Acta fytotechn. zootechn., 17, 2014(2): 65–71

Review

Received 20. February 2014 | Accepted 7. March 2014 | Available online 23. June 2014

Advances in genomic sequencing using Bovine SNP BeadChip in Deer

Radovan Kasarda, Nina Moravčíková*, Anna Trakovická

Slovak University of Agriculture in Nitra, Slovakia

The aim of this work was to describe the progress made in particular area and summarizes a variety of SNPs discovery and genotyping studies in deer species. Increased interest of breeding of other animal species than traditional livestock has been recorded in recent years. One of these is also "deer livestock". Deer (*Cervidae*) is currently one of attractive species farmed in many countries as well as one of wild game animal used. Deer species as non-model organisms therefore do not have a large scale genomic sequence and adequate supporting tools to determine genetic markers for associations with traits of interest. Identification and understanding of loci that explain fitness variation is one of the crucial problems for application of molecular-based animal breeding to predict performance with the potential of increasing genetic improvement. Single nucleotide polymorphisms (SNPs) are growing in popularity as genetic markers not only investigating evolutionary processes but also for analyses of quantitative trait loci and candidate genes. SNPs have gained wide use in model species and are becoming the marker of choice for applications in other species. Technology that was developed for work in model species may provide useful tools for SNPs detection and genotyping in non-model organisms.

Keywords: *Cervidae*, SNPs, non-model organisms, genetic markers

Organisms traditionally considered of „minor" importance by national and international funding agencies generally suffer from a paucity of genome-wide sequence and polymorphism data which severely limits the implementation of genomic approaches for addressing biological question in these species (Seabury et al., 2011). One of such underserved species is deer, a highly successful and widely distributed ruminant mammal species of the order *Artiodactyla* and family *Cervidae* (Wilson and Reeder, 2005).

1. Characterization of deer species based on mitochondrial DNA variations

The family *Cervidae* includes 40 species of deer distributed throughout the northern hemisphere, as well as in South America and Southeast Asia, and an additional five species which has been assigned to the *Moschidae* family (Gilbert et al., 2006; Grubb and Groves, 2003). The subfamily *Cervinae* are found in Eurasia, with the exception of the North American wapiti (*Cervus elaphus*), and are referred to as the Old World deer species. The *Odocoileinae*, or New World deer species, can be found in both North America, such as the white-tailed deer (*Odocoileus viginianus*), in South America such as the brocket deer (*Mazama*), and in Eurasia, such as the roe deer (*Capreolus capreolus*). Tribal status within the *Cervidae* has been assigned to the holarctic deer species of reindeer (caribou; *Rangifer* sp.) and moose (*Alces alces*). More difficult to place have been the muntjac deer, which now have subfamily status within the *Cervidae* (*Muntiacinae*), and even more so the Chinese water deer (*Hydropotes inermis*) which is the only extant species in the subfamily of *Hydropotinae*. Complication of the taxonomic designations were the various hybridizations that occured between deer species, such as the well-described hybridizations between members of the genera *Cervus*, particularly for Sika (*C. nippon*), red deer and North American wapiti (*C. elaphus*). Further complications have arisen due to the various morphotypes of *C. elaphus*, where the subspecies status has been even more controversal (Ludt et al., 2004). The red deer (*Cervus elaphus*) is one of the biggest free-ranging mammals of Central Europe and, although not endangered in terms of population numbers, is the perfect model for study the population genetic effects of a multitude of deliberate and unintentional anthropogenic influences on natural populations over a long period of time. Red deer gene pools were affected by habitat fragmentation, keeping of populations in enclosures, translocations, (re) introductions, and trophy hunting. Various schedules of population regulation by hunting were applied throughout Europe. Many autochthonous stocks have been hybridized with the introduced animals, thus

***Correspondence:** Nina Moravčíková, Slovak University of Agriculture in Nitra, Faculty of Agrobiology and Food Resources, Department of Animal Genetics and Breeding biology, Trieda A. Hlinku 2, 949 76 Nitra, Slovakia, e-mail: nina.moravcikova1@gmail.com

Faculty of Agriobiology and Food Resources, 2014
http://www.fapz.uniag.sk/
DOI: 10.15414/afz.2014.17.02.65–71

blurring the historical boundaries between formerly natural populations (Hartl et al., 2003; Zachos et al., 2003).

Complete mitochondrial DNA sequence represents data for determination of the population structure and also identification of subspecies and species of deer (Wan et al., 2004). In recent years has been recorded a rapid expansion in the sequencing of mitochondrial genomes of different species in family *Cervidae*. The complete mitochondrial genome sequence of deer for determining phylogenetic positions, providing also important information for molecular-based animal breeding and genetic improvement was determined on the semidomestic red deer (*Cervus elaphus*) of New Zealand by Wada et al. (2010). Database homology searches showed that the mitochondrial DNA (mtDNA) sequence from the New Zealand semidomestic deer was similar to partial mtDNA sequences from the European, Norwegian (*C. e. atlanticus*) and Spanish red deer (*C. e. hispanicus*). Saebury et al. (2011) generated complete mitochondrial genome sequence and identified putative SNPs distributed throughout the white-tailed deer (*Odocoileus virginianus*) nuclear and mitochondrial genomes. A SNP validation study designed to test specific classes of putative SNPs provided evidence of 10,476 genome-wide SNPs in the dataset. Based on cytogenetic evidence for homology between cattle (*Bos taurus*) and white-tailed deer chromosomes, they demonstrated that a divergent genome may be used for estimation of the relative distribution and density of de *novo* contigs as well as putative SNPs for species without draft genome assemblies. Yang et al. (2012a) and Pan et al. (2013) determined complete mitochondrial genome of the Chinese Sika deer – Sichuan Sika deer (*Cervus nippon sichuanicus*) and the South China Sika deer (*Cervus nippon kopschi*). Kim et al. (2013) completed mitochondrial genome of a water deer subspecies (*Hydropotes inermis argyropus*). The close relatedness between Siberian red deer (*C. e. sibirica*) and North American wapiti (*C. e. canadensis*) based on mitochondrial DNA variation of cytochrome B gene confirmed Kuznetsova et al. (2012). Zhang and Zhang (2012) used mitochondrial DNA sequences to estimated phylogenetic relationships among animal taxa and for molecular phylogenetic evolution analysis. They prepared phylogenetic analyses of 19 species of *Cervidae*, with *Bos taurus* as the outgroup and used neighbour joining, maximum likelihood, maximum parsimony, and Bayesian inference methods on whole mitochondrial genome sequences.

Current studies prepared to examination in order to understand the origin, phylogeny, and phylogeography of the family *Cervidae* are mainly based on DNA sequence variation of mitochondrial protein – coding genes, analysed in species of deer represent most of the taxonomic diversity of the family.

2. Utilization of SNPs in deer as non-model species

The development of genetic markers in deer has followed the development of biochemistry and molecular biology, from the initial studies that utilized allozymes to studies that incorporate molecular markers derived from both mitochondrial DNA and the nuclear genome. Much of the work in the development of nuclear DNA markers has relied upon comparative work already completed for other species, in particular other ruminants (Hall, 2009). Single nucleotide polymorphisms (SNPs) are growing in popularity as a genetic markers for investigating evolutionary processes. A panel of SNPs is often developed by comparing large quantities of DNA sequence data across multiple individuals to identify polymorphic sites (Haynes and Latch, 2012). Genomic sequencing programmes in livestock species such as cattle and sheep have enabled the building and application of large SNP chip containing more than 50,000 markers. Other livestock species (non-model), including deer do not have a large scale genomic sequence or they do have other adequate supporting tools to enable trait to marker associations to be established (Bixley et al., 2009).

Single nucleotide polymorphisms are the most abundant type of genetic polymorphism in most, if not all, genomes (Slate et al., 2009). Genetic markers that were applied in past studies fall into two general categories: markers that identify anonymous genetic variation and markers that identify genetic variation in specific segments of genome. SNPs fall into the second category, but are broadly distributed and can represent variation in all of the different genomic regions (coding, non-coding, microsatellite, mitochondrial and chloroplast DNA) (Garvin et al., 2010). SNPs are attractive markers for many reasons, including the availability of high numbers of annotated markers, low-scoring error rates, relative ease of calibration among laboratories compared to length-based markers and the associated ability to assemble combined temporal and spatial data sets from multiple laboratories (Helyar et al., 2011). Additionally, the potential for high-throughput genotyping improved genotyping results for poor quality samples, a simple mutation model, and the ability to examine both neutral variation and regions under selection offers unparalleled scope for expansive screening of genomes and large sample sizes from natural populations (Smith et al., 2011). SNP discovery in many non-model organisms is still primarily performed with chain-termination (Sanger) sequencing (Seeb et al., 2011). Most of the studies attempted to address ascertainment bias including representative samples in the discovery panel, and some were able to use large sample sizes, but most included only a handful of samples. The number of potential

Faculty of Agriobiology and Food Resources, 2014
http://www.fapz.uniag.sk/
DOI: 10.15414/afz.2014.17.02.65–71

SNPs discovered and reported ranged from 2 to 1700, which demonstrated that large numbers of SNPs can be discovered with Sanger sequencing, although coast associated with larger studies were not available (Garvin et al., 2010). In model organisms, which are species with fully sequenced genomes, can be panels of SNPs devised to allow marker-trait association studies of high statistical power and accuracy (Brooks et al., 2010). Utilization of SNPs in study of non-model organisms is different, in connection with microsatellite markers can be used to detection of kinship and parentage (Hauser et al., 2011), individuals (Wiliams et al., 2010) and population structure (Morin et al., 2009). The newly mature next-generation sequencing technologies provide access to a wealth of sequence information on non-model organisms (Tautz et al., 2010).

Even though the next generation sequencing should reduce the cost of DNA sequencing, it is still outside the resources of many projects. One means of SNP discovery that does not require extensive sequencing is to use commercially available SNP chips developed for a related, well-studied model species (Haynes and Latch, 2012). In the last period have been used SNP chips from livestock to identify SNPs in closely related species to non-model species (Miller et al., 2011; Pertoldi et al., 2010), including deer. Bixley et al. (2009) have produced a reduced representational sequence of >160 million base pairs (Mbp), of which they mapped 44 Mbp to unique positions on the bovine genome. From this was selected 768 SNPs to be included in a Golden Gate (IlluminaTM) SNP chip. Subsequently have been assembled a mapping pedigree in order to quality control check these and other SNPs and to produce a genetic map. This mapping population was also used to assess recombination rates and to reorder the deer sequence from bovine physical order to deer order. Other immediate outputs from this SNP chip were new parentage assignment and breed composition panels. Haynes and Latch (2012) used the Bovine SNP50 BeadChip developed in cattle (*Bos taurus*) for identifying polymorphic SNPs in *Cervids Odocoileus hemionus* (mule deer and black-tailed deer) and *O. virginianus* (white-tailed deer) in the Pacific Northwest. They found that 38.7 % of loci could be genotyped, of which 5 % (n = 1068) were polymorphic. Of these 1068 polymorphic SNPs, a mixture of putatively neutral loci (n = 878) and loci under selection (n = 190) were identified with the F_{ST}-outlier method. A range of population genetic analyses were implemented using these SNPs and a panel of 10 microsatellite loci. The three types of deer could readily be distinguished with both the SNP and microsatellite datasets. This study demonstrates that commercially developed SNP chips are a viable means of SNP discovery for non-model organisms, even when used between very distantly related species (the *Bovidae* and *Cervidae* families diverged some 2 512 301 million years before present).

3. Significance of SNPs in genes important for different deer traits

Until now has been described in family *Cervidae* a number of genetic markers (or candidate genes) affecting fitness-related traits. At the present are identified through sequencing mainly SNPs of individual genes such as the major histocompatibility complex, reproductive and growth hormones and the prion protein genes (Hall, 2009; Slate et al., 2002).

3.1 Genes encoding major histocompatibility complex

The major histocompatibility complex (MHC) is highly polymorphic genomic region that is divided into three tightly linked regions, termed class I, class II, and class III (Wan et al., 2011). Genes encoding MHC molecules are the most polymorphic genes described in vertebrates with polymorphism occurring predominantly at peptide binding site (Winter et al., 1995). DR and DQ genes have been identified as two-principal class II molecule in ruminants. They are tightly linked with class III and class I genes (Van Eijk et al., 1995). The primarily role of the MHC is recognize foreign proteins, present them to specialist immune cells and initiate an immune response. The MHC can reflect the fitness and adaptive potential of a given species due to its association with the immune system (Liu et al., 2013). MHC genes encode cell surface glycoproteins that bind and present antigenic peptides to T cells. Individuals from natural populations deal constantly with diverse range of pathogens and the polymorphism at MHC loci determines the diversity of foreign antigens that the host immune system can recognize (Fernández de Mera et al., 2009). The MHC has also been implicated in mate selection and antler development may be associated with pathogen resistance in deer and thus could be a signal of genetic quality (Kennedy et al., 2010). The MHC class II genes encode polymorphic cell-surface glycoproteins comprising non-covalently linked α and β subunits. These play a pivotal role in the initiation of the immune response to pathogen-derived peptide antigens (Hughes and Yeager, 1998). The second exon has been shown to be highly polymorphic and under positive selection, and the class II DQA gene has recently attracted more attention (Goüy et al., 2009). In artiodactyls, research on the DQ gene structure and polymorphisms of economically important animals such as cattle and sheep is remarkably extensive (Zhou and Hickford, 2004). In contrast, studies on MHC class II genes in deer are largely restricted to the DRB locus (Fernández de Mera et al., 2009; Kennedy et al., 2010; Li et al., 2012; Li

Faculty of Agriobiology and Food Resources, 2014
http://www.fapz.uniag.sk/
DOI: 10.15414/afz.2014.17.02.65–71

et al., 2013), only rarely considering the DQ gene (Wan et al., 2011; Wu et al., 2012; Liu et al., 2013).

3.2 Growth hormone gene

Many studies in this case evaluated genes, which affect antler growth, because antler belongs to the most important products of deer farming with great economic value. Antler is one of the fastest growing parts of deer body and can be considered as the secondary sex characteristics of male deer (Bartos et al., 2009). Antler formation and growth is mainly controlled by the concentration of sex hormones including progesterone, thyroid hormone, adrenocortical hormone and chorionic gonadotropin (Bubenik et al., 1997; Li et al., 2003; Bartos et al., 2009), but few molecular studies analysed and associated antler growing traits with candidate genes encoding growth hormone (GH) and major histocompatibility complex (Li, 2003; Du and Bai, 2004; Wallis et al., 2006).

Pituitary growth hormone (GH) is a protein hormone from the pituitary gland which is found in most vertebrates, and which regulates overall somatic growth and various aspects of metabolism. In mammals, GH is generally a strongly conserved protein, but in primates and cetartiodactyls (*Cetacea* plus *Artiodactyla*) bursts of rapid evolution led to GHs that differ considerably from those of other mammals (Wallis et al., 2006).

Growth hormone secretion from anterior pituitary is regulated by the hypothalamus and the principal physiological regulation mechanisms of GH secretion are neural endogenous rhythm, sleep, stress, exercise, and nutritional and metabolic signals (Møller and Jørgensen, 2009). Growth hormone is essential for normal linear growth and the attainment of an adult mature height, and it also has roles during cartilage growth and the attainment of normal bone mass (Bennett, 2005). The genetic polymorphism and potential effects of GH gene have been intensively studied in domestic animals such as cattle and pigs and wild animals like red deer (Wallis et al., 2006; Zhang et al., 2011; Yang et al., 2012b).

Another analyzed gene as candidate for antler growth was gene encoding androgen receptor (AR) (Xiong et al., 2012). Androgen is important for male reproductive organ development and function maintenance. Androgen receptor is one of type I steroid receptors and is a ligand-development transregulator protein. Bubenik et al. (2002) showed that the antler cycle is very sensitive to manipulation of androgen levels. These studies showed that antler growing is process affected with several genes and therefore is screening more candidate very important. Potential molecular markers related to antler growth could be utilized for marked assisted selection programs in deer farming.

3.3 Prion protein gene

The genetic of the prion protein (PRNP) play a crucial role in determining the relatively susceptibility to transmissible spongioform encephalopathies (TSEs) in several mammalian species (Peletto et al., 2009). Transmissible spongiform encephalopathy (TSE), or prion diseases, are a group of infectious neurodegenerative diseases, which leads the hosts to death. Without available healing and prevention programs, TSE becomes more important as new researches have shown its comprehensive global spread and the large number of animal groups susceptible to developing TSEs. The most popular TSEs are Creutzfeldt-Jacob disease in humans, Bovine Spongiform Encephalopathy (BSE), and scrapie in ovine. Another prion disease less known, but not less important, is the Chronic Wasting Disease (CWD) which attacks animals from *Cervidae* family, and is the only form of TSE that attacks wild animals (Falcão and Garcia, 2012). CWD is a prion disease of North American cervids, currently affecting both captive and wild elk (*Cervus elaphus*), mule deer (*Odocoileus hemionus*), white-tailed deer (*Odocoileus virginianus*), and moose (Alces alces) (Matsumoto et al., 2012). Disease management in wild cervids populations has been severaly impeded by efficient horizontal transmission of the disease agent, which has resulted in substantial economic losses to farming, gaming, and tourism industries (Bishop, 2004). Direct and indirect transmission is result from prion infectivity in various tissues fluids, and carcasses of infected animals (Mathiason et al., 2006). The degree of similarity of amino acid sequence of the *Prnp* gene among different species will have consequences on the transmission of TSEs among these species. Often, the same polymorphisms in two species result in similar effects with respect to susceptibility to prion disease (Goldmann, 2008). Associations between variation in the primary sequence of the prion protein gene and disease modulation have been shown for CWD and a number of studies have analysed the genetic variability of the PRNP gene in cervids species (Peletto et al., 2009; Jeong et al., 2009; Ernest et al., 2010; Cullingham et al., 2011).

4. Conclusions

Finally, single nucleotide polymorphisms are used for number of different applications in molecular genetics research of deer species, which are important for conservation and utilization of their genetic diversity. In addition SNPs can be used also as genetic markers for fitness-related or economic important traits of deer. The application of SNPs to genetic studies will continue to expand because SNPs are abundant, co-dominant markers that are broadly distributes in genomes and amenable to high-throuhput screening. Advances in DNA sequencing and genotyping technologies are now

Faculty of Agriobiology and Food Resources, 2014
http://www.fapz.uniag.sk/
DOI: 10.15414/afz.2014.17.02.65–71

viable also for any non-model organisms, but much progress is likely to be made in deer through the use of genome sequence data from other ruminants. Few studies demonstrates that commercially developed SNP chips are a viable means of SNP discovery for non-model organisms, even when used between very distantly related species.

5. Acknowledgements

This work was supported by the Slovak Research and Development Agency under the contract No. APVV-0636-11.

6. References

BARTOS, L., SCHAMS, D. and BUBENIK, G. A. (2009) Testosterone, but not IGF-1,LH, prolactin or cortisol, may serve as antler-stimulating hormone in red deer stags (*Cervus elaphus*). In *Bone*, vol. 44, no. 4, pp. 691–698.
DOI: http://dx.doi.org/10.1016/j.bone.2008.12.004.

BENNETT, R. (2005) Growth hormone in musculoskeletal pain states. In *Current Pain and Headache Reports*, vol. 9, no. 5, pp. 331–338. DOI: http://dx.doi.org/10.1007/s11916-005-0009-4.

BISHOP, R. C. (2004) The economic impacts of chronic wasting disease (CWD) in Wisconsin. In *Human Dimensions of Wildlife*, vol. 9, no. 3, pp. 181–192.
DOI: http://dx.doi.org/10.1080/10871200490479963.

BIXLEY, M. J. et al. (2009) Building a deer SNP chip. In *Matching genetics and environment: a new look at an old topic*. In *Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics*, Barossa Valley, South Australia, 28.9 – 1.11. 2009, Australia, pp. 300–303.

BO, L., YANCHUN, X. and JIANZHANG, M. (2013) Allelic characterization of the second DRB locus of major histocompatibility complex class II in Ussuri sika deer (*Cervus nippon hortulorum*): highlighting the trans-species evolution of DRB alleles within *Cervidae*. In *Animal Cells and Systems*, vol. 17, no. 4, pp. 269–276.
DOI: http://dx.doi.org/10.1080/19768354.2013.826280.

BROOKS, S. A. et al. (2010) Whole-genome SNP association in the horse: identification of a deletion in myosin Va responsible for lavender foal syndrome. In *PLoS Genetics*, vol. 6, e1000909. DOI: http://dx.doi.org/10.1371/journal.pgen.1000909.

BUBENIK, G. A. et al. (1997) Seasonal levels of reproductive hormones and their relationship to the antler cycle of male and female reindeer (*Rangifer tarandus*). In *Comparative Biochemistry and Physiology – Part B*, vol. 116, no. 2, pp. 269–277.
DOI: http://dx.doi.org/10.1016/S0305-0491(97)00183-1.

BUBENIK, G. A. et al. (2002) Effect of antiandrogen cyproterone acetate on the development of the antler cycle in Southern pudu (*Pudu puda*). In *Journal of Experimental Zoology*, vol. 292, no. 4, pp. 393–401. DOI: http://dx.doi.org/10.1002/jez.10046.

CULLINGHAM, C. I. et al. (2011) Multi-scale population genetic analysis of mule deer (*Odocoileus hemionus hemionus*) in western Canada sheds new light on chronic wasting disease spread. In *Canadian Journal of Zoology*, vol. 89, no. 2, pp. 134–147. DOI: http://dx.doi.org/10.1139/Z10-104.

DU, Z. H. and BAI, X. J. (2004) Cloning and sequencing analysis of GH-I gene in sika deer. In *Journal of Economic Animal*, vol. 8, no. 3, pp. 131–134.

ERNEST, H. B. et al. (2010) Molecular genealogy tools for white--tailed deer with chronic wasting disease. In *Canadian Journal of Veterinary Research*, vol 74, no. 2, pp. 153–156.

FALCÃO, C. B. R. and GARCIA, J. E. (2012) Chronic wasting disease: the prion disease of cervids. In *ARS veterinaria, Jaboticabal, SP*, vol. 28, no. 1, pp. 13–21.

FERNÁNDEZ DE MERA I. G. et al. (2009) Impact of major histocompatibility complex class II polymorphisms on Iberian red deer parasitism and life history traits. In *Infection, Genetics and Evolution*, vol. 9, no. 6, pp. 1232–1239.
DOI: http://dx.doi.org/10.1016/j.meegid.2009.07.010.

GARVIN, M. R., SAITOH, K. and GHARRETT, A. J. (2010) Application of single nucleotide polymorphisms to non--model species: a technical review. In *Molecular Ecology Resources*, vol. 10, no. 6, pp. 915–934.
DOI: http://dx.doi.org/10.1111/j.1755-0998.2010.02891.x.

GILBERT, C., ROPIQUET, A. and HASSANIN, A. (2006) Mitochondrial and nuclear phylogenies of *Cervidae* (*Mammalia*, *Ruminantia*). In *Systematics, morphology, and biogeography. Molecular Phylo-genetics and Evolution*, vol. 40, no. 1, pp. 101–117. DOI: http://dx.doi.org/10.1016/j.ympev.2006.02.017.

GOLDMANN, W. (2008) PrP genetics in ruminant transmissible spongiform encephalopathies. In *Veterinary Research*, vol. 39, no. 4, pp. 30. DOI: http://dx.doi.org/10.1051/vetres:2008010.

GOÜY DE BELLOCQ, J. et al. (2009) Evolutionary history of an MHC gene in two leporid species: characterisation of Mhc-DQA in the European brown hare and comparison with the European rabbit. In *Immunogenetics*, vol. 61, no. 2, pp. 131–44.
DOI: http://dx.doi.org/10.1007/s00251-008-0349-4.

GRUBB, P. and GROVES, C. P. (2003) *Relationships of living deer. In: WEMMER, C. M. (eds.) Biology and Management of the Cervidae*. Washington: Smithsonian Institution Press, pp. 21–59.

HALL, R. J. (2009) Deer. In Cockett, N. E. and Chittaranjan, K. (eds.) *Genome Mapping and Genomics in Domestic Animals*. Heidelberg: Springer-Verlag Berlin, pp. 47–74.

HARTL, G. B., ZACHOS, F. and NADLINGER, K. (2003) Genetic diversity in European red deer (*Cervus elaphus* L.): anthropogenic influences on natural populations. In *Comptes Rendus Biologies*, vol. 326, supplement 1, pp. 37–S42.
DOI: http://dx.doi.org/10.1016/S1631-0691(03)00025-8.

HAUSER, L. et al. (2011) An empirical comparison of SNPs and microsatellites for parentage and kinship assignment in a wild sockeye salmon (*Oncorhynchus nerka*) population. In *Molecular Ecology Resources*, vol. 11, supplement 1, pp. 150–161. DOI: http://dx.doi.org/10.1111/j.1755-0998.2010.02961.x.

HAYNES, G. D. and LATCH, E. K. (2012) Identification of novel single nucleotide polymorphisms (SNPs) in deer (*Odocoileus* spp.) using the BovineSNP50 BeadChip. In *PLoS One*, vol. 7, e36536. DOI: http://dx.doi.org/0.1371/journal.pone.0036536.

HELYAR, S. J. et al. (2011) Application of SNPs for population genetics of nonmodel organisms: new opportunities and challenges. In *Molecular Ecology Resources*, vol. 11, supplement 1, pp. 123–136.
DOI: http://dx.doi.org/10.1111/j.1755-0998.2010.02943.x.

HUGHES, A. L. and YEAGER, M. (1998) Natural selection at major histocompatibility complex loci of vertebrates. In *Annual Review of Genetics*, vol. 32, no. , pp. 415–435.
DOI: http://dx.doi.org/10.1146/annurev.genet.32.1.415.

JEONG, H. J. et al. (2009) Single-nucletide polymorphisms in prion protein gene of Korean subspecies of Chinese water deer

(*Hydropotes inermis argyropus*). In *Korean Journal of Veterinary Research*, vol. 49, no. 1, pp. 59–62.

KENNEDY, L. J. et al. (2010) Genetic diversity of the major histocompatibility complex class II in *Alaskan caribou* herds. In *International Journal of Immunogenetics*, vol. 38, no. 2, pp. 109–119. DOI: http://dx.doi.org/10.1111/j.1744-313X.2010.00973.x.

KIM, E. K. et al. (2013) Complete mitochondrial genome of a water deer subspecies, Hydropotes inermis argyropus (*Cervidae*: *Hydropotinae*). In *Mitochondrial DNA*, vol. 24, no. 1, pp. 17–18.
DOI: http://dx.doi.org/10.3109/19401736.2012.710229.

KUZNETSOVA, M. V., DANILKIN, A. A. and KHOLODOVA, M. V. (2012) Phylogeography of red deer (*Cervus elaphus*): Analysis of MtDNA cytochrome b polymorphism. In *Biology Bulletin*, vol. 39, no. 4, pp 323–330.
DOI: http://dx.doi.org/10.1134/S1062359012040048.

LI, B. (2003) *A Study on the Polymorphism of MHC-DRB Genes and Their Relatedness to the Antler Productivity in Sika Deer (Cervus Nippon*). Northeast Forestry University.

LI, L. et al. (2012) Characterization of major histocompatibility complex DRA and DRB genes of the forest musk deer (*Moschus berezovskii*). In *Chinese Science Bulletin*, vol. 58, no. 18, pp. 2191–2197. DOI: http://dx.doi.org/10.1007/s11434-012-5581-5.

LIU, D. Z. et al. 2013. Polymorphisms in major histocompatibility complex class IIα genes are associated with resistance to infectious hematopoietic necrosis in rainbow trout, Oncorhynchus mykiss (Walbaum, 1792). In *Journal of Applied Ichthyology*, vol. 29, no. 6, pp. 1234–1240.
DOI: http://dx.doi.org/10.1111/jai.12326.

LUDT, C. J. et al. (2004) Mitochondrial DNA phylogeography of red deer (*Cervus elaphus*). In *Molecular Phylogenetics and Evolution*, vol. 31, no. 3, pp. 1064–1083.
DOI: http://dx.doi.org/10.1016/j.ympev.2003.10.003.

MATHIASON, C. K. et al. (2006) Infectious prions in the saliva and blood of deer with chronic wasting disease. In *Science*, vol. 314, no. 5796, pp. 133–136.
DOI: http://dx.doi.org/10.1126/science.1132661.

MATSUMOTO, T. et al. (2012) Association mapping of genetic risk factors for chronic wasting disease in wild deer. In *Evolutionary Applications*, vol. 6, no. 2, pp. 340–342.
DOI: http://dx.doi.org/10.1111/eva.12003.

MILLER, J. et al. (2011) A genome-wide set of SNPs detects population substructure and long range disequilibrium in wild sheep. In *Molecular Ecology Resources*, vol. 11, no. 2, pp. 314–322. DOI: http://dx.doi.org/10.1111/j.1755-0998.2010.02918.x.

MØLLER, N. and JØRGENSEN, J. O. (2009) Effects of growth hormone on glucose, lipid, and protein metabolism in human subjects. In *Endocrine Reviews*, vol. 30, no. 2, pp. 152–177. DOI: http://dx.doi.org/10.1210/er.2008-0027.

MORIN, P. A., MARTIEN, K. K. and TAYLOR, B. L. (2009) Assessing statistical power of SNPs for population structure and conservation studies. In *Molecular Ecology Resources*, vol. 9, no. 1, pp. 66–73.
DOI: http://dx.doi.org/10.1111/j.1755-0998.2008.02392.x.

PAN H. CH. et al. (2013) The complete mitochondrial genome of sika deer *Cervus nippon* (*Cetartiodactyla*: *Cervinae*) South Anhui population. In *Mitochondrial DNA*, Ahead of Print, pp. 1–2.

PELETTO, S. et al. (2009) Genetic variability of the prion protein gene (PRNP) in wild ruminants from Italy and Scotland. In *Journal of Veterinary Science*, vol. 10, no. 2, pp. 115–20.

PERTOLDI, C. et al. (2010) Genome variability in European and American bison detected using BovineSNP50 BeadChip. In *Conservation Genetics*, vol. 11, no. 2, pp. 627–634.
DOI: http://dx.doi.org/10.1007/s10592-009-9977-y.

SEABURY, C. M. et al. (2011) Genome-wide polymorphism and comparative analyses in the whitetailed deer (*Odocoileus virginianus*): a model for conservation genomics. In *Plos One*, vol. 6, e15811.
DOI: http://dx.doi.org/10.1371/journal.pone.0015811.

SEEB, J. E. et al. (2011) Single nucleotide polymorphism (SNP) discovery and application of SNP genotyping in nonmodel organisms. In *Molecular Ecology Resources*, vol. 11, supplement 1, pp. 1–8.
DOI: http://dx.doi.org/10.1111/j.1755-0998.2010.02979.x.

SIGURDSON, C. J. and AGUZZI, A. 2007. Chronic wasting disease. In *Biochimica et Biophysica Acta*, vol. 1772, no. 6, pp. 610–618.
DOI: http://dx.doi.org/10.1016/j.bbadis.2006.10.010.

SLATE, J. et al. (2002) A deer (subfamily *Cervinae*) genetic linkage map and the evolution of ruminant genomes. In *Genetics*, vol. 160, no. 4, pp. 1587–1597.

SLATE, J. et al. (2009) Gene mapping in the wild with SNPs: guidelines and future directions. In *Genetica*, vol. 136, no. 1, pp. 97–107. DOI: http://dx.doi.org/10.1007/s10709-008-9317-z.

SMITH, M. (2011) Multiplex preamplification PCR and microsatellite validation allows accurate single nucleotide polymorphism (SNP) genotyping of historical fish scales. In *Molecular Ecology Resources*, vol. 11, supplement 1, pp. 268–277. DOI: http://dx.doi.org/10.1111/j.1755-0998.2010.02965.x.

TAUTZ, D., ELLEGREN, H. and WEIGEL, D. (2010) Next generation molecular ecology. In *Molecular Ecology*, vol. 19, supplement 1, pp. 1–3.
DOI: http://dx.doi.org/10.1111/j.1365-294X.2009.04489.x.

VAN EIJK, M. J. (1995) Genetic mapping of BoLA-A, CYP21, DRB3, DYA, and PRL on BTA23. In *Mammalian Genome*, vol. 6, no. 2, pp. 151–152. DOI: http://dx.doi.org/10.1007/BF00303266.

WADA, K. et al. (2010) The Complete Mitochondrial Genome of the Domestic Red Deer (*Cervus elaphus*) of New Zealand and Its Phylogenic Position within the Family *Cervidae*. In *Journal of Animal Science*, 2010, vol. 81, no. 5, pp. 551–557.
DOI: http://dx.doi.org/10.1111/j.1740-0929.2010.00799.x.

WALLIS, O. C. et al. (2006) Polymorphism of the growth hormone gene of red deer (*Cervus elaphus*). In *General and Comparative Endocrinology*, vol. 146, no. 2, pp. 180–185.
DOI: http://dx.doi.org/10.1016/j.ygcen.2005.10.001.

WAN, Q. H. et al. (2004) Which genetic marker for which conservation genetics issue?. In *Electrophoresis*, vol. 25, no. 14, pp. 2165–2176.
DOI: http://dx.doi.org/10.1002/elps.200305922.

WAN, Q. H. et al. (2011) A Novel HURRAH Protocol Reveals High Numbers of Monomorphic MHC Class II Loci and Two Asymmetric Multi-Locus Haplotypes in the Père David's Deer. In *PLoS One*, vol. 6, no. 1, e14518.
DOI: http://dx.doi.org/10.1371/journal.pone.0014518.

WILLIAMS, L. M. et al. (2010) SNP identification, verification, and utility for population genetics in a non-model genus. In *BMC Genetics*, vol. 11, no. 32.
DOI: http://dx.doi.org/10.1186/1471-2156-11-32.

WILSON, D. E. and REEDER, D. M. (2005) Mammals Species of the World: A taxonomic and Geographic Reference. 3rd ed. Baltimore: The Jonhs Hopkins University Press.

WINTER, W. E. BUCK, R. H. and VERGA-HOUSE, D. A. (1995) Class I and class II major histocompatibility complex molecules. In *Neuroimmunology*, vol. 24, pp. 61–88.

WU, H. L. et al. (2012) Insight into gene evolution within *Cervidae* and *Bovidae* through genetic variation in MHC-DQA in the black muntjac (*Muntiacus crinifrons*). In *Genetic Molecular Research*, vol. 11, no. 3, pp. 2888–2898.
DOI: http://dx.doi.org/10.4238/2012.May.15.13

XIONG, J. et al. (2012) Identification of Genetic Variants Within Androgen Receptor Gene of Sika Deer and its Association with Antler Production. In *Journal of Animal and Veterinary Advances*, vol. 11, no. 12, pp. 2059–2063.
DOI: http://dx.doi.org/10.3923/javaa.2012.2059.2063.

YANG, F. et al. (2012b) Investigation of genetic effect of growth hormone gene on antler production in Chinese Sika deer *Cervus nippon*. In *African Journal of Biotechnology*, vol. 11, no. 101, pp. 16630–16634. DOI: http://dx.doi.org/10.5897/AJB11.2659.

YANG, CH. et al. (2012a) The complete mitochondrial genome of the Chinese Sika deer (*Cervus nippon* Temminck, 1838), and phylogenetic analysis among *Cervidae*, *Moschidae* and *Bovidae*. In *Journal of Natural History*, vol. 46, no. 27–28, 2012, pp. 1747–1759. DOI: http://dx.doi.org/10.1080/00222933.2012.693959.

ZACHOS, F. E. et al. (2003) On the phylogeographic origin of the Corsican red deer (*Cervus elaphus corsicanus*): evidence from microsatellites and mitochondrial DNA. In *Mammalian Biology*, vol. 68, no. 5, pp. 284–298.
DOI: http://dx.doi.org/10.1078/1616-5047-00097.

ZHANG C. et al. (2011). The association of two single nucleotide polymorphisms (SNPs) in growth hormone (GH) gene with litter size and superovulation response in goat-breeds. In *Genetics and Molecular Biology*, vol. 34, no. 1, pp. 49–55.
DOI: http://dx.doi.org/10.1590/S1415-47572010005000110.

ZHANG, W. Q. and ZHANG, M. H. (2012) Phylogeny and evolution of *Cervidae* based on complete mitochondrial genomes. In *Genetic Molecular Research*, vol. 11, no. 1, pp. 628–635. DOI: http://dx.doi.org/10.4238/2012.March.14.6.

ZHOU, H. and HICKFORD, J. G. (2004) Allelic polymorphism in the ovine DQA1gene. In *Journal of Animal Science*, vol. 82, no. 1, pp. 8–16.

Faculty of Agriobiology and Food Resources, 2014
http://www.fapz.uniag.sk/
DOI: 10.15414/afz.2014.17.02.65–71