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Agricultural Science and Technology
Faculty of Agriculture, Trakia University
Student’s campus, 6000 Stara Zagora
Bulgaria
Telephone.: +359 42 699330
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Technical Assistance:
Nely Tsvetanova
Telephone.: +359 42 699446
E-mail: editoffice@agriscitech.eu
Classical and modern concepts of inbreeding and effects of inbreeding depression in animals

S. Tanchev*

Department of Genetics, Breeding and Reproduction, Faculty of Agriculture, Trakia University, 6000 Stara Zagora, Bulgaria

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Abstract. An overview of the literature on inbreeding and inbreeding depression in animals was made with focus on the development of scientific concepts from Darwin times to present days. The opinions and hypothesis of numerous researchers about the genetic nature of these events are presented. The effects of inbreeding on different biological traits of animals and manifestations of inbreeding depression as a possible result of various allele and gene interactions are discussed. The analysis of information demonstrated that despite the new body of knowledge about inbreeding and inbreeding depression accumulated during the last 10 – 15 years, some issues are still not clear thus posing important research tasks to genetics. They are associated to: 1. The number of genes, the nature and features of specific allele and gene interactions which determine inbreeding depression; 2. The investigation and discovery of genes mutations related to this event; 3. Performance of structural and functional analyses of genes, RNA transcripts, proteins and metabolites related to inbreeding depression; 4. Investigation of the interaction of inbred genotypes with environmental factors etc. From a future perspective, the author believes that in the omic technologies era, the long-standing topic about inbreeding and inbreeding depression could acquire a new meaning and renew the interest of scientists. In conclusion, the implementation of modern technologies of research could assist for gathering new detailed information about the genetic nature of inbreeding and the effects of inbreeding depression.

Keywords: Inbreeding, inbreeding depression, animals

Introduction

It is logical to assume that after the domestication of a number of plant and animal species since most ancient times, people have been aware that in many instances, inbreeding had adverse consequences. Later, similar observations of scientific nature were probably made by ancient scientists from Greece, the Persian Empire, Egypt, the Roman Empire etc. It becomes clear that the historical body of evidence based on empirical experiments and speculations on inbreeding has not provided a reliable explanation of the biological nature of this phenomenon (Tanchev, 2006).

The problem with inbreeding has been reviewed most thoroughly and objectively by Charles Darwin. The principal conclusion on the adverse impact of continuous narrow inbreeding made on the basis of a huge amount of factual material was so convincing that the broad implication of inbreeding in agriculture and livestock farming has been limited for a long time (Darwin, 1868).

A renaissance of the scientific and applied interest to inbreeding occurred in the early XIX century. By that time, an intense development of agrobiological science has begun. On the basis of its studies on self-pollinating plants, Johansen (1903) created the ‘pure lines’ theory. Practically, pure lines are inbred lines obtained via continuous self-pollination. The progeny is relatively homogenous, and most genes are in a homozygous state (Johansen, 1903). In parallel to and immediately after the experiments of Johansen with plants, comprehensive trials on the inheritance of traits in laboratory animals using various breeding schedules including inbreeding have begun: Bateson (1903) with mice and rats, Castle et al (1906) with Drosophila, King (1911) with rats, Little (1913) with mice, Wright (1921a, 1921b, 1922) with guinea pigs etc.

These early observations, experiments and reports have become the background for later more detailed studies on inbreeding until recent days. Therefore, from both historical and modern perspective, the analysis of scientific knowledge on the genetic nature of inbreeding and inbreeding depression and their significance for theoretical and practical biology are still appealing.

Genetic nature of inbreeding and inbreeding depression

As stated, the first relatively consistent scientific explanations about the biological nature of inbreeding are given by Darwin (1868) in its work “The variation of animals and plants under domestication” and more specifically, in the chapter “On the good effects of crossing, and on the evil effects of close interbreeding”. The explanation about the biological nature of inbreeding compares its negative effects and the positive influence of crossbreeding on several biological traits in living beings. In the view of Darwin, these two phenomena should be always discussed together. He also outlined the advantage of breeding organisms which are not related genetically resulting in the fusion of gametes of different parental forms and consequently, in improved biological diversity of the progeny. As a result of the inbreeding, fusion of a similar genetic material occurs, which reduced the biodiversity and the adaptation potential of the new organism.

The first genetic hypotheses explaining the genetic nature of inbreeding and heterosis appeared after the differentiation of genetics as an independent science and the introduction of specific genetic terminology. The first one is the dominance hypothesis (Davenport, 1908). It affirms that the major part of mutations were neutral or deleterious and, in most instances, recessive, therefore
remaining hidden. Inbreeding leads to increased homozygosity and from its part it creates preconditions for phenotype appearance of more recessive mutations. The same year has witnessed the birth of the Overdominance hypothesis (East, 1908; Shull, 1908). According to it, the traits of heterozygous genotypes within populations are better than those of homozygous genotypes. The inbreeding results in decrease in heterozygous individuals and increase in homozygous ones, thus increasing the probability for appearance of deleterious mutations.

At the example of Darwin, East and Jones (1919) concluded that the inbreeding and the hybrid vigour (heterosis) obtained after crossing are the two faces of the same phenomenon, namely, the alteration of the heterozygosity extent after various types of mating. Thus, inbreeding results in increased homozygosity of animals creating conditions not only for appearance of abnormalities and other deleterious effects, but also could result in increased production performance and a certain positive effect in a given trait. On the contrary, crossbreeding reduces the extent of homozygosity with respect to all traits. Later, other studies have confirmed the view that inbreeding increased the homozygosity of all genes in the individual genotype (Bogdanov, 1922). The adverse impact of inbreeding consists namely in the higher level of homozygosity causing negative effects on different traits and events during the ontogeny of inbred organisms. A part of dominance and overdominance effects are lost, and conditions for phenotypic appearance of unwanted recessive genes are created. In general, this state is termed „inbreeding depression“. It is established that the response to inbreeding was different in the various descent groups. The features of parental genotypes determine the extent of the inbreeding depression (Serebrovskii, 1968; Ovyanickov, 1974; Tanchev, 2006). Along with nuclear heredity, the role of cytoplasmic heredity should be also considered. It is assumed that apart nuclear inbreeding depression, a cytoplasmic inbreeding depression also exists, probably associated with the maternal organism role (Kushner, 1967; Yohanson, 1970). It is also proved that the increased homozygosity in inbreeding creates preconditions for phenotypic appearance of deleterious recessive genes. Outbred animal populations possess many recessive genes in an occult state, which are responsible for a number of abnormalities in case of inbreeding (Chai 1969; Wiesner and Willer, 1974; Lesley, 1982; Gronert et al., 1986; Lojda, 1993; Welchman et al., 1994; Tanchev, 2006). Not all abnormalities are associated with visible phenotypic effects; some of them are manifested on biochemical and physiological level at different stages of the ontogeny.

On the basis of analysis of synopsis of existing reports and own data, Charlesworth and Willis (2009) suggest three hypotheses for genetic determination of inbreeding depression. According to the first hypothesis this phenomenon is determined by a single locus (single-locus hypotheses). It includes two variants of allele interactions with various effects – model of dominance (partial or full) and model of overdominance. It is suggested that for both models the relationship between genotype and inbreeding depression is linear. It is also assumed that apart the two models, inbreeding depression could result also from antagonistic pleiotropy. The second hypothesis affirms that inbreeding depression is determined by two or more loci located in a single chromosome. The interaction could entail a pseudo-overdominance, hence inbreeding depression. The third hypothesis suggests that inbreeding depression is a product of multiplicative and non-multiplicative interactions among genes, including negative forms of epistasis. It is also hypothesised that epistatic interaction among genes is responsible for the non-linear character of the relationship between the genotype and the inbreeding depression.

In an analysis on the nature of hypotheses, Kristensen et al. (2010) concluded that the relative contribution of partial dominant versus overdominant loci to inbreeding depression is still unresolved, but that most researchers supported partial dominance as the primary mechanism – for example Charlesworth and Charlesworth (1999), Crow (1999). A contribution of epistatic interactions to inbreeding depression has also been proposed (Yu et al., 1997). Epistatic interactions are usually treated as statistical effects, but can be interpreted as the fixation of incompatible gene combinations during inbreeding events, owing to the increased effect of genetic drift (Charlesworth and Charlesworth, 1999).

Despite the numerous studies on inbreeding depression conducted within past 150 years and hypotheses for the genetic determination of this phenomenon, some questions are still unresolved, for instance, the exact number of loci causing the depression (Frankham et al., 2002), the exact interactions of genes from these loci and pathways of inbreeding depression expression (Paige, 2010). The development of molecular biology, genetics, biochemistry, ecology, informatics and other science during the last decades contributed a lot to obtain new information about the genetic nature of inbreeding and inbreeding depressions in sexually reproducing organisms. The development and implementation of new molecular genetic and genomic methods of research allowed for detection of homoygous and heterozygous loci, identification of gene related to inbreeding depression, as well as evaluation of the dynamics of genetic diversity of populations on the basis of specific qualitative and quantitative traits. These studies however generated a huge amount of information about the DNA of the different species leading to development of highly efficient software for storage, analysis and processing of information about the genetic events proper to inbreeding depression (Schenne et al., 1995; White et al., 1999; Amundson, 2008). A lot of interesting results have been obtained from the investigation of various inbred and non-inbred lines and hybrids of D. melanogaster (Kristensen et al., 2005, 2006; Demontis et al., 2009; Reed, 2009; Ayroles et al., 2009). Comparative analyses have established that inbreeding depression was associated with many differentially expressed genes. This group includes various numbers of genes responsible for the synthesis of specific proteins, genes coding antibacterial peptides, genes related to metabolism and systemic defense responses etc. For example, using a genome-wide approach to assess the genomic basis of inbreeding depression, Ayroles et al. (2009) identified 567 genes involved in inbreeding depression among inbred Drosophilia melanogaster lines, 75 percent of them being additive, partially additive or dominant, and 25 percent expressing patterns of overdominance.

Molecular epigenetic studies are of special interest to the research on the genetic nature of inbreeding depression. These relatively novel studies suggested that epigenetic DNA modifications were involved in embryonic survival, initial stages of growth during the postnatal development and probably, in inbreeding depression (Remington and O'Malley, 2000a, 2000b; Li, 2001; Bossdorf et al., 2008; Huang et al., 2009; Biémont, 2010; Vergeer et al., 2012; Schmitz et al., 2013; Liebl et al., 2013; Biémont and Vieira, 2014).

Molecular and genomic studies made possible large-scale analysis of DNA sequences in different organisms. This fact entailed the discovery of synonymous and nonsynonymous mutations in coding and non-coding DAN regions, supposed to be involved in inbreeding depression. (Yang et al., 2003; Haddrill et al., 2005; Parmley et al., 2006; Loewe and Charlesworth 2006; Keightley and
It was also suggested that deleterious mutations associated with inbreeding depression could affect cis-regulatory regions, trans-acting factors of transcription or a kind of combined effect from their simultaneous action (Meiklejohn et al., 2003; Schadt et al., 2003; Hughes et al., 2006; Lemos et al., 2008; Charlesworth and Willis, 2009; Paige, 2010). The accumulation of a lot of such mutations probably determines a genomic instability in inbred animals, causing inbreeding depression.

During the last 10 – 15 years, the researchers – geneticists, biochemists, ecologists etc. have focused their attention on the study of probable genetic and functional relationships of inbreeding depression and stress in animals, caused by various factors in experimental and natural conditions. In most instances, the studies demonstrated that inbred animals from different species were more susceptible to stress than outbred and hybrid animals (Tanchev et al., 2003; Tanchev and Gadjeva, 2006; Tanchev, 2006; Kristensen et al., 2005, 2006; Charlesworth and Willis, 2009; Paige, 2010; Okada et al., 2011; Vermeulen et al., 2013).

Effect of inbreeding on some biological traits of animals

Numerous studies have shown that in many cases, inbreeding has adverse consequences. The traits which are most negatively affected are associated with reproduction performance, livability and adaptation of animals to the changing environment. In domestic animals, growth traits, feed conversion and the performance in general are worsened. These negative effects are incurred from inbreeding depression which accompanies the development of existence of inbred offspring. It is generally explained by the transition of many gene allele pairs into homozygous state (Ovsyannikov, 1974). The increased homozygosity creates conditions for the phenotypic appearance of unwanted recessive genes and consequently, to occurrence of morphological, biochemical, physiological and other types of damage (Tanchev, 2006). Often, they include mutant genotypes and phenotypes, which are lethal and are expressed in early ontogeny (Mc Cune et al., 2002). The increased homozygosity reduces the genetic heterogeneity of allele pairs in the genotype of the inbred individual, and affects some important functions as synthesis of enzymes, hormones, proteins etc. It could be logically assumes that the increase in homozygosity depletes the ability of the body to produce a broader spectrum of biologically active substances, as heterozygous outbred or crossbred organisms are capable to.

Effects on reproduction traits

The maintenance of normal reproduction is essential both for the existence of populations within a given species, and for the existence of the species in general. It is confirmed that reproduction traits of animals are most sensitive to inbreeding and with most substantial expression of inbreeding depression. According to multiple studies, when the inbreeding level is equal to or higher than 25% (F >0.25) the following disturbances are reported:

- Impaired synthesis of sex steroids (O’Brein, 1994; Kosowska and Zdrojewiez, 1998; Bickley et al., 2013);
- Reduced conception rates (Falconer and Mackey, 1996; Bouzat et al., 1998; Westermeer et al., 1998; Meagher et al., 2000; Robert et al., 2005; Brown et al., 2009; Demontis et al., 2011; Johnson et al., 2011; Leroy 2014);
- Reduced fertility of female animals (Chai, 1969; Hinkovski et al., 1975; Li, 1977; Poupardieu and Toure, 1980; Hradecky et al., 1985; Geras, 1986; Torro et al., 1988; Park et al., 1990; Ferraz et al., 1992; Bielanski et al., 1993; Rodriguez et al., 1998; Culbertson et al., 1998; Farghaly, 2000; Tanchev, 2006);
- Reduced milk yields and deteriorated milk quality in mammals (Hinkovski et al., 1975; Cassell, 1999; Tompson et al., 2000; Kristensen and Sorensen, 2005; Kasarda and Kadlecik, 2007; Danchin-Burge et al., 2011; Leroy 2014).

Effects on embryonic development, livability, growth, adaptation potential and life span

The investigations in inbred animals demonstrated that apart the strong negative impact on reproduction performance, in many instances inbreeding depressions exerted an adverse influence on livability, growth and the entire body development (Hinkovski et al., 1975; Li, 1977; Erohin et al., 1985). This is supported by studies reporting:

- Impaired embryonic development and embryonic death (Sittman et al., 1966; Cordero et al., 2004; Brown et al., 2009; Lazzari et al., 2011; Bickley et al., 2012; Bezdicek et al., 2014);
- Negative effects on the livability (Poupardieu and Toure, 1980; Falconer and Mackey, 1996; De Rose and Roff, 1999; Farghaly, 2000; Kock et al., 2009; Paige, 2010);
- Adverse effects on growth performance (Swiger et al., 1961; Dinkel et al., 1968; Burrow, 1993; Rodrigues et al., 1994; Falcao et al., 2001; Mc Parland et al., 2009; Kock et al., 2009);
- Negative influence on the synthesis of growth hormones Growth hormone (GH) and thyroxine (T₄) (Chai, 1958; Erohin et al., 1985; Kosowska, 1992; Tanchev, 2006; Santana et al., 2012);
- Reduced ability for adaptation and lower life span (Moskalev and Zainullin, 2006; Sasaki and Fukuda, 2006; Moskalev, 2008; Tanchev et al., 2015).

Effect on immunity and resistance to diseases

A number of authors affirmed that inbreeding depression influence negatively immunity and the resistance to various diseases (Palladino, 1977; Cassinello et al., 2001; Keller and Waller, 2002; Reid et al., 2003; Tanchev et al., 2005; Stanilova et al., 2005; Tanchev, 2006; Whiteman, 2006; Paneto et al., 2008; Charlesworth and Willis, 2009; Townsend et al., 2009,2010; Paige, 2010). In studies on insects however, no adverse effect of inbreeding on immune system was evidenced (Calleri et al., 2008; Rantalal and Roff, 2007; Gerishman, 2010; Vilikainen and Sundstrom, 2011; Franke and Fisher, 2013). In some of studies, researchers concluded that the effects of inbreeding depression on immune system and resistance to diseases in vertebrates and invertebrates were different.

Inbreeding and stress

At the background of stress, important biochemical and physiological reactions could be identified. Some of them are related to functional changes of endocrine glands and altered levels of produced hormones (Selye, 1971; Madzharov, 1980, 1988; Desautes et al., 1994; Maksimov et al., 1998; Avilov, 2001;
existence of the genetic diversity requires maintenance of an 
2014 (Kosowska and Zdrojewie, 1991; Kosowska and Zdrojewiez, 1996a, 1996b; Tanchev, 2006; Brown et al., 2009; Tanchev et al., 2014). Others reported that inbred animals were more sensitive to the effects of 
Ros, hence to oxidative stress. This was closely associated to impaired reproduction, growth performance, immunity and adaptation to abruptly changing environmental conditions (Franklin, 1980; Blount et al., 2001; Tanchev et al., 2003; Kristensen et al., 2005; Tanchev and Gadjeva, 2006; Charlesworth and Willis, 2009; Dowling and Simmons, 2009; Bolund et al., 2010; Okada et al., 2010; Ruiz-Lopes et al., 2010; Paige, 2010).

Inbreeding within small populations

The inbreeding is a factor with fundamental influence on genetic diversity within populations. It reduces the heterozygosity level and lead to corresponding increase in homozygosity. Populations subjected to inbreeding for a long time suffer from inbreeding depression exerted negative effects on reproductiveness, livability and growth performance of lambs, wool yields etc. (Ercanbrack and Knight, 1981, 1983, 1991, 1993; Rzewuska et al., 2005; Hussain et al., 2006; Ceyhan et al., 2011; Jafari, 2014).

Inbreeding was reported to have an adverse effect on genetic diversity; similarly inbreeding depression influenced negatively various economic traits (egg production, fertility, hatchability, livability, growth performance) in poultry from egg-laying and meat types. (Bermier et al., 1951; Sewaleem et al., 1999; Szwaczko et al., 2004; Ghorbani et al., 2007; Muir et al., 2008; Bahmanimehr al., 2012). According to some studies, the effect of inbreeding in livestock husbandry depends on the production system and the extent of its controlled implementation (Borisenko, 1967; Lush, 1973; Dickerson, 1973; Falkoner, 1985), the fast and slow increase in homozygosity (Kristensen et al., 2005, 2006; Demontis et al., 2009; Reed, 2009; Leroy, 2014) and on the role of already accumulated levels of old and new inbreeding (Hinrishs et al., 2007; Leroy 2014).

Positive effects

Along with the negative effects of inbreeding, the positive genetic effects from its purposeful implementation in livestock breeding to improve some important production quantitative traits (QTL) should not be ignored. With this regard, it should be noticed that the inbreeding applied in the livestock production practice does not result in very rapid increase in homozygosity similar to what occurs in self-pollinating plants (Kislovska, 1939). What is more, in most cases, inbred breeders selected for specific important economic traits, transfer well and strongly the positive traits to their progeny (Glembocksi and Nahimson, 1945; Glembocki, 1947; Borisenko, 1967; Arzumanyan, 1977; Falkoner, 1985; Erohin et al., 1985). On the other hand, it is considered that the prolonged and intensive selection results in systemic elimination of lethal and sublethal genes so the inbreeding in such populations guarantees to a certain extent a less pronounced inbreeding depression (Ven

Significance of inbreeding for livestock husbandry

Negative effects

Both genetic studies and livestock husbandry practices proved that inbreeding had a negative impact on several economically relevant traits in domestic animals. This could entail economic losses and to reduce the efficiency of farms produce. The results of numerous reports could be cited in support of that statement. For example, in dairy cattle farming, most studies reported that a level of inbreeding over 10% resulted in marked decrease in reproduction performance and milk yields. In most cases, milk fat and milk protein remained unaffected by inbreeding depression or only a slight negative effect was present (Wiggans et al., 1995; Migliore et al., 1992; Kawahara et al., 2006; Charlieh et al., 2008; Bjeland et al., 2013; Besdzic et al., 2014; Pryce et al., 2012, 2014). The inbreeding had also a negative influence on the duration of the productive lifetime of dairy cows (Smith et al., 1998; Cassell, 1999; Sorensen et al., 2006; Croquet et al., 2007; Pryce, 2014; Leroy, 2014) and weak adverse effect on growth performance and slaughter traits in beef cattle (Carolinio and Gama, 2008).

In sheep, inbreeding depression exerted negative effects on reproduction performance, livability and growth performance of lambs, wool yields etc. (Ercanbrack and Knight, 1981, 1983, 1991, 1993; Rzewuska et al., 2005; Hussain et al., 2006; Ceyhan et al., 2011; Jafari, 2014).

Multiple abnormal traits (pigs and rabbits) are particularly sensitive to inbreeding depression. Apart the negative impact on reproduction traits, adverse effects on livability of the neonates and juvenile animals from the progeny, growth performance, weak adaptation potential, higher frequency of skeletal and other abnormalities, marked susceptibility to stress etc. (Chai, 1969; Ford, 1970; Lim, 1977; Poujardieu and Toure, 1980; Hradecky et al., 1985; Gerash, 1986; Jawrska, 1988; Park et al., 1990; Ferraz et al., 1992; Bielanski et al., 1992; Culbertson et al., 1998; Tanchev, 2006; Tanchev et al., 2011).

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various phenotypic expressions expressed genes and for establishment of their relationship to analyses in this field allow for the identification of differentially inbreeding within populations and the homozygosity level (Keller et al., 2011; Purfield et al., 2012; Kim et al., 2015; Saura et al., 2015). It is believed that genome information obtained via runs genome level significantly more detailed information about the genetic nature of the synergic associations of inbreeding with the nature of the synergic associations of inbreeding with the environment still has to be elucidated (Kristensen et al., 2009; Paige, 2010; Leroy, 2014).

Perspectives on inbreeding and inbreeding depression research

The progress in new scientific branches – genomics, transcriptomics, proteomics, metabolomics and genetic engineering reveal broader possibilities for elucidation of the genetic nature of inbreeding and inbred depression. The implementation of “omic” technologies already gives solutions to some problems and opens up new perspectives for solving issues related to the number of genes associated with inbreeding depression, mechanisms of allelic and genetic interactions, specifics of protein synthesis and the genetic background of metabolic processes in inbred animals. The nature of the synergic associations of inbreeding with the environment still has to be elucidated (Kristensen et al., 2009; Paige, 2010; Leroy, 2014).

The achievements of the structural, functional and comparative genomics and the results in these directions are the base for genome-wide studies and analysis. New methods for sequencing, gene mapping and elaboration of DNA microchips made possible the composition of list of genes and candidate genes related to inbreeding depression (Paige, 2010), and also provides opportunities for detection of specific genetic determinants of this phenomenon (Ayroles et al., 2009).

The investigations with the methods of genomics provide significantly more detailed information about the genetic nature of inbreeding and its effects (Kristensen et al., 2005; Charlesworth and Willis, 2009; Paige, 2010; Bjelland et al., 2013; Kardos et al., 2015; Saura et al., 2015). The application of genome-wide studies introduced new terms as Genomic inbreeding and Genomic inbreeding coefficients (Fi) to reflect the status of inbreeding at genome level (VanRaden et al., 2011). For instance, it is now believed that genome information obtained via runs of homozygosity (ROH) allowed attaining a most accurate evaluation of the effects of inbreeding within populations and the homozygosity level (Keller et al., 2011; Purfield et al., 2012; Kim et al., 2015; Saura et al., 2015).

Transcriptomics is associated to the study of the entire set of RNA transcripts produced on the basis of genome. Comparative analyses in this field allow for the identification of differentially expressed genes and for establishment of their relationship to various phenotypic expressions (Shiu and Borevitz, 2008). For instance, the use of transcriptomic analysis in the study on inbreeding showed that the different populations within a species reacted in a different way to inbreeding depression (Kristensen et al., 2005, 2006; Ayroles et al., 2009).

The proteomics branch is related to the quantitation of final gene products – proteins and their posttranslational modifications (Patterson and Aebersohn, 2003; Mann and Jensen, 2003). The investigations and analyses in inbred and outbred Drosophila lines and their crosses showed that the different groups possessed different protein characteristics (Pedersen et al., 2009). According to the authors, these differences were at a background of the expression of inbreeding depression and its association to reduced adaptation capability in high temperatures conditions.

Another new field – metabolomics (Paige, 2010) is important for research on effects of inbreeding depression. It investigates the genetic determination of metabolic processes and the quantitative features of end products – metabolites (Fiehn, 2002; Goodacre et al., 2004; Kristensen et al., 2005; Paige, 2010). The studies of Pedersen et al. (2008, 2009) demonstrated the differences between inbred and outbred Drosophila with regard to some metabolites. The authors suggested that these metabolic disparities were probably related to the poorer reproduction traits of inbred animals and their reduced ability to cope with stress.

During the last years, the modern methods of molecular biology and genomics are increasingly applied in the research on inbreeding in livestock husbandry. A group of genome studies is devoted to the detection of genes and candidate genes involved in negative and positive effects of inbreeding on different biological and economic traits, as well as on the evaluation of the genetic diversity within the populations (Bielanski et al., 2013; Silio et al., 2013; Gomez et al., 2013; Ginja et al., 2013; Pryce et al., 2014; Pienaar et al., 2014; Saura et al., 2015) Another group of genome studies is focused on the opportunities for accurate and efficient control on inbreeding in domestic animals species in conditions of genome selection (Daetwyler et al., 2007; de Roos et al., 2011; Sonesson et al., 2012; Rodriguez-Ramilo et al., 2015; Saura et al., 2015; Kim et al., 2015; Bouquet et al., 2015; Boichard and Friz, 2015).

Conclusion

The literature overview demonstrated that the subject of inbreeding and inbreeding depression is still of great interest for scientists from both theoretical and practical points of view. From Darwin times to present, several hypotheses about the genetic nature of inbreeding and the effects of inbreeding depression have been advanced. Most studies are unanimous on the primary points although specific differences and contradictions are also present.

The overview made obvious that despite the new body of evidence about inbreeding and inbreeding depression from the last 10 – 15 years, some issues are still unclear thus posing important research tasks to genetics. They are associated to: 1. The number of genes, the nature and features of specific allele and gene interactions which determine inbreeding depression; 2. The investigation and discovery of gene mutations related to this event; 3. Performance of structural and functional analyses of genes, RNA transcripts, proteins and metabolites related to inbreeding depression; 4. Investigation of the interaction of inbred genotypes with environmental factors etc.

From a future perspective, authors believe that in the omic technologies era, the old subject of inbreeding and inbreeding
depression could acquire a new meaning and renew the interest of scientists. It could be therefore anticipated that the implementation of modern technologies of research could assist for gathering new detailed information about the genetic nature of inbreeding and the effects of inbreeding depression.

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