



Epigenetics and phenotypic variability: some interesting insights from birds

Laure Fresard, Mireille Morisson, Jean- Michel Brun, Anne Collin, Bertrand Pain, Francis Minvielle, Frederique Pitel

► To cite this version:

Laure Fresard, Mireille Morisson, Jean- Michel Brun, Anne Collin, Bertrand Pain, et al.. Epigenetics and phenotypic variability: some interesting insights from birds. 10. World Congress on Genetics Applied to Livestock Production (WCGALP), Aug 2014, Vancouver, Canada. American Society of Animal Science, 2014, 10th World Congress on Genetics Applied to Livestock Production. hal-01194041

HAL Id: hal-01194041

<https://hal.science/hal-01194041>

Submitted on 3 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Epigenetics and phenotypic variability: some interesting insights from birds

L. Frésard^{1†}, M. Morisson^{1†}, J.-M. Brun¹, A. Collin², B. Pain³, F. Minvielle⁴, F. Pitel¹

¹UMR 1388 INRA / INPT ENSAT / INPT ENVT, GenPhySE, Castanet-Tolosan, France, ²INRA, UR83, Recherches Avicoles, Nouzilly, France, ³INSERM, U846, INRA, USC1361, Institut Cellule Souche et Cerveau, Bron, France, ⁴UMR 1313

INRA/AgroParisTech, GABI, Jouy-en-Josas, France. [†]Equal contributors.

ABSTRACT: Little is known about epigenetic mechanisms in birds, except the phenomenon of dosage compensation of sex chromosomes, although such mechanisms could be involved in the phenotypic variability of birds, as in several livestock species. This paper reviews the literature on epigenetic mechanisms that could contribute significantly to trait variability in birds, and compares the results to the existing knowledge of epigenetic mechanisms in mammals. The main issues addressed in this paper are: (1) How does the embryo environment influence the adult phenotype in avian species? (2) Does the embryo environment have an impact on phenotypic variability across several successive generations? The potential for epigenetic studies to improve the performance of individual animals through the implementation of limited changes in breeding conditions or the addition of new parameters in selection models is still an open question.

Keywords:

epigenetics

bird

phenotypic variability

Introduction

This review reproduces to a large extent the article by Frésard et al., 2013 ([Frésard et al., \(2013\)](#)). Several results obtained in the laboratory will also be presented.

Most economically relevant traits in animal production exhibit continuous phenotypic variations due to polygenic and environmental factors. Whereas many quantitative trait loci (QTL) have been identified for agronomic traits, in most cases, the underlying genes remain largely unknown. Genome-wide association studies have shown that, except for rare monogenic traits, the variability of complex traits is only partially explained by genetic variation ([Manolio et al., \(2009\)](#)). Possible explanations include epistatic effects, structural variations, and insufficient detection power due to lack of individuals or markers ([Manolio et al., \(2009\)](#), [Makowsky et al., \(2011\)](#)). Both epidemiological studies in humans and genetic studies in animals have revealed that, in addition to the DNA sequence, epigenetic marks may be transmitted across generations and influence the phenotype of offspring ([Jablonka and Raz., \(2009\)](#)). There are many discussions in the literature on what the term “epigenetics” refers to and this leads to numerous definitions ([Jablonka and Lamb., \(2002\)](#), [Holliday., \(2006\)](#), [Bird., \(2007\)](#), [Goldberg et al., \(2007\)](#), [Ptashne., \(2007\)](#), [Jablonka and Raz., \(2009\)](#), [Krause et](#)

[al., \(2009\)](#), [Ho and Burggren., \(2010\)](#), [Ptashne., \(2013\)](#)). While some definitions restrict epigenetics to modifications of the phenotype without changes of the DNA sequence that are transmitted to the next generations ([Ho and Burggren., \(2010\)](#)), other broader definitions include any form of information storage that maintains the DNA sequence intact, as described by Bird: “the structural adaptation of chromosomal regions so as to register, signal or perpetuate altered activity states” ([Bird., \(2007\)](#)). The former definitions link the term “epigenetic” to inheritance and the latter also refer to any phenomenon that leads to phenotypic plasticity. These two visions share a common feature i.e. the molecular mechanisms involved. The epigenetic machinery encompasses chromatin folding and its attachment to the nuclear matrix, packaging of DNA around nucleosomes, covalent modifications of histone tails, DNA methylation, and regulatory non coding RNA (such as miRNA, snoRNA, lncRNA). Epigenetic marks have been shown to actively contribute to the determination of patterns of gene silencing or active transcription and to participate in the lineage and tissue-specific expression of genes ([Youngson and Whitelaw., \(2008\)](#), [Feil and Fraga., \(2012\)](#), [Mazzio and Soliman., \(2012\)](#)). Epigenetic marks are heritable from cell to cell through lineage development, and when acquired in early life, they can have an impact on the adult phenotype. They can also have an impact on the phenotypes of subsequent generations through multigenerational effects that occur either via epigenetic changes acquired during embryonic development, or through the inheritance of epigenetic marks via the gametes ([Jablonka and Raz., \(2009\)](#), [Daxinger and Whitelaw., \(2012\)](#)). In this review, we retain the definition given by Feil and Fraga ([Feil and Fraga., \(2012\)](#)): “Epigenetics is the study of mitotically and/or meiotically heritable changes in gene function that cannot be explained by changes in DNA sequence”.

Understanding the epigenetic regulation of gene expression due to environmental factors should provide important new insights into animal breeding, since the same genetic information may be used differently by individuals grown in different environments. However, epigenetic regulation of gene expression is not always environment-dependent as for parental imprinting in which parent-of-origin-specific expression of a subset of genes is regulated by epigenetic mechanisms. Examples of such loci have been documented in livestock species i.e. the locus responsible for the callipyge phenotype in sheep ([Cockett et al., \(1996\)](#)) and the locus that controls *IGF2* expression in pigs ([Van Laere et al., \(2003\)](#)).

The first agricultural species to be fully sequenced was the chicken, however, to date, there are few studies on the relationship between epigenetic processes and economically important phenotypes in birds. This review is focused on how epigenetic phenomena can have an impact on the adult phenotype of farmed birds.

The importance of sex-linked genes that account for part of the phenotypic variability has been shown in the chicken ([Park et al., \(2006\)](#)) and X inactivation that involves epigenetic mechanisms is well known in mammals ([Lyon, \(1961\)](#), [Morey and Avner, \(2011\)](#)). In birds, only partial dosage compensation between the hetero- (ZW, female) and homogametic (ZZ, male) sexes has been described ([Ellegren et al., \(2007\)](#), [Itoh et al., \(2010\)](#)) and this was previously known as "lack of global dosage compensation" ([Julien et al., \(2012\)](#)). A region of hypermethylation (MHM for Male Hypermethylated Region, ([Teranishi et al., \(2001\)](#)) is associated with dosage-compensation of several genes in the male chicken ([Melamed and Arnold, \(2007\)](#), [Mank and Ellegren, \(2009\)](#), [Zhang et al., \(2010\)](#)), but not in zebra finch ([Itoh et al., \(2010\)](#)). Many questions about the mechanisms of regional dosage-compensation still remain ([Mank and Ellegren, \(2009\)](#), [Livernois et al., \(2012\)](#)). Since this topic has already been extensively reviewed, we refer the reader to the literature, including the references given above. By contrast, little is known about the mechanisms of genomic imprinting, if present, or developmental programming in birds although they may play a role in phenotypic variability as shown in mammalian farm animals. Similarly, epigenetic information that can be transmitted through several generations could have a significant impact on animal selection.

This review addresses the following questions: (1) While the influence of fetal environment on adult phenotypes is largely documented in mammals, what are the developmental and metabolic phenotypes due to specific environmental cues in birds? (2) Are there examples indicating that embryo environment has multigenerational effects in birds?

Environmental epigenomics

The environment can influence developmental plasticity and thus phenotypes in a wide variety of animals, from insects to man ([Feil and Fraga, \(2012\)](#)). Environmental epigenomics refers to the study of how environmental exposures (e.g., toxins, stress or maternal nutrition) during early development influence gene regulation through epigenetic mechanisms (e.g., marks as DNA methylation or histone modifications) that, in turn, influence the adult phenotype ([Szyf et al., \(2008\)](#), [Jammes et al., \(2010\)](#), [Faulk and Dolinoy, \(2011\)](#), [Feil and Fraga, \(2012\)](#)). As described below, the environment may have a much broader impact on the adult phenotype when the marks occur early during development.

Post-hatch environmental influences

Several studies on DNA and histone methylation levels in chicks subjected to heat stimulation demonstrated

that epigenetic marks vary with the environmental conditions experienced during the post-hatch period ([Yossifoff et al., \(2008\)](#), [Kisliouk and Meiri, \(2009\)](#), [Kisliouk et al., \(2010\)](#), [Kisliouk et al., \(2011\)](#)). They showed that the expression of BDNF (brain-derived neurotrophic factor), which is a key regulator of thermotolerance acquisition in the chick hypothalamus, differs between control birds and animals acclimated to heat early in their post-hatch life. Furthermore, alterations were observed in the methylation level of CpG sites in the promoter of the *BDNF* gene. It was also shown that modifications of histone H3 lysine 9 (H3K9) and methylation of histone H3 lysine residue 27 (H3K27) in the promoter of *BDNF* occur in the hypothalamus during thermotolerance acquisition on day 3 post-hatch.

Epigenetic modifications are involved in the immune mechanisms underlying chicken susceptibility to *Salmonella enteritidis* ([Gou et al., \(2012\)](#)) or Marek disease ([Luo et al., \(2012a\)](#), [Luo et al., \(2012b\)](#)) and include changes in the DNA methylation pattern of host defense genes. Indeed, the Marek disease virus (MDV) can induce changes in the expression levels of all three *DNMT* genes (*DNMT1*, *DNMT3A*, and *DNMT3B*). Various histone profiles and gene promoters were identified as being differentially modified and methylated in MDV-sensitive and -resistant chicken strains, indicating that epigenetic mechanisms may participate in the modulation of the resistance and/or susceptibility to specific poultry diseases ([Luo et al., \(2012a\)](#), [Luo et al., \(2012b\)](#)).

Other environmental changes are known to affect the adult phenotype, but to date, no molecular evidence of epigenetic phenomena is available. For instance, phosphorus- or calcium-restricted diets during the early growing period trigger a compensatory adaptation of the chicken ([Yan et al., \(2005\)](#)), possibly mediated by epigenetic mechanisms ([Ashwell and Angel, \(2010\)](#)). Although little is known about the underlying molecular mechanisms in birds, it seems that feed stress may alter gene transcription at least partly via epigenetic mechanisms. For example, Xu et al. ([Xu et al., \(2012\)](#)) reported that 3-day-old chicks subjected to a 24-hour fasting underwent histone H3 methylation modifications in the preoptic anterior hypothalamus, which is the center of body temperature and food intake control.

Influence of the environment during development

In addition to post-hatch environmental factors, changes applied directly to the egg or the resources contained in the egg (e.g., nutrients, hormones, carotenoids, vitamins or RNA transcripts) can have an impact on newborn fitness and later on the adult phenotype ([Ho et al., \(2011\)](#), [Reed and Clark, \(2011\)](#)). Thus, these environmental effects on development are either directly applied to the embryo itself, or are transmitted by the mother.

In birds, direct abiotic environmental factors (e.g., temperature) can influence embryonic development and the adult phenotype (see ([Renaudeau et al., \(2012\)](#))). It has been shown that exposure of embryos to different temperatures at the end of egg incubation, which is a critical developmental period, can be a way of adapting poultry embryos to later climatic conditions (see ([Renaudeau et al., \(2012\)](#))). Epigenetic processes are good candidates for mediating these

mechanisms ([Nichelmann et al., \(1999\)](#), [Tzschentke and Basta, \(2002\)](#), [Piestun et al., \(2008\)](#), [Shinder et al., \(2011\)](#)). Another example of abiotic stress influencing embryonic development is the exposure to green monochromatic LED light during embryogenesis that has a growth-promoting effect observed on adult turkeys and broiler chickens ([Rozenboim et al., \(2003\)](#), [Rozenboim et al., \(2004\)](#), [Halevy et al., \(2006\)](#), [Zhang et al., \(2012\)](#)). One explanation may be enhanced proliferation and differentiation of adult myoblasts and myofiber synchronization ([Halevy et al., \(2006\)](#)), but further work is needed to better characterize the underlying processes.

The impact of the mother's environment on the F1 generation phenotype has been well documented in mammals. For example, it has been reported in humans, that the gestational diet affects offspring phenotypes (part of the "nutritional programming") (see ([Gabory et al., \(2011\)](#))). A well-documented example comes from studies after the Dutch famine during World War II, which revealed that prenatal under-nutrition had an effect on later health ([Lumey et al., \(2007\)](#)) and that epigenetic mechanisms were involved ([Heijmans et al., \(2008\)](#)). The resulting chronic degenerative diseases associated with this famine include cardiovascular diseases, metabolic diseases, breast cancer and obesity. Another famous example of an adult phenotype induced by maternal nutrition in mammals is the viable yellow agouti (A^y) mouse model, in which the *Agouti* gene is genetically and epigenetically dysregulated by an upstream retrotransposon insertion. In this model, the diet of the mother influences coat color and other pleiotropic outcomes, such as diabetes, obesity and tumorigenesis in the offspring. Both DNA methylation patterns and histone modifications are involved in the epigenetic variations of this mutation ([Dolinoy, \(2008\)](#), [Dolinoy et al., \(2010\)](#)).

Maternal under-nutrition can also affect the phenotype of offspring in birds. For example, Rao et al. showed that 4-week-old chicks from mothers fed a low-protein diet had significantly heavier body weight and *Pectoralis major* muscle weight ([Rao et al., \(2009\)](#)). Another approach consists in experimentally increasing brood size, which induces developmental deficits (including nutrient deficits) in the early life of birds. For example, in zebra finches, Naguib et al. ([Naguib and Gil, \(2005\)](#), [Naguib et al., \(2006\)](#)) imposed different degrees of developmental stress on nestlings by forming broods ranging in size from two to six nestlings, and then examined the offspring of the dams that had been differentially stressed as nestlings. As the brood size experienced by the dams increased, the weight of their offspring decreased. The effects on body mass and size were sex-specific. Female offspring grew larger than male offspring when their dam was raised in a small brood, but females from dams reared in large broods were smaller than their brothers. Furthermore, the reproductive success of the female progeny was negatively associated with the brood size in which the dam was raised ([Naguib and Gil, \(2005\)](#), [Naguib et al., \(2006\)](#)). These maternal effects could result from modifications in egg content of the females that were stressed during their early development, leading to sex-dependent impacts on the phenotype of F1 individuals. Epigenetic mechanisms might be involved in this process,

and deserve to be examined in this context. Several studies have also proven the existence of a maternal influence on the immune system of F1 individuals in birds (see ([Hasselquist and Nilsson, \(2009\)](#)) for a review).

From a genetic point of view, it is interesting that the priming effect of these induced responses seems to depend on the maternal genetic background ([Navara and Pinson, \(2010\)](#)).

The most in-depth research on epigenetic effects in birds over a single generation focused on the effects of environmental challenges on behavioral traits, gene expression and DNA methylation in offspring ([Lindqvist et al., \(2007\)](#), [Natt et al., \(2009\)](#), [Goerlich et al., \(2012\)](#), [Natt et al., \(2012\)](#)). In one of these studies ([Lindqvist et al., \(2007\)](#)), spatial learning was affected in individuals subjected to unpredictable light rhythms compared to animals exposed to predictable light rhythms. In the White Leghorn but not the Red Jungle Fowl, these effects were transmitted to the F1 generation reared under normal conditions, indicating a difference in the transmission of information to the next generation between these two chicken breeds. Exposure of commercial chicks to an unpredictable light schedule also triggered transmission of adaptive behavior to the next generation, with female offspring showing greater effects than males ([Natt et al., \(2009\)](#)). Molecular analyses showed that transcription differences acquired by the parents in response to environmental challenges are partially passed on to the F1 generation, and that the *BDNF* gene ([Lindqvist et al., \(2007\)](#)), immune genes ([Natt et al., \(2009\)](#)), and stress-related genes ([Goerlich et al., \(2012\)](#)) seem to be involved in these transmitted effects. This work also provides new insight into the role of DNA methylation in multigenerational epigenetic effects, by showing heritable differences of DNA methylation between different chicken breeds ([Natt et al., \(2012\)](#)). The influence of the genetic background is a particularly interesting feature and it has been reported that the impact of the parental environment on the offspring's phenotype depends on the chicken line ([Lindqvist et al., \(2007\)](#)). Observations in quail have also demonstrated a genetic component of maternal influence. Cross-fostering of chicks by mothers from two quail lines, divergently selected for tonic immobility (a fear-related behavioral trait), showed that the level of maternal influence on the offspring's behavioral development depends on the chick's genetic origin ([Houdelier et al., \(2011\)](#)). This maternal influence is at least partially carried by egg composition, as shown in a study of F1 quails from stressed females ([Guibert et al., \(2011\)](#)) and using an *ex-ovo* embryo transfer strategy between chicken layers and broilers ([Ho et al., \(2011\)](#)).

Collectively, the above-described examples yield two noteworthy conclusions. First, some of the early environmental effects on the offspring's phenotype are sex-specific in both birds and mammals. Second, the environment experienced during early development seems to have a greater impact on the adult phenotype than that experienced later in life.

Taken together, these examples show that the environment influences gene expression in avian species, perhaps via epigenetic mechanisms. An interesting feature in the context of poultry production and selection is the

possibility that these influences may be retained across several successive generations.

Transgenerational memory of the ancestors' environment

An example of transgenerational epigenetic transmission comes from the plant world. Johannes et al. showed that alterations in DNA methylation can be inherited for several generations in *Arabidopsis thaliana* ([Johannes et al., \(2009\)](#)). Using epiRIL (epigenetic Recombinant Inbred Lines), these authors and others ([Reinders et al., \(2009\)](#)) examined the transmission of epigenetic marks for at least eight generations, and observed that some were conserved while others gradually returned to their original methylation state.

Similarly, interesting cases have been highlighted in animals. Erasure of methylation patterns during meiosis results in the establishment of new parent-specific imprints in oocytes and spermatocytes ([Law and Jacobsen, \(2010\)](#), [Cedar and Bergman, \(2012\)](#)). However, some loci can escape DNA methylation reprogramming, as for example, repeated elements such as retrotransposons ([Law and Jacobsen, \(2010\)](#), [Daxinger and Whitelaw, \(2012\)](#)). Moreover, miRNA were shown to be involved in the transmission of epigenetic information via the gametes ([Daxinger and Whitelaw, \(2012\)](#), [Marczylo et al., \(2012\)](#)). Thus, epigenetic information can be transmitted and have an impact on the next generations.

Parental environment has an effect on the F1 generation and this is particularly clear in mammals, since the mother hosts the offspring's development from the zygote stage to birth. Such effects will also occur in the F2 generation, since the developing F1 generation bears the primordial germ cells that will differentiate into gamete precursor cells and eventually form an F2 animal. In this way, the maternal environment can affect the next two generations, which means that the first generation for which an individual's cells are not directly exposed to an environmental effect is the F3 generation if it was the female that was exposed and the F2 generation if it was the male. Thus, evidence for transgenerational epigenetic transmission, i.e. incomplete erasure of epigenetic marks between generations resulting in unusual patterns of inheritance from one generation to the next, is unquestionable only if the effect is detected in the F3 generation or beyond ([Skinner, \(2011a\)](#)). Investigating the male-path is an interesting approach to examine transgenerational epigenetic impacts.

Paternal environmental influences on the phenotype of the F1 generation (or even the F2 generation) have been shown in mammals (reviewed in [Curley et al., \(2010\)](#)). For example, the female offspring of adult male rats fed a high-fat diet showed modified β -cell functions that were associated with an altered expression of more than 600 genes in the F1 generation, and hypomethylation of a cytosine proximal to the transcription start site of the *IL13RA2* gene ([Ng et al., \(2010\)](#)). Similarly, offspring from male rats fed a low-protein diet showed impaired lipid metabolism, notably associated with increased methylation at a putative enhancer of the *PPAR α* gene ([Carone et al., \(2010\)](#)). These results

strongly suggest transmission of epigenetic information, but since the methylation patterns were not examined in the following generation, it is difficult to conclude to an unquestionable transgenerational epigenetic phenomenon, as defined above.

Transgenerational epigenetic transmission may be rare, but it has already been reported in different mammalian species. In man, Pembrey reported that the paternal grandfather's food supply affected the mortality rate of grandsons but not of granddaughters, whereas the paternal grandmother's food supply affected the mortality rate of granddaughters but not of grandsons ([Kaati et al., \(2007\)](#), [Pembrey, \(2010\)](#)). Another study by Heijmans and collaborators showed that the risk of mortality in grandchildren, with respect to the grandparents' food supply, was associated with modifications of DNA methylation in the differentially methylated region of the *IGF2* gene ([Heijmans et al., \(2008\)](#)).

Recently, Zeybel et al. ([Zeybel et al., \(2012\)](#)) described an adaptive mechanism involving epigenetic mechanisms in rats. After inducing liver injury in F0 and/or F1 males, they showed a reduction of liver fibrogenesis in F2 male offspring, illustrating an unquestionable transgenerational inheritance. The authors observed epigenetic modifications in a number of genes, with alterations observed in CpG methylation (*PPAR γ* , *PPAR α* and *TGF- β 1*), histone H3 acetylation (*PPAR γ* and *TGF- β 1*) and other chromatin modifications (*PPAR γ*). However, the mechanisms that transmit epigenetic modifications from the environment to the sperm and from the sperm to the offspring's liver have not yet been deciphered ([Zeybel et al., \(2012\)](#)). In rats, an epigenetic inheritance induced by different environmental components was observed in the sperm of the F3 generation by detecting differentially methylated regions depending on the environmental exposure of the ancestors ([Manikkam et al., \(2012\)](#)).

Some studies have even revealed transmission of epigenetic marks to at least the F4 generation. Recently, Wolstenholme et al. reported that exposure to bisphenol A during the gestation of female mice reduced the expression of the genes encoding two neuropeptides (oxytocin and vasopressin) in the brain of the F1 individuals. The expression of oxytocin was still reduced in the brain of the F4 males and females, whereas decreased vasopressin expression was maintained only in the F4 males. Moreover, impacts on social behavior were detected until the F4 generation ([Wolstenholme et al., \(2012\)](#)). Another report on the analysis of the phenotype and epigenetic marks of female rats subjected to a high-energy diet for four generations, demonstrated that transgenerational effects involving altered epigenetic marks at each generation were induced (at least partly) *de novo* ([Burdge et al., \(2011\)](#)). Finally, the best-studied example of transgenerational epigenetic inheritance in vertebrates concerns the influence of vinclozolin on the health (fertility problems or organic diseases) of rat male offspring in the F1 to F4 generations. This occurs via DNA methylation and a putative induction of copy number variation to generate new imprinted-like sites that are transmitted to subsequent generations through the male germ line, thus creating transgenerational transmission of adult

phenotypes ([Anway et al., \(2005\)](#), [Chang et al., \(2006\)](#), [Guerrero-Bosagna et al., \(2010\)](#), [Skinner et al., \(2012\)](#)). Other studies have suggested putative intergenerational transmission of epigenetic marks through the gametes ([Daxinger and Whitelaw, \(2012\)](#), [Marczylo et al., \(2012\)](#)).

To our knowledge, no transgenerational transmission of epigenetic marks has been reported in birds, either prior to the exhaustive reviews by Jablonka and Raz ([Jablonka and Raz, \(2009\)](#)) and Ho and Burggren ([Ho and Burggren, \(2010\)](#)), or since then.

Conclusions

A phenotype results from the interplay between the genome and the epigenome, which itself depends on the environment the animal experiences during its development and adult life. Epigenetic variations during early life play a role in producing inter-individual differences in phenotypes. Consequently, analyses of inter-individual phenotypic diversity should consider both epigenetic and genetic variations ([Szyf et al., \(2008\)](#)). In this review, we describe epigenetic phenomena in birds in comparison to the related studies in mammals. Much more work is needed to fully comprehend the importance of epigenetics in the phenotypic variability of birds, and hence to exploit it for genetic selection.

In the chicken, epigenetic modifications occur from the first egg stage, i.e. a stage at which the dam provides an environmental signature through the egg content ([Monaghan, \(2008\)](#)). These environmental influences may have agronomic value via their effect on the adult phenotype. Given the likelihood that climate will change in the more or less near future and demands for food supplies will increase, a better understanding of the epigenetic mechanisms governing the embryo's response to environmental changes could open new ways to improve efficiency, animal welfare and food quality. For example, one interesting issue is the nutrient profile and restriction level of the diet of breeders, which is tailored to produce the largest possible number of fertile eggs and may thus not fill the requirements for future adult broiler performance ([Leeson, \(2012\)](#)).

Transgenerational inheritance associated with mechanisms other than DNA sequence variation (i.e., epigenetics, parental effects or "cultural inheritance") is thought to affect evolutionary dynamics ([Danchin et al., \(2011\)](#)). This "non-classical" inheritance is known to play a role in phenotypic variability, especially in the response to environmental changes ([Liu, \(2007\)](#)). An important question in animal selection is the extent to which this non-genetic inheritance also affects the efficiency of genetic selection. Indeed, epigenetics may help to better explain environmental and non-Mendelian variability of complex traits ([Petronis, \(2010\)](#)). Several authors have proposed quantitative models including epigenetic inheritance and environmental interactions ([Tal et al., \(2010\)](#), [Furrow et al., \(2011\)](#), [Johannes and Colome-Tatche, \(2011\)](#)), potentially paving the way for future inclusion of these mechanisms in genetic selection studies. The reversibility of epigenetic modifications (i.e., their potentially transient nature) could constitute a challenge in the modeling of inheritance

([Slatkin, \(2009\)](#)). Aside from putative epigenetic inheritance, Feinberg and coworkers proposed a model in which DNA mutations could, via epigenetic mechanisms, modify phenotypic variability without changing the mean phenotype ([Feinberg and Irizarry, \(2009\)](#)). This model should be considered by geneticists aiming at studying the adaptation of livestock to changing environments.

From a genetic point of view, the contribution of heritable epigenetic effects to important phenotypic variations is an exciting research area, not only for fundamental science, but also because of its possible breeding applications, as recently suggested by a primary poultry genetics organization ([Fulton, \(2012\)](#)).

Literature Cited

- Anway, M. D., A. S. Cupp, M. Uzumcu, et al. (2005). *Science* 308: 1466-1469.
- Ashwell, C. and R. Angel (2010). *R. Bras. Zootec.* 39: 268-278.
- Bird, A. (2007). *Nature* 447: 396-398.
- Burdge, G. C., S. P. Hoile, T. Uller, et al. (2011). *PLoS One* 6: e28282.
- Carone, B. R., L. Fauquier, N. Habib, et al. (2010). *Cell* 143: 1084-1096.
- Cedar, H. and Y. Bergman (2012). *Annu Rev Biochem* 81: 97-117.
- Chang, H. S., M. D. Anway, S. S. Rekow, et al. (2006). *Endocrinology* 147: 5524-5541.
- Cockett, N. E., S. P. Jackson, T. L. Shay, et al. (1996). *Science* 273: 236-238.
- Curley, J. P., R. Mashoodh and F. A. Champagne (2010). *Horm Behav* 59: 306-314.
- Danchin, E., A. Charmantier, F. A. Champagne, et al. (2011). *Nat Rev Genet* 12: 475-486.
- Daxinger, L. and E. Whitelaw (2012). *Nat Rev Genet* 13: 153-162.
- Dolinoy, D. C. (2008). *Nutr Rev* 66 Suppl 1: S7-11.
- Dolinoy, D. C., C. Weinhouse, T. R. Jones, et al. (2010). *Epigenetics* 5: 637-644.
- Ellegren, H., L. Hultin-Rosenberg, B. Brunstrom, et al. (2007). *BMC Biol* 5: 40.
- Faulk, C. and D. C. Dolinoy (2011). *Epigenetics* 6: 791-797.
- Feil, R. and M. F. Fraga (2012). *Nat Rev Genet* 13: 97-109.
- Feinberg, A. P. and R. A. Irizarry (2009). *Proc Natl Acad Sci U S A* 107 Suppl 1: 1757-1764.
- Frésard, L., M. Morisson, J. M. Brun, et al. (2013). *Genet Sel Evol* 45: 16.
- Fulton, J. E. (2012). *Animal Frontiers* 2: 30-36.
- Furrow, R. E., F. B. Christiansen and M. W. Feldman (2011). *Genetics* 189: 1377-1387.
- Gabory, A., L. Attig and C. Junien (2011). *World J Diabetes* 2: 164-175.
- Goerlich, V. C., D. Natt, M. Elfving, et al. (2012). *Horm Behav* 61: 711-718.
- Goldberg, A. D., C. D. Allis and E. Bernstein (2007). *Cell* 128: 635-638.
- Gou, Z., R. Liu, G. Zhao, et al. (2012). *PLoS One* 7: e33627.
- Guerrero-Bosagna, C., M. Settles, B. Luckner, et al. (2010). *PLoS One* 5: e13100.
- Guibert, F., M.-A. Richard-Yris, S. Lumineau, et al. (2011). *Appl Anim Behav Sci.* 132: 51-60.
- Halevy, O., Y. Piastun, I. Rozenboim, et al. (2006). *Am J Physiol Regul Integr Comp Physiol* 290: R1062-1070.
- Hasselquist, D. and J. A. Nilsson (2009). *Philos Trans R Soc Lond B Biol Sci* 364: 51-60.

- Heijmans, B. T., E. W. Tobi, A. D. Stein, et al. (2008). *Proc Natl Acad Sci U S A* 105: 17046-17049.
- Ho, D. H. and W. W. Burggren (2010). *J Exp Biol* 213: 3-16.
- Ho, D. H., W. L. Reed and W. W. Burggren (2011). *J Exp Biol* 214: 619-628.
- Holliday, R. (2006). *Epigenetics* 1: 76-80.
- Houdelier, C., S. Lumineau, A. Bertin, et al. (2011). *PLoS One* 6: e14604.
- Itoh, Y., K. Replogle, Y. H. Kim, et al. (2010). *Genome Res* 20: 512-518.
- Jablonka, E. and M. J. Lamb (2002). *Ann N Y Acad Sci* 981: 82-96.
- Jablonka, E. and G. Raz (2009). *Q Rev Biol* 84: 131-176.
- Jammes, H., C. Junien and P. Chavatte-Palmer (2010). *Reprod Fertil Dev* 23: 64-74.
- Johannes, F. and M. Colome-Tatche (2011). *Genetics* 188: 215-227.
- Johannes, F., E. Porcher, F. K. Teixeira, et al. (2009). *PLoS Genet* 5: e1000530.
- Julien, P., D. Brawand, M. Soumillon, et al. (2012). *PLoS Biol* 10: e1001328.
- Kaati, G., L. O. Bygren, M. Pembrey, et al. (2007). *Eur J Hum Genet* 15: 784-790.
- Kisliouk, T. and N. Meiri (2009). *Eur J Neurosci* 30: 1909-1922.
- Kisliouk, T., S. Yosefi and N. Meiri (2011). *Eur J Neurosci* 33: 224-235.
- Kisliouk, T., M. Ziv and N. Meiri (2010). *Dev Neurobiol* 70: 100-113.
- Krause, B., L. Sobrevia and P. Casanello (2009). *Curr Vasc Pharmacol* 7: 513-520.
- Law, J. A. and S. E. Jacobsen (2010). *Nat Rev Genet* 11: 204-220.
- Leeson, S. (2012). *Poultry Science* 91: 1281-1285.
- Lindqvist, C., A. M. Janczak, D. Natt, et al. (2007). *PLoS One* 2: e364.
- Liu, Y. (2007). *EMBO Rep* 8: 798-803.
- Livernois, A. M., J. A. Graves and P. D. Waters (2012). *Heredity (Edinb)* 108: 50-58.
- Lumey, L. H., A. D. Stein, H. S. Kahn, et al. (2007). *Int J Epidemiol* 36: 1196-1204.
- Luo, J., A. Mitra, F. Tian, et al. (2012b). *PLoS One* 7: e41849.
- Luo, J., Y. Yu, S. Chang, et al. (2012a). *Front Genet* 3: 20.
- Lyon, M. F. (1961). *Nature* 190: 372-373.
- Makowsky, R., N. M. Pajewski, Y. C. Klimentidis, et al. (2011). *PLoS Genet* 7: e1002051.
- Manikkam, M., C. Guerrero-Bosagna, R. Tracey, et al. (2012). *PLoS ONE* 7: e31901.
- Mank, J. E. and H. Ellegren (2009). *Heredity (Edinb)* 102: 312-320.
- Manolio, T. A., F. S. Collins, N. J. Cox, et al. (2009). *Nature* 461: 747-753.
- Marczylo, E. L., A. A. Amoako, J. C. Konje, et al. (2012). *Epigenetics* 7: 432-439.
- Mazzio, E. A. and K. F. Soliman (2012). *Epigenetics* 7: 119-130.
- Melamed, E. and A. P. Arnold (2007). *Genome Biol* 8: R202.
- Monaghan, P. (2008). *Philos Trans R Soc Lond B Biol Sci* 363: 1635-1645.
- Morey, C. and P. Avner (2011). *PLoS Genet* 7: e1002212.
- Naguib, M. and D. Gil (2005). *Biol Lett* 1: 95-97.
- Naguib, M., A. Nemitz and D. Gil (2006). *Proc Biol Sci* 273: 1901-1905.
- Natt, D., N. Lindqvist, H. Stranneheim, et al. (2009). *PLoS One* 4: e6405.
- Natt, D., C. J. Rubin, D. Wright, et al. (2012). *BMC Genomics* 13: 59.
- Navara, K. J. and S. E. Pinson (2010). *Poult Sci* 89: 1509-1513.
- Ng, S. F., R. C. Lin, D. R. Laybutt, et al. (2010). *Nature* 467: 963-966.
- Nichelmann, M., J. Hochel and B. Tzschentke (1999). *Comp Biochem Physiol A Mol Integr Physiol* 124: 429-437.
- Park, H. B., L. Jacobsson, P. Wahlberg, et al. (2006). *Physiol Genomics* 25: 216-223.
- Pembrey, M. E. (2010). *Hum Fertil (Camb)* 13: 268-271.
- Petronis, A. (2010). *Nature* 465: 721-727.
- Piestun, Y., D. Shinder, M. Ruzal, et al. (2008). *Poult Sci* 87: 1516-1525.
- Ptashne, M. (2007). *Curr Biol* 17: R233-236.
- Ptashne, M. (2013). *Faseb J* 27: 1-2.
- Rao, K., J. Xie, X. Yang, et al. (2009). *Br J Nutr* 102: 848-857.
- Reed, W. L. and M. E. Clark (2011). *Integr Comp Biol* 51: 73-80.
- Reinders, J., B. B. Wulff, M. Mirouze, et al. (2009). *Genes Dev* 23: 939-950.
- Renaudeau, D., A. Collin, S. Yahav, et al. (2012). *Animal* 6: 707-728.
- Rozenboim, I., R. Huisinga, O. Halevy, et al. (2003). *Poult Sci* 82: 1181-1187.
- Rozenboim, I., Y. Piestun, N. Mobarkey, et al. (2004). *Poult Sci* 83: 1413-1419.
- Shinder, D., M. Ruzal, M. Giloh, et al. (2011). *Poult Sci* 90: 633-641.
- Skinner, M. K. (2011a). *Epigenetics* 6: 838-842.
- Skinner, M. K., M. Mohan, M. M. Haque, et al. (2012). *Genome Biol* 13: R91.
- Slatkin, M. (2009). *Genetics* 182: 845-850.
- Szyf, M., P. McGowan and M. J. Meaney (2008). *Environmental and Molecular Mutagenesis* 49: 46-60.
- Tal, O., E. Kisdi and E. Jablonka (2010). *Genetics* 184: 1037-1050.
- Teranishi, M., Y. Shimada, T. Hori, et al. (2001). *Chromosome Res* 9: 147-165.
- Tzschentke, B. and D. Basta (2002). *Comp Biochem Physiol A Mol Integr Physiol* 131: 825-832.
- Van Laere, A. S., M. Nguyen, M. Braunschweig, et al. (2003). *Nature* 425: 832-836.
- Wolstenholme, J. T., M. Edwards, S. R. Shetty, et al. (2012). *Endocrinology* 153: 3828-3838.
- Xu, P., C. J. Denbow, N. Meiri, et al. (2012). *Physiol Behav* 105: 276-282.
- Yan, F., R. Angel, C. Ashwell, et al. (2005). *Poult Sci* 84: 1232-1241.
- Yossifoff, M., T. Kisliouk and N. Meiri (2008). *Eur J Neurosci* 28: 2267-2277.
- Youngson, N. A. and E. Whitelaw (2008). *Annu Rev Genomics Hum Genet* 9: 233-257.
- Zeybel, M., T. Hardy, Y. K. Wong, et al. (2012). *Nat Med* 18: 1369-1377.
- Zhang, L., H. J. Zhang, X. Qiao, et al. (2012). *Poult Sci* 91: 1026-1031.
- Zhang, S. O., S. Mathur, G. Hattem, et al. (2010). *BMC Genomics* 11: 13.