traits despite the genotyping costs of a single bird. That is because genomic selection improves the accuracy of selection in traits with low heritability or with difficult to obtain phenotypes such as FE traits.

Further reduction of environmental footprint in broiler production

Between the years 1988 and 2007, the decrease in wastes emission by exploiting the genetic potential of broilers has been shown to be on the level of 20% for methane, 23% for nitrous oxide, and 10% for ammonia (Hume et al. 2011). As poultry remains the second largest (after cattle) producer of ammonia, phosphorus, nitrogen, carbon dioxide, and methane (FAO/OECD), and with the growing population of broilers reduction of wastes emission is still an important issue. However, not only the selection and genetic information can be used to continue the

improvement of FE traits.

Precision feeding

Precision feeding is not a new concept for livestock production. In an ideal situation, such a feeding strategy would provide to an animal only the amount and composition of feed required by their individual needs. This would maximize feed digestibility and reduce the amount of waste produced by the animal. First concepts were, however, based on adjusting the feeding only to a weight of individual or production stage and only lately complex feeding stations were developed that can provide real-time precision feeding (Brossard et al. 2017). The new feeding stations allow adjusting diet based on body weight, feed intake as well as environmental conditions and with the application of models for nutrient requirements they offer feed “designed” for an animal in a specific production stage (Brossard et al. 2017). This not only improves the FE, but also by spending 1% more on feed, the drop in wastes emission can be expected on the level of 10-20% (Santos et al. 2017).

Microbiome studies

Another answer to further improve waste reduction in broiler breeding might be the composition of the microbiota. Microbiota can be defined as the complex community of microbes that is coexisting internally and externally with an animal (Oakley et al. 2014; Qaisrani et al. 2015), and can be seen as a link between their diet and health (Sergeant et al. 2014) as it helps in assimilating nutrients, producing vitamins and amino acids (Apajalahti 2005). Furthermore, the undigested protein in the birds digestive system can become a source of amino acids for microbiota living in the gut (Qaisrani et al. 2015) as well as the bird itself. Studies have indicated that microbiota is involved in nitrogen recycling by its ability to breakdown uric acid, whereas ammonia utilization is enabled by transformation into bacterial protein (Rist et al. 2011), which are important aspect of nitrate utilization in poultry breeding (Qaisrani et al. 2015). Currently more than 640 different bacterial species in the chicken gut are known (Apajalahti 2005). Modern technologies based on genomic information allow the separation of the effects of microbiota from that of the host and the study of its effect on the immune system and its importance for poultry nutrition including FE traits (Oakley et al. 2014; Mignon-Grasteau et al. 2015a). It is expected that better understanding of the host-microbial interactions could improve feed digestibility, and decrease waste emission.

Conclusions

The need for sustainable poultry meat production is more important than ever as the world’s poultry consumption is continuously increasing. Even though decades of selection improved FE in poultry tremendously, the considerable heritability of this trait enables its continued change. Since the genomic studies indicated a highly polygenic and complex background of FE, application of genomic selection would be the best use of genomic information, especially when applied to FE traits related to individual’s ability to digest certain ingredients. However, we should not only focus on genetic aspects of FE as advanced technologies enabling precision

feeding and microbiome studies yield new opportunities for even further decreasing waste emissions. In conclusion, when considering combination of genomic selection, use of individual digestibility traits, precision feeding and microbiome studies further reducing the environmental footprint of poultry meat production is still achievable.

Acknowledgment

The study was supported by the European Union Seventh Framework Programme (FP7/2007-2013) as part of the ECO-FCE project under grant agreement No. 311794. as well as this scientific work is co-financed from funds for science allocated to an international project in the years 2013-2017. ESK acknowledges the financial support of the Foundation for Polish Science (FNP START 2016 grant no. 94.2016).

Table 1. Different measures/traits of feed efficiency in broilers; from Sell-Kubiak et al. (2017).

Measure/Trait	Abbr.	Formula ¹
Feed conversion ratio (gross efficiency)	FCR	FCR=FI/PO
Residual feed intake	RFI	RFI=FI – E(FI) E(FI) = $\alpha + \beta_1 BW^{0.5} + \beta_2 \Delta BW + \beta_3 EW$
Coefficient of digestibility	CDU	CDU = 100 – 100(DEW/FI)

¹FI – feed intake, PO – production outputs, BW – body weight, FI_n – feed intake at zero change of body weight, BW^{0.5} – metabolic body weight, E(FI) – expected FI, EW – average egg weight, DEW – weighted dried excreta.

²Maintenance efficiency is defined as the feed needed to maintain the energy requirements of the animal, i.e. to keep temperature level, body movement, and basal metabolism level, without affecting the body weight.

Table 2. Heritability estimates of most commonly used feed efficiency traits (feed conversion ratio, residual feed intake and coefficient of digestibility).

Heritability estimates	References
FCR	
0.16-0.20 (sire population)	Bernon and Chambers (1988)
0.28-0.35 (dam population)	
0.13-0.34 (adjusted for weight)	
0.11-0.43 (not adjusted for weight)	Wang et al. (1991); Chambers et al. (1994) e.g. Wang et al. (1991); Beaumont et al. (1998); Zhang et al. (2003); Howie et al. (2011)
RFI	
0.23-0.45	Pakdel et al. (2005); Melo et al. (2006); N'dri et al. (2006); Gaya et al. (2006); Aggrey et al. (2014); Begli et al. (2016)
CDU	
0.04-0.26 (corn diet)	Mignon-Grasteau et al. (2010)

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