DETECTION OF POLYMORPHISMS AND FECUNDITY DETERMINATION IN Axis axis Erxleben, Rusa timorensis Blainville AND Rusa unicolor Kerr RAISED IN LENGGONG, PERAK, MALAYSIA

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In animal breeding and conservation programmes selection is usually based on fecundity traits. Selection methods such as the traditional marker-assisted selection, which is based on observable phenotypes and genomic selection, which uses genomic features for selection and it can be genome-wide scanning or the candidate gene approach are employed. These candidate genes are polymorphic and their polymorphism is associated with traits of interest. Polymorphisms in form of SNPs and RFLPs have been employed to select animals for breeding and or conservation. This study is therefore, aimed at discovering polymorphisms in the protein-coding region of five fecundity genes: BMP15, FOXL2, GDF9, MHCDQA1 and MTNR1A in *Axis axis Erxleben*, *Rusa timorensis Blainville* and *Rusa unicolor Kerr* reared at PTH Lenggong.

This study applied cytogenetic methods to detect morphological and numeric chromosomal aberrations in three breeds of deer comprising 60 individuals. Following the discovery of chromosomal aberrations, DNA was obtained from 45 individuals to amplify the protein coding regions of the fecundity genes, through high fidelity PCR. The genes were confirmed by mapping on metaphase chromosomes through Fluorescent *in situ* Hybridization (FISH). The PCR products were thereafter sequenced by Sanger's method. Following sequencing, a combination of Bioinformatic tools were used to detect SNPs and RFLPs in the fecundity genes. The genes were translated into proteins and analyzed for structure and function. Prediction programs and phylogenetic analysis were used to generate wild type proteins, which were used as templates to predict protein structure and the effect of amino acid substitutions on protein function.

Fifteen of the 60 animals were found to carry chromosome aberrations. High fidelity PCR produced 225 sequences, which were confirmed by FISH and used in the downstream analysis. A total of 117 SNPs and 13 restriction sites with utility in animal selection were discovered in the protein coding regions of the fecundity genes through scan. After protein translation 19 variants were discovered; 3 in BMP15, 4 in FOXL2, 2 in GDF9, 3 in MHCDQA1 and 7 in MTNR1A. 11 of the variants carry neutral substitution and are therefore predicted to be functional. Based on the protein analysis 10 out of the 45 animals; TP27F, TF375, TP14F, TN60M, SJ4M, AX1, AX4F, AX3F, AX6F, AX7F were predicted to carry a combination of functional fecundity proteins.

A large number of animals within the study population carry chromosomal aberration. Significant genetic diversity exists in the study population and some animals carry defective fecundity protein variants. The presence of chromosomal anomaly and protein polymorphisms, with some variant predicted to carry deleterious amino acid substitutions, may be one of the reasons for fertility decline in the study population. There is evidence of hybridization between *R. timorensis Blainville* and *R. unicolor Kerr*. *Axis axis Erxleben* is likely to have undergone inbreeding and allele fixation. It is concluded that the type of husbandry practiced in PTH Lenggong, Perak, where animals of different breeds are kept together, and the absence of a well-designed breeding program for the deer, might be responsible for these fertility problems.

Keywords: Cytogenetics, Chromosomal aberration, Deer, Fecundity, Fertility decline, Protein prediction

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

PENGESANAN KELAINAN KROMOSOM DAN POLIMORFISME DALAM SEGMEN PENGEKODAN PROTEIN DARIPADA LIMA GEN KESUBURAN DALAM *Axis axis* Erxleben, *Rusa timorensis* Blainville dan *Rusa unicolor* Kerr DI LENGGONG, PERAK, MALAYSIA

Oleh

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Dalam program untuk pembiakan dan pemuliharaan haiwan, secara lazimnya pemilihan adalah berdasarkan ciri-ciri kesuburan. Kaedah pemilihan seperti pemilihan tradisi berbantu penanda berasaskan ciri fenotip dan pemilihan genomik berasaskan imbasan sebaran genom atau pendekatan gen calon telah digunakan. Calon gen ini adalah polimorfik dan polimofismenya berkait dengan ciri yang berkepentingan. Polimorfisme dalam bentuk SNP dan RFLP telah digunakan untuk memilih haiwan untuk tujuan pembiakan dan pemuliharaan. Dari itu kajian ini menumpu kepada pencarian polimorfisme dalam bahagian pengekodan protein untuk 5 gen kesuburan: BMP15, FOXL2, GDF9, MHCDQA1 dan MTNR1A dalam kumpulan rusa baka-baka *Axis axis Erxleben, Rusa timorensis Blainville* dan *Rusa unicolor Kerr* yang dipelihara di PTH Lenggong.

Kajian ini menggunakan kaedah sitogenetik untuk mengesan kecacatan morfologi dan kromosom numerik dalam 3 jenis baka rusa yang terdiri daripada 60 individu. Berikutan terdapatnya kecacatan kromosom, DNA telah diperolehi daripada 45 individu untuk meluaskan bahagian pengekodan protein bagi gen kesuburan dengan menggunakan PCR berketepatan tinggi. Gen ditentukan secara pemetaan kromosom metafasa melalui *Fluorescent in situ Hybridization* (FISH). Produk PCR kemudianya disusun mengikut kaedah Sanger. Dengan menggunakan sekumpulan peralatan Bioinformatik, SNP dan RFLP untuk gen kesuburan telah dikenal pasti. Gen kemudiannya diterjemahkan kepada protein untuk analisis struktur dan fungsi. Program ramalan dan analisis filogenetik digunakan untuk menghasilkan protein bentuk liar yang dijadikan templat untuk meramalkan struktur protein dan kesan penggantian asid amino terhadap fungsi protein.

Sebanyak 15 daripada 60 individu didapati membawa kecacatan kromosom. PCR berketepatan tinggi menghasilkan 225 susunan yang disahkan secara FISH dan digunakan dalam analisis hiliran. Dengan menggunakan teknik imbasan, 117 SNP dan 13 tapak sekatan yang berguna untuk pemilihan haiwan dalam bahagian pengekodan protein bagi gen kesuburan telah ditemui. Selepas penterjemahan protein, 19 varian ditemui: 3 dalam BMP15, 4 dalam FOXL2, 2 dalam GDF9, 3 dalam MHCDQA1 dan 7 dalam MTNR1A. Sejumlah 11 varian membawa penggantian neutral, dari itu diramalkan berfungsi. Analisis protein mendapati 10 daripada 45 individu: TP27F, TF375, TP14F, TN60M, SJ4M, AX1, AX3F, AX4F, AX6F dan AX7F diramalkan membawa satu kombinasi protein kesuburan yang berfungsi.

Sejumlah besar individu dalam kumpulan yang dikaji membawa kecacatan kromosom. Terdapat wujudnya kepelbagaian genetik yang signifikan dalam kumpulan kajian ini dan sebahagian individu membawa varian terencat bagi protein kesuburan. Kehadiran anomali kromosom dan polimorfisme protein dengan beberapa varian diramalkan membawa penggantian asid amino mungkin menyebabkan penurunan tahap kesuburan dalam kumpulan kajian ini. Terdapat bukti berlakunya hibridisasi di antara *Rusa timorensis Blainville* dan *Rusa unicolor Kerr*. *Axis axis Erxleben* berkemungkinan juga telah melalui pembiakan dalaman dan pengekalan allel. Kesimpulannya, masalah kesuburan dalam kumpulan rusa di PTH Lenggong, Perak boleh dikaitkan dengan amalan menempatkan haiwan pelbagai baka dalam satu kumpulan dan tidak mengamalkan program pembiakan haiwan yang teratur.

Kata kunci: Sitogenetik, kecacatan kromosom, Rusa, kesuburan, masalah kesuburan, ramalan protein

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This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Doctor of Philosophy. The members of the Supervisory Committee were as follows:

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LIST OF ABBREVIATIONS

AF	Agitation Frequency
BCIP	5-bromo-4-chloro-3-indolyl-phosphate
BLAST	Basic Local Alignment Search Tool
BMP	Bone Morphogenetic Proteins
CCI	Calving-conception interval
CNV	Copy number variations
CCD	Charge-coupled Device
CGH	Comparative Genomic Hybridization
CM	Culture Medium
CI	Centromeric index
DOP-PCR	Degenerate Oligonucleotide Primed PCR
DKCL	Duration of cells in KCL
DAPI	4′,6-diamidino-2-phenylindole
ExPASy	Expert Protein Analysis System
FISH	Fluorescent *in situ* hybridization
FPG	Fluorochrome-Photolysis Giemsa
FBS	Fetal Bovine Serum
GDF	Growth Differentiation Factors
ISH	*in situ* hybridization
KCl	Potassium chloride
MEGA	Molecular Evolutionary Genetics Analysis
MHCDQA	Major Histocompatibility Complex DQ Alpha
MTNR1A	Melatonin Receptor 1A

NOR	Nucleolar Organizer Region
NBT	Nitro Blue Tetrazolium
OECD	Organization for Economic Co-operation and Development
PBMC	Peripheral Blood Mononuclear Cells
PGD	Preimplantation genetic diagnosis
QTL	Quantitative Trait Loci
PRINS	Primed *in situ* DNA
ProtParam	Protein Parameters tool
PROVEAN	Protein Variation Effect Analyzer
RFLP	Restriction Fragment Length Polymorphisms
SNP	Single Nucleotide Polymorphisms
STELA	Single Telomere Lengths
SMS	Sequence Manipulation Suite
SIFT	Sorting the intolerant from tolerant
TGF-beta	Transforming Growth Factor Beta
TL	Total Chromosome Length

CHAPTER 1

INTRODUCTION

1.1 Background of the study

Fecundity traits are an important selection requirement for animal breeding and conservation programmes. Animals, which are prolific and adaptive to environmental conditions, are desirable, as they fit the objective of many of such production systems. To select animals for breeding a number of selection methods are employed; these methods include the traditional marker-assisted selection, which is based on observable phenotypes and genomic selection, which uses genomic features for selection (Meuwissen, Hayes, & Goddard, 2016) and it can either be genome-wide scanning or the candidate gene approach. The latter is largely considered today because of its reliability and shorter time requirement. Selection based on candidate genes is a molecular-marker-assisted selection that has gained acceptance and is widely used among breeders and researchers (Meuwissen *et al.,* 2016)

Loss of fecundity is a serious issue that must be addressed immediately whenever it is reported in livestock production centers. It often results in immeasurable economic losses to the livestock industry (Lee & Kim, 2007).To address loss of fecundity in livestock, adequate supporting tools such as fertility and fitness data are used. Fertility data include non-return rate, calving-conception interval (CCI), calving-to-first service interval, conception (pregnancy) rate, heat detection assessment, In-calf rate. Other composite measures include; fertility factor, FERTEX score and fertility index and data on fitness such as disease resistance and so on (Buaban *et al.,* 2015). The application of these data to propagate animals has played a pivotal role in the animal industry through both traditional and molecular animal selection methods (Matoušek, 1986). The advancement in molecular methods along with phenotypic records has contributed to genomic data for more accurate and rapid propagation of animal genetic resources. Currently, without fertility data it is almost impossible to attempt fertility assessment and its improvement (Nani *et al.,* 2019).

Generally, genetic evaluation starts by the analysis of phenotypes to identify genetic influences, while molecular genetics usually begins with known alleles or DNA sequences and later analyze their influence on phenotypes (Rexroad *et al.,* 2019).

The identification of genome regions and genes related to important phenotypic traits allows for selecting animals based on genetic markers that are linked with such traits. These genetic markers include genes or DNA sequences with observable variations, known as polymorphisms, among members of animal groups (Rexroad *et al.,* 2019).

Genetic polymorphisms in the form of Chromosomal polymorphisms, Copy number variations (CNVs), mini and microsatellites, Restriction Fragment Length Polymorphisms (RFLPs), Single Nucleotide Polymorphisms (SNPs), and other forms of variations within DNA sequences have been used as markers in population and evolutionary genetics (Bauduer et al, 2009), systematics, molecular phylogeny and agricultural genetics (Spiridonova et al, 2017). They have afforded scientists the ability to tag genes and other pieces of DNA through multiple alleles at individual loci. Polymorphisms have been used in areas from genotype investigations; mapping of quantitative loci affecting economic traits in animals and plants; mapping of disease genes; and evolutionary comparisons of DNA sequences to chromosome organizations between related species (Borowski *et al.,* 2016; Carranza *et al.,* 2016). Genes with such variations are known as candidate genes.

Candidate genes are sequenced genes and genetic variations with known biological pathway that are involved in the physiology or development of traits of interest. Biological understanding of the role of the product of the wild-type of these genes forms the basis for their selection as candidate gene (Katzeff *et al.,* 2019). Those candidate genes with distinct role in reproduction and survival are referred to as fecundity genes (Abdoli *et al.,* 2016). Mutation in these genes can sometimes affect the intensity of their effects. This could be lower or higher than the effects of the wild-type version of the genes (Slota *et al.,* 2016). The FecX gene, for example, was found to increase ovulation rate by up to 1.0 in some heterozygous animals but homozygous ones were found to be sterile (Nicol *et al.,* 2009). Other genes related to fecundity, which have the same implications, are members of the Transforming Growth Factor Beta (TGF-beta) superfamily, particularly Bone Morphogenetic Proteins (BMPs), Growth Differentiation Factors (GDFs) (Nicol *et al.,* 2009) and most of these work was done on cattle, sheep, goat and swine (Han *et al.,* 2015a). Others are the melatonin receptor1 A (Yang *et al.,* 2014) and forkhead box (FOXL2) genes (Krepelova *et al.,* 2016). Identification and utilization of these genes is well described in the animal industry (Davis, 2004).

However, some animals suffer from a paucity of genetic and fertility data such as genome wide sequences and polymorphism data, and breeding record which severely limits the implementation of genomic approaches for addressing biological question in these species (Sabury *et al.,* 2011). One of the understudied species in this regard is the deer, which is a widely distributed ruminant species of the order *Artiodactyla* and family *Cervidae* (Solari & Baker, 2007). The *R. timorensis Blainville*, *R. unicolor Kerr* and *Axis axis Erxleben* fall within the category of understudied deer breeds (Zakaria *et al.,* 2016)

In the last few decades Malaysia has witnessed changes in deer farming, where the species has become popular as a source of protein in the livestock industry with immense potential for both local consumption and export capacity (Fitri *et al.,* 2017). To maintain this capacity, deer has been imported into the country from a number of different countries (El-Jaafari, Panandam, Idris, & Siraj, 2008) and kept together, breeding freely, exposing the animals to the risk of genetic mixture, introgression and

possible loss of some desirable, adaptive traits (Berthouly-Salazar *et al.*, 2012; El-Jaafari *et al.*, 2008). The conflict between the desire to use wild animals both as sources of animal protein and conserve them as wild game animals limits the ability of some deer farms to maintain useful fertility record, thereby affecting the development of the deer industry in the country. Consequently, the deer in Malaysia receives less attention, regarding research interest, compared to cattle, buffaloes and small ruminants in terms of efforts geared towards fertility improvement and genetic conservation. There are reports of dramatic and progressive loss of fertility in the Malaysian deer, particularly the *Axis axis Erxleben, Cervus nippon, Rusa timorensis Blainville and Rusa. unicolor.* Although some of these reports have been (El-Jaafari *et al.*, 2008; Zakaria *et al.*, 2016), most of them remain with farmers who keep grappling with the problems (Lee, 2014). The aim of any breeding program is to improve the potential of animals for maximum fecundity, which can be achieved by improving the genetic worth of the stock through methods that ensure proper selection (Rauw & Gomez-Raya, 2015). As it is difficult to measure fecundity because of paucity of adequate supporting tools, such as genomic and fertility data, in these farms, indirect methods through cytogenetics and molecular characterization of their fecundity genes may generate useful information for the improvement of animals in this category.

1.2 Statement of research problem

As the world's population continues to grow exponentially, the demand for animal protein has become more intense. This requires 1) efforts to improve strategies in livestock breeding by exploring faster and more efficient ways of propagating animals. 2) breeding of nonconventional livestock (Thornton, 2010). Deer is one of such animals currently farmed in many countries including Malaysia. Several farms were set up to serve as nucleus for the production and distribution of deer stock to smallholder farms across the country (El-Jaafari *et al.*, 2008). One of such farms is the Pusat Ternakan Haiwan (PTH) Lenggong. Many of these nucleus farms are grappling with fertility issues in the deer. Ordinarily with the current advancement in the area of animal breeding, especially the molecular genetics component, increasing such animal resources through existing selection methods should be rapid to address such fertility problems. For example, Restriction Length Fragment Polymorphisms (RFLPs) and Single nucleotide polymorphisms (SNPs) are important genetic markers, which in combination with onsite fecundity record can be used for animal improvement (Rexroad *et al.*, 2019). The utilization of SNPs as genetic makers for selection is quite mature in animals with abundant genomic data (model animals). Development of SNP panel, for identification of polymorphic sites, requires the comparison of large amount of DNA sequence data across multiple individuals (Haynes & Latch, 2012a). In model animals such as cattle, the availability of such data through genomic sequencing programmes has made possible the production and application of large SNP chip containing more than 50,000 markers. Unfortunately, other non-model animals do not possess large amount of genomic data to facilitate such development (BIXLEY, 2009). Another important issue is that of lack of comprehensive fertility record on some animal facilities (Zakaria *et al.*, 2016). Therefore, even when polymorphisms data become available there is need for

phenotype data to associate with the polymorphisms. Determination of fecundity status through candidate gene analysis, using computational methods will reduce this bottleneck and provide a viable alternative in reproduction studies.

1.3 Justification

Loss of fertility in the deer across Malaysia is militating against the deer industry by causing immeasurable economic losses. The husbandry practice of allowing semi domesticated animals of different breeds, or even species living together that were allowed to interbreed complicates the problem. The problem resulted in lack of proper farm record, such as fertility record on these farms. These coupled with the general lack sufficient genomic data in *A. axis Erxleben, R. timorensis Blainville and R. unicolor Kerr* in the public domain limit the application of high-end genomic method such as SNP chips for genotyping to investigate fecundity issues in these breeds. Additionally, *A. axis Erxleben, R. timorensis Blainville and R. unicolor Kerr* are currently designated as vulnerable by the IUCN (Hedges, Duckworth, Timmins, Semiadi, & Dryden, 2015). Bone Morphogenetic Protein 15 (BMP15) gene, Growth Differentiation Factor 9 (GDF9) gene, Forkhead protein (FOXL2) gene, Major Histocompatibility Complex DQ Alpha (MHCDQA) and Melatonin Receptor 1A (MTNR1A) gene are fecundity genes that are well characterized in animals (Abdolahi & Shokrollahi, 2019) (Snibson *et al.*, 1998). They are known to be directly involved in fecundity. Polymorphisms in these genes in the form of both Single Nucleotide Polymorphisms (SNPs) and Restriction Fragment Length (RFLPs) have been associated with fecundity in animals. Likewise, protein variations within them have been associated with fecundity; such that individuals who carry defective variants of the proteins were infertile. Cytogenetic investigation coupled with the study of these fecundity genes can provide insight into the fecundity problems involving these animals.

Molecular computational methods can scan these genes for polymorphisms and their proteins for variations as well as predict the effects of the variants on the fecundity of individuals. Combining cytogenetic and molecular computational resources to determine the fecundity status of these animals will shed light into future reproduction studies as well as make available a wealth of polymorphism data for future use in animal selection.

1.4 Research hypotheses

Cytogenetics and computational analysis of five fecundity genes; Bone Morphogenetic Protein 15 (BMP15), Growth Differentiation Factor 9 (GDF9), Forkhead Box L 2 (*FOXL2*) , Melatonin Receptor 1A (*MTNR1A*) and Major Histocompatibility complex- DQAlpha (MHC-DQA) can be used to determine the fecundity status of three breeds of deer that are currently housed at PTH Lenggong.

1.5 Aim of the study

To determine the chromosomal and genetic polymorphisms, utilize the data to determine the fecundity status and to predict which animals are suitable for use in breeding in *Axis axis Erxleben, Rusa timorensis Blainville* and *Rusa unicolor Kerr* reared in Perak, Malaysia

1.6 Research objectives

The specific objective of this research are:

i. To determine the karyotypes of three breeds of deer (*R. timorensis Blainville, R. unicolor Kerr and Axis axis Erxleben*) in Lenggong, Perak
ii. To identify five fecundity genes (*BMP15, FOXL2, GDF9, MHCDQA and MTNR1A*) in deer through PCR
iii. To confirm congruence and complementarity between the PCR products and the in situ genes through FISH in three breeds of deer in Lenggong, Perak
iv. To determine Single Nucleotide Polymorphisms (SNPs) and Restriction Fragment Length Polymorphisms (RFLPs) in the fecundity genes of three breeds of deer in Lenggong,, Perak
v. To predict the proteins encoded by (*BMP15, FOXL2, GDF9, MHCDQA and MTNR1A*) genes, their variants and functional status in three breeds of deer in Lenggong, Perak

REFERENCES

Abdolahi, S., Shokrollahi, B., Saadati, N., & Morammazi, S. (2019). No polymorphism of melatonin receptor 1A (MTNR 1A) gene was found in Markhoz goat. *Veterinary Medicine and Science*, *5*(2), 157–161. https://doi.org/10.1002/vms3.146

Abdoli, R, Zamani, P., Mirhoseini, S., Ghavi Hossein-Zadeh, N., & Nadri, S. (2016). A review on prolificacy genes in sheep. *Reproduction in Domestic Animals*, *51*(5), 631–637. https://doi.org/10.1111/rda.12733

Abdoli, Ramin, Ziaeddin Mirhoseini, S., Ghavi Hossein-Zadeh, N., & Zamani, P. (2018). Screening for Causative Mutations of Major Prolificacy Genes in Iranian Fat-Tailed Sheep. *International Journal of Fertility & Sterility*, *12*(1), 51–55. https://doi.org/10.22074/ijfs.2018.5247

Abrams, E. T., & Miller, E. M. (2011). The roles of the immune system in Women's reproduction: Evolutionary constraints and life history trade-offs. *American Journal of Physical Anthropology*, *146*(SUPPL. 53), 134–154. https://doi.org/10.1002/ajpa.21621

Aghamohammadi, S. Z., Henderson, L., & Cole, R. J. (1984). The human lymphocyte micronucleus assay: Response of cord blood lymphocytes to γ-irradiation and bleomycin. *Mutation Research/Environmental Mutagenesis and Related Subjects*, *130*(6), 395–401. https://doi.org/10.1016/0165-1161(84)90011-6

Agnarsson, I., & May-Collado, L. J. (2008). The phylogeny of Cetartiodactyla: The importance of dense taxon sampling, missing data, and the remarkable promise of cytochrome b to provide reliable species-level phylogenies. *Molecular Phylogenetics and Evolution*, *48*(3), 964–985. https://doi.org/10.1016/j.ympev.2008.05.046

Ahmad, T., Ganai, T. A. S., Magotra, A., Sharma, R. K., & Aarif, O. (2015). Genetic polymorphism of melatonin receptor 1A (*MTNR1* A) gene in Corriedale sheep of Kashmir, India. *Indian Journal of Animal Research*, *49*(4), 448. https://doi.org/10.5958/0976-0555.2015.00119.3

Ahmed, S., & Othman, O. E. (2006). A PCR-RFLP method for the analysis of Egyptian goat MHC class II DRB gene. *Biotechnology*, *5*(1), 58–61. https://doi.org/10.3923/biotech.2006.58.61

Akinyemi, M., Osaiyuwu, H., & Adegoke, I. (2017). Computational Molecular Analysis of the Sequences of PAPPA2 Gene of Selected Ruminants and Non Ruminants. *Biotechnology Journal International*, *19*(1), 1–8. https://doi.org/10.9734/bji/2017/33125

Alam, Md Hasanur, Lee Jibak, M. T. (2018). GDF9 and BMP15 induce development of antrum-like structures by bovine granulosa cells without oocytes. *Journal of Reproduction and Development*, *64*(5), 423–431. https://doi.org/10.1262/jrd.2018-078

Albertson, D. G., & Pinkel, D. (2015). Comparative genomic hybridization. *Molecular Oncology: Causes of Cancer and Targets for Treatment*, 21–27. https://doi.org/10.1017/CBO9781139046947.004

Aleksandr Morgulis, George Coulouris, Yan Raytselis, Thomas L. Madden, Richa Agarwala, A. A. S. (2008). Database Indexing for Production MegaBLAST Searches. *Bioinformatics*, *24*, 1757–1764.

Ana Paula A. Guimarães , Adriana C. Guimarães, D. Á. A., Luiz Raimundo Cunha , Patrícia L. Lima, M. C. V., Raquel C. Montenegro , Bruno M. Soares, M. M. A., & Burbano, and R. R. (2014). Chromosomal Aberration Test Utilities In Vitro and In Vivo. In A. R. Collins & A. Azqueta (Eds.), *Genotoxicity and DNA Repair* (pp. 365–376). https://doi.org/10.1007/978-1-4939-1068-7

Andres, R. J., & Kuraparthy, V. (2013). Development of an Improved Method of Mitotic Metaphase Chromosome Preparation Compatible for Fluorescence in situ Hybridization in Cotton. *The Journal of Cotton Science*, *156*(17), 149–156.

Aricò, A., Ferraresso, S., Bresolin, S., Marconato, L., Comazzi, S., Te Kronnie, G., & Aresu, L. (2014). Array-based comparative genomic hybridization analysis reveals chromosomal copy number aberrations associated with clinical outcome in canine diffuse large B-cell lymphoma. *PloS One*, *9*(11), e111817. https://doi.org/10.1371/journal.pone.0111817

Asher, G. W., Gallagher, D. S., Tate, M. L., & Tedford, C. (1999). Hybridization between sika deer (Cervus nippon) and axis deer (*Axis axis Erxleben*). *Journal of Heredity*, *90*(1), 236–240. https://doi.org/10.1093/jhered/90.1.236

Asher, G. W. W. (2011). Reproductive cycles of deer. *Animal Reproduction Science*, *124*(3–4), 170–175. https://doi.org/10.1016/j.anireprosci.2010.08.026

Aubert, G., Hills, M., & Lansdorp, P. M. (2012). Telomere length measurement—Caveats and a critical assessment of the available technologies and tools. *Mutation Research/Fundamental and Molecular Mechanisms of Mutagenesis*, *730*(1–2), 59–67. https://doi.org/10.1016/J.MRFMMM.2011.04.003

Aujame, L., Seguin, D., Droy, C., & Hessler, C. (2000). Experimental Design Optimization of Filamentous Phage Transfection into Mammalian Cells by Cationic Lipids. *BioTechniques*, *28*(6), 1202–1213. https://doi.org/10.2144/00286rr01

Ballingall, K. T., Rocchi, M. S., McKeever, D. J., & Wright, F. (2010). Trans-species polymorphism and selection in the MHC class II DRA genes of domestic sheep. *PloS One*, *5*(6), e11402. https://doi.org/10.1371/journal.pone.0011402

Balogh, O., Kovács, K., Kulcsár, M., Gáspárdy, A., Zsolnai, A., Kátai, L., … Huszenicza, G. (2009). AluI polymorphism of the bovine growth hormone (GH) gene, resumption of ovarian cyclicity, milk production and loss of body condition at the onset of lactation in dairy cows. *Theriogenology*, *71*(4), 553–559. https://doi.org/10.1016/j.theriogenology.2008.06.032

Barakat, I. A., Salem, L. M., Daoud, N. M., Khalil, W. K., & Mahrous, K. F. (2017). Genetic polymorphism of candidate genes for fecundity traits in Egyptian sheep breeds. *Biomedical Research (India)*, *28*(2), 851–857. Retrieved from http://www.alliedacademies.org/articles/genetic-polymorphism-of-candidate-genes-for-fecundity-traits-in-egyptian-sheep-breeds.html

Barnes, R. P., Fouquerel, E., & Opresko, P. L. (2019). The impact of oxidative DNA damage and stress on telomere homeostasis. *Mechanisms of Ageing and Development*, *177*(February 2018), 37–45. https://doi.org/10.1016/j.mad.2018.03.013

Bateson, M. (2016). Cumulative stress in research animals: Telomere attrition as a biomarker in a welfare context? *BioEssays*, *38*(2), 201–212. https://doi.org/10.1002/bies.201500127

Bauduer, F., Degioanni, A., & Dutour, O. (2009, February). Medical genetic polymorphisms as markers of evolutionary forces within the human genome: Hypotheses focusing on natural selection in the basque population. *Human Biology*, Vol. 81, pp. 23–42. https://doi.org/10.3378/027.081.0103

Bębenek, A., & Ziuzia-Graczyk, I. (2018). Fidelity of DNA replication—a matter of proofreading. *Current Genetics*, *64*(5), 985–996. https://doi.org/10.1007/s00294-018-0820-1

Benkert, P., Biasini, M., & Schwede, T. (2011). Toward the estimation of the absolute quality of individual protein structure models. *Bioinformatics*, *27*(3), 343–350. https://doi.org/10.1093/bioinformatics/btq662

Berthouly-Salazar, C., Thévenon, S., Van, T. N., Nguyen, B. T., Pham, L. D., Chi, C. V., & Maillard, J.-C. (2012). Uncontrolled admixture and loss of genetic diversity in a local Vietnamese pig breed. *Ecology and Evolution*, *2*(5), 962–975. https://doi.org/10.1002/ece3.229

Bertoni, M., Kiefer, F., Biasini, M., Bordoli, L., & Schwede, T. (2017). Modeling protein quaternary structure of homo- and hetero-oligomers beyond binary interactions by homology. *Scientific Reports*, *7*(1), 10480. https://doi.org/10.1038/s41598-017-09654-8

Beuzen, N. D., Stear, M. J., & Chang, K. C. (2000). Molecular markers and their use in animal breeding. *Veterinary Journal*, *160*(1), 42–52. https://doi.org/10.1053/tvjl.2000.0468

Bhushan, B., Patra, B. N., Das, P. J., Dutt, T., Kumar, P., Sharma, A., … Ahlawat, S. P. S. (2007). Polymorphism of exon 2-3 of bovine major histocompatibility complex class I BoLa-A gene. *Genetics and Molecular Biology*, *30*(3), 560–566. https://doi.org/10.1590/s1415-47572007000400009

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

Blagodatskikh, K. A., Kramarov, V. M., Barsova, E. V., Garkovenko, A. V., Shcherbo, D. S., Shelenkov, A. A., … Ignatov, K. B. (2017). Improved DOP-PCR (iDOP-PCR): A robust and simple WGA method for efficient amplification of low copy number genomic DNA. *PLoS ONE*, *12*(9), e0184507. https://doi.org/10.1371/journal.pone.0184507

Bogdanovska-Todorovska, M., Petrushevska, G., Janevska, V., Spasevska, L., & Kostadinova-Kunovska, S. (2018). Standardization and optimization of fluorescence in situ hybridization (FISH) for HER-2 assessment in breast cancer: A single center experience. *Bosnian Journal of Basic Medical Sciences*, *18*(2), 132–140. https://doi.org/10.17305/bjbms.2018.2519

Borowski, Z., Wisocka, M., Matosiuk, M., Mirski, P., Krysiuk, K., Czajkowska, M., … Ratkiewicz, M. (2016). Purifying selection, density blocking and unnoticed mitochondrial DNA diversity in the red deer, Cervus elaphus. *PLoS ONE*, *11*(9), 1–17. https://doi.org/10.1371/journal.pone.0163191

Boulanger, L., Pannetier, M., Gall, L., Allais-Bonnet, A., Elzaiat, M., Le Bourhis, D., … Pailhoux, E. (2014). FOXL2 Is a Female Sex-Determining Gene in the Goat. *Current Biology*, *24*(4), 404–408. https://doi.org/10.1016/j.cub.2013.12.039

Brauning, R., Fisher, P. J., McCulloch, A. F., Smithies, R. J., Ward, J. F., Bixley, M. J., … McEwan, J. C. (2015). Utilization of high throughput genome sequencing technology for large scale single nucleotide polymorphism discovery in red deer and Canadian elk. In *bioRxiv*. https://doi.org/10.1101/027318

Buaban, S., Duangjinda, M., Suzuki, M., Masuda, Y., Sanpote, J., & Kuchida, K. (2015). Genetic analysis for fertility traits of heifers and cows from smallholder dairy farms in a tropical environment. *Journal of Dairy Science*, *98*(7), 4990–4998. https://doi.org/10.3168/jds.2014-8866

Bugno-Poniewierska, M., Sołek, P., Potocki, L., Pawlina, K., Wnuk, M., Jezewska-Witkowska, G., & Słota, E. (2013). Polymorphism of cytogenetic markers in wild and farm red fox (Vulpes vulpes) populations. *Folia Biologica (Poland)*, *61*(3–4), 155–163. https://doi.org/10.3409/fb61_3-4.155

Bugno, M., Jabłońska, Z., & Słota, E. (2009). Optimalization of fluorescence in situ hybridization conditions in mare oocytes and mouse embryos. *Folia Biologica*, *57*(1–2), 49–55. Retrieved from http://www.ncbi.nlm.nih.gov/pubmed/19459461

Calvo, J. H., Serrano, M., Martinez-Royo, A., Lahoz, B., Sarto, P., Ibañez-Deler, A., … Alabart, J. L. (2018). SNP rs403212791 in exon 2 of the MTNR1A gene is associated with reproductive seasonality in the Rasa aragonesa sheep breed. *Theriogenology*, *113*, 63–72. https://doi.org/10.1016/j.theriogenology.2018.02.013

Carranza, J., Salinas, M., de Andrés, D., & Pérez-González, J. (2016). Iberian red deer: Paraphyletic nature at mtDNA but nuclear markers support its genetic identity. *Ecology and Evolution*, *6*(4), 905–922. https://doi.org/10.1002/ece3.1836

Chaudhary, R., Singh, B., Kumar, M., Gakhar, S. K., Saini, A. K., Parmar, V. S., & Chhillar, A. K. (2015, July 3). Role of single nucleotide polymorphisms in pharmacogenomics and their association with human diseases. *Drug Metabolism Reviews*, Vol. 47, pp. 281–290. https://doi.org/10.3109/03602532.2015.1047027

Cheema, R. S., Kaur, A., Ghuman, S. P. S., & Dhindsa, S. S. (2016). *Melatonin receptor 1a gene polymorphism in murrah buffaloes with possible impact on summer anestrous*. *5*(3), 386–394.

Chemineau, P., Guillaume, D., Migaud, M., Thiry, J., Pellicer-Rubio, M., & Malpaux, B. (2008). Seasonality of Reproduction in Mammals: Intimate Regulatory Mechanisms and Practical Implications. *Reproduction in Domestic Animals*, *43*, 40–47. https://doi.org/10.1111/j.1439-0531.2008.01141.x

Chen, H., Liu, C., Jiang, H., Gao, Y., Xu, M., Wang, J., … Dai, L. (2017). Regulatory Role of miRNA-375 in Expression of BMP15/GDF9 Receptors and its Effect on Proliferation and Apoptosis of Bovine Cumulus Cells. *Cellular Physiology and Biochemistry*, *41*(2), 439–450. https://doi.org/10.1159/000456597

Choi, Y., Sims, G. E., Murphy, S., Miller, J. R., & Chan, A. P. (2012). Predicting the Functional Effect of Amino Acid Substitutions and Indels. *PLoS ONE*, *7*(10), e46688. https://doi.org/10.1371/journal.pone.0046688

Chooseangjaew, S., Tanyaros, S., Maneechot, N., Buasriyot, P., Getlekha, N., & Tanomtong, A. (2017). Chromosomal characteristics of the tropical oyster, Crassostrea belcheri Sowerby, 1871 (Ostreoida, Ostreidae) by conventional and Ag-NOR banding techniques. *Cytologia*, *82*(1), 3–8. https://doi.org/10.1508/cytologia.82.3

Chu, M. X., Cheng, D. X., Liu, W. Z., Fang, L., & Ye, S. C. (2006). Association between melatonin receptor 1A gene and expression of reproductive seasonality in sheep. *Asian-Australasian Journal of Animal Sciences*, *19*(8), 1079–1084. https://doi.org/10.5713/ajas.2006.1079

Cinzia Marcitelli, P. V. and A. N. (2009). Characterization of single nucleotide polymorphisms in BMP15, GDF9 and BMBR1B genes in Maremmana cattle breed. *Italian Journal of Animal Science*, *8*(2), 214.

Coizet, B., Frattini, S., Nicoloso, L., Iannuzzi, L., Coletta, A., Talenti, A., … Crepaldi, P. (2018). Polymorphism of the *STAT5A*, *MTNR1A* and *TNFα* genes and their effect on dairy production in *Bubalus bubalis*. *Italian Journal of Animal Science*, *17*(1), 31–37. https://doi.org/10.1080/1828051X.2017.1335181

Corvi, R., & Madia, F. (2017). In vitro genotoxicity testing–Can the performance be enhanced? *Food and Chemical Toxicology*, *106*, 600–608. https://doi.org/10.1016/J.FCT.2016.08.024

Crisponi, L., Deiana, M., Loi, A., Chiappe, F., Uda, M., Amati, P., … Pilia, G. (2001). The putative forkhead transcription factor FOXL2 is mutated in blepharophimosis/ptosis/epicanthus inversus syndrome. *Nature Genetics*, *27*(2), 159–166. https://doi.org/10.1038/84781

Croitor, R. (2014). Deer from Late Miocene to Pleistocene of Western Palearctic: Matching fossil record and molecular phylogeny data. *Zitteliana Reihe B: Abhandlungen Der Bayerischen Staatssammlung Fur Palaontologie Und Geologie*, *32*(32), 115–153.

Cui, C., Shu, W., & Li, P. (2016). Fluorescence In situ Hybridization: Cell-Based Genetic Diagnostic and Research Applications. *Frontiers in Cell and Developmental Biology*, *4*(SEP), 89. https://doi.org/10.3389/fcell.2016.00089

Cursino, M. S., Salviano, M. B., Abril, V. V., Dos Santos Zanetti, E., & Duarte, J. M. B. (2014). The role of chromosome variation in the speciation of the red brocket deer complex: The study of reproductive isolation in females. *BMC Evolutionary Biology*, *14*(1). https://doi.org/10.1186/1471-2148-14-40

Da Silva, A., Gaillard, J.-M., Yoccoz, N. G., Hewison, A. J. M., Galan, M., Coulson, T., … Luikart, G. (2009). Heterozygosity-Fitness Correlations Revealed by Neutral and Candidate Gene Markers in Roe Deer from a Long-Term Study. *Evolution*, *63*(2), 403–417. https://doi.org/10.1111/j.1558-5646.2008.00542.x

Dagong, M. I. A., A Bugiwati, R. R. S. R., & Purnomo, N. (2019). Melatonin receptor 1A (MTNR1A) gene polymorphisms in the local goat population in South Sulawesi region of Indonesia. *IOP Conference Series: Earth and Environmental Science*, *270*(1), 012009. https://doi.org/10.1088/1755-1315/270/1/012009

Dagong, M. I. A., Bugiwati, R. R. S. R. A., & Purnomo, N. (2019). Melatonin receptor 1A ({MTNR}1A) gene polymorphisms in the local goat population in South Sulawesi region of Indonesia. *{IOP} Conference Series: Earth and Environmental Science*, *270*, 12009. https://doi.org/10.1088/1755-1315/270/1/012009

Danielak-czech, B., & Rejduch, B. (2016). *Cytogenetic and molecular diagnostics of XX/XY chimerism in cattle, sheep, and goats – a review*. *16*(4), 989–1005. https://doi.org/10.1515/aoas-2016-0028

Darzynkiewicz, Z., Smolewski, P., Holden, E., Luther, E., Henriksen, M., François, M., … Fenech, M. (2011). Laser scanning cytometry for automation of the micronucleus assay. *Mutagenesis*, *26*(1), 153–161. https://doi.org/10.1093/mutage/geq069

Davis, G. H. (2004). Fecundity genes in sheep. *Animal Reproduction Science*, *82–83*, 247–253. https://doi.org/10.1016/j.anireprosci.2004.04.001

De Baere, E., Copelli, S., Caburet, S., Laissue, P., Beysen, D., Christin-Maitre, S., … Fellous, M. (2005). Premature ovarian failure and forkhead transcription factor FOXL2: blepharophimosis-ptosis-epicanthus inversus syndrome and ovarian dysfunction. *Pediatric Endocrinology Reviews : PER*, *2*(4), 653–660. Retrieved from http://www.ncbi.nlm.nih.gov/pubmed/16208278

De Lorenzi, L., Morando, P., Planas, J., Zannotti, M., Molteni, L., & Parma, P. (2012). Reciprocal translocations in cattle: frequency estimation. *Journal of Animal Breeding and Genetics*, *129*(5), 409–416. https://doi.org/10.1111/j.1439-0388.2011.00983.x

Dehouck, Y., Kwasigroch, J. M., Gilis, D., & Rooman, M. (2011). PoPMuSiC 2.1: A web server for the estimation of protein stability changes upon mutation and sequence optimality. *BMC Bioinformatics*, *12*. https://doi.org/10.1186/1471-2105-12-151

Demyda-Peyrás, S., Membrillo, A., Bugno-Poniewierska, M., Pawlina, K., Anaya, G., & Moreno-Millán, M. (2013). The Use of Molecular and Cytogenetic Methods as a Valuable Tool in the Detection of Chromosomal Abnormalities in Horses: A Case of Sex Chromosome Chimerism in a Spanish Purebred Colt. *Cytogenetic and Genome Research*, *141*(4), 277–283. https://doi.org/10.1159/000351225

Di Berardino, D., & Burguete, I. (2003). High resolution RBA-banding comparison between early prometaphase chromosomes of cattle (*Bos taurus* L.) and goat (*Capra hircus* L.) at 700 band level. *Cytogenetic and Genome Research*, *83*(1–2), 130–138. https://doi.org/10.1159/000015148

Dixit, M., & Kumar, A. (2018). Chapter 4 - In Vitro Gene Genotoxicity Test Methods. In A. Dhawan & S. Kwon (Eds.), *In Vitro Toxicology* (pp. 67–89). https://doi.org/https://doi.org/10.1016/B978-0-12-804667-8.00004-3

Dolmatova, I. I., & Il'iasov, I. G. (2011). [Association of cattle growth hormone gene polymorphism with milk productivity]. *Genetika*, *47*(6), 814–820. Retrieved from http://www.ncbi.nlm.nih.gov/pubmed/21866862

Dong Xu and Yang Zhang. (2012). Ab initio protein structure assembly using continuous structure fragments and optimized knowledge-based force field. *Proteins*, *80*, 1715–1735.

Dong Xu and Yang Zhang. (2013). Toward optimal fragment generations for ab initio protein structure assembly. *Proteins*, *81*, 229–239.

Du, P., Ye, L., Yang, Y., & Jiang, W. G. (2014). Reduced expression of growth and differentiation factor-9 (GDF9) is associated with aggressive behaviour of human clear-cell renal cell carcinoma and poor patient survival. *Anticancer Research*, *34*(11), 6515–6520. Retrieved from http://www.ncbi.nlm.nih.gov/pubmed/25368253

Dubey, A. A., Singh, M. I., & Jain, V. (2016). Rapid and robust PCR-based all-recombinant cloning methodology. *PLoS ONE*, *11*(3), 1–11. https://doi.org/10.1371/journal.pone.0152106

Duckworth, J.W., Kumar, N.S., Anwarul Islam, M., Sagar Baral, H. & Timmins, R. (2015). *Axis axis Erxleben , Chital. 8235*.

Ducos, A., Revay, T., Kovacs, A., Hidas, A., Pinton, A., Bonnet-Garnier, A., … Iannuzzi, L. (2008). Cytogenetic screening of livestock populations in Europe: An overview. *Cytogenetic and Genome Research*, Vol. 120, pp. 26–41. https://doi.org/10.1159/000118738

Dyrendahl, Ivar and Gustavsson, I. (1979). Sexual functions, semen characteristics and fertility of bulls carrying the 1/29 chromosome translocation. *Hereditas*, *90*(2), 281–289. https://doi.org/10.1111/j.1601-5223.1979.tb01315.x

Eklöf, J., Rydell, J., Eklöf, J., & Rydell, J. (2017). Evolution and Diversity. In *Bats* (pp. 9–20). https://doi.org/10.1007/978-3-319-66538-2_1

El-Bayomi, K. M., EL-Araby, I. E. S., & Zaglool, A. W. (2011). Cytogenetic analysis related to some infertility problems in Cattle. *Global Veterinaria*, *7*(4), 323–329.

El-Jaafari, H. A. A., Panandam, J. M., Idris, I., & Siraj, S. S. (2008). RAPD analysis of three deer species in Malaysia. *Asian-Australasian Journal of Animal Sciences*, *21*(9), 1233–1237. https://doi.org/10.5713/ajas.2008.60227

El Fiky, Z. A., Hassan, G. M., & Nassar, M. I. (2017). Genetic polymorphism of growth differentiation factor 9 (GDF9) gene related to fecundity in two Egyptian sheep breeds. *Journal of Assisted Reproduction and Genetics*, *34*(12), 1683–1690. https://doi.org/10.1007/s10815-017-1007-2

Farhadi, V. Genualdo, A. Perucatti, S. H. Hafezian, G. Rahimi-mianji, L. De lorenzi P. Parma, L. I. and A. I. (2013). Comparative FISH mapping of BMPR1B, BMP15 and GDF9 fecundity genes on cattle, river buffalo, sheep and goat chromosomes. *Journal of Genetics*, *92*(3), 595–597. https://doi.org/10.1007/s12041-013-0301-8

Fathy, H. A., Gouda, E. M., Gafer, J. A., Galal, M. K., & Nowier, A. M. (2018). Genetic polymorphism in melatonin receptor 1A and arylalkylamine N-acetyltransferase and its impact on seasonal reproduction in Egyptian sheep breeds. *Archives Animal Breeding*, *61*(4), 505–516. https://doi.org/10.5194/aab-61-505-2018

Felsenstein, J. (1985). Confidence Limits on Phylogenies: an Approach Using the Bootstrap. *Evolution*, *39*(4), 783–791. https://doi.org/10.1111/j.1558-5646.1985.tb00420.x

Fenech, M., & Morley, A. A. (1985). Measurement of micronuclei in lymphocytes. *Mutation Research/Environmental Mutagenesis and Related Subjects*, *147*(1–2), 29–36. https://doi.org/10.1016/0165-1161(85)90015-9

Fitri, W. N., Wahid, H., Rosnina, Y., Jesse, F. F. A., Aimi-Sarah, Z. A., Mohd-Azmi, M. L., … Baiee, F. H. A. (2017). Semen characteristics, extension, and cryopreservation of Rusa deer (*Rusa timorensis Blainville*). *Veterinary World*, *10*(7), 779–785. https://doi.org/10.14202/vetworld.2017.779-785

Ford CE, Pollok DL, G. I. (1980). Reading Conference. In G. I. Ford CE, Pollok DL (Ed.), *Proceedings of the First International Conference for the Standardization of Banded Karyotypes of Domestic Animals* (pp. 145–162). Reading.

Fowler, D. M., & Fields, S. (2014). Deep mutational scanning: A new style of protein science. *Nature Methods*, Vol. 11, pp. 801–807. https://doi.org/10.1038/nmeth.3027

Frohlich, J., Kubickova, S., Musilova, P., Cernohorska, H., Muskova, H., Vodicka, R., & Rubes, J. (2017). Karyotype relationships among selected deer species and cattle revealed by bovine FISH probes. *PloS One*, *12*(11), e0187559. https://doi.org/10.1371/journal.pone.0187559

Gafter-Gvili, A., Zingerman, B., Rozen-Zvi, B., Ori, Y., Green, H., Lubin, I., … Herman-Edelstein, M. (2013). Oxidative Stress-Induced DNA Damage and Repair in Human Peripheral Blood Mononuclear Cells: Protective Role of Hemoglobin. *PLoS ONE*, *8*(7), e68341. https://doi.org/10.1371/journal.pone.0068341

Gaildrat, P., Becq, F., & Falcón, J. (2002). First cloning and functional characterization of a melatonin receptor in fish brain: a novel one? *Journal of Pineal Research*, *32*(2), 74–84. https://doi.org/10.1034/j.1600-079x.2002.1817.x

Gall, J. G. and, & Pardue, M. L. (1969). . Formation and detection of RNA–DNA hybrid molecules in cytological preparations. *Proc. Natl Acad. Sci. USA*, *63*(1), 378–383.

Galloway SM, McNatty KP, Cambridge LM, L. M., Juengel JL, Jokiranta TS, McLaren RJ, Luiro K, D., & KG, Montgomery GW, Beattie AE, Davis GH, R. O. (2000). Mutations in an oocyte-derived growth factor gene (BMP15) cause increased ovulation rate and infertility in a dosage-sensitive manner. *Nature Genetics*, *25*, 279–283. https://doi.org/https://doi.org/10.1038/77033

Garibyan, L., & Avashia, N. (2013). Polymerase chain reaction. *Journal of Investigative Dermatology*, *133*(3), 1–4. https://doi.org/10.1038/jid.2013.1

Gasteiger, E., Gattiker, A., Hoogland, C., Ivanyi, I., Appel, R. D., & Bairoch, A. (2003). ExPASy: The proteomics server for in-depth protein knowledge and analysis. *Nucleic Acids Research*, *31*(13), 3784–3788. https://doi.org/10.1093/nar/gkg563

Gasteiger, E., Hoogland, C., Gattiker, A., Duvaud, S., Wilkins, M. R., Appel, R. D., & Bairoch, A. (2005a). Protein Analysis Tools on the ExPASy Server. *The Proteomics Protocols Handbook Protein Identification and Analysis Tools on the ExPASy Server*, 571–607. https://doi.org/10.1385/1592598900

Gasteiger, E., Hoogland, C., Gattiker, A., Duvaud, S., Wilkins, M. R., Appel, R. D., & Bairoch, A. (2005b). The Proteomics Protocols Handbook - Chapter 52: Protein Identification and Analysis Tools on the ExPASy Server. In *The Proteomics Protocols Handbook*. https://doi.org/10.1385/1592598900

Geigl, J. B., Uhrig, S., & Speicher, M. R. (2006). Multiplex-fluorescence in situ hybridization for chromosome karyotyping. *Nature Protocols*, *1*(3), 1172–1184. https://doi.org/10.1038/nprot.2006.160

Genualdo, V., Spalenza, V., Perucatti, A., Iannuzzi, A., Di Meo, G. P., Caputi-Jambrenghi, A., … Iannuzzi, L. (2011). Fluorescence in situ hybridization mapping of six loci containing genes involved in the dioxin metabolism of domestic bovids. *Journal of Applied Genetics*, *52*(2), 229–232. https://doi.org/10.1007/s13353-011-0043-3

Giantsis, I. A., Laliotis, G. P., Stoupa, O., & Avdi, M. (2016). Polymorphism of the melatonin receptor 1A (MNTR1A) gene and association with seasonality of reproductive activity in a local Greek sheep breed. *Journal of Biological Research-Thessaloniki*, *23*(1), 9. https://doi.org/10.1186/s40709-016-0050-y

Gilbert, C., Ropiquet, A., & Hassanin, A. (2006). Mitochondrial and nuclear phylogenies of Cervidae (Mammalia, Ruminantia): Systematics, morphology, and biogeography. *Molecular Phylogenetics and Evolution*, *40*(1), 101–117. https://doi.org/10.1016/j.ympev.2006.02.017

Giles, T. C., & Emes, R. D. (2017). Inferring function from homology. In *Methods in Molecular Biology* (Vol. 1526, pp. 23–40). https://doi.org/10.1007/978-1-4939-6613-4_2

Glei M., S. T. & S. W. (2016). Comet assay: an essential tool in toxicological research. *Archives of Toxicology*, *90*, 2315–36.

Gomes, N. M. V., Ryder, O. A., Houck, M. L., Charter, S. J., Walker, W., Forsyth, N. R., … Wright, W. E. (2011). Comparative biology of mammalian telomeres: hypotheses on ancestral states and the roles of telomeres in longevity determination. *Aging Cell*, *10*(5), 761–768. https://doi.org/10.1111/j.1474-9726.2011.00718.x

González-Pérez, A., & López-Bigas, N. (2011). Improving the assessment of the outcome of nonsynonymous SNVs with a consensus deleteriousness score, Condel. *American Journal of Human Genetics*, *88*(4), 440–449. https://doi.org/10.1016/j.ajhg.2011.03.004

Grievink, H. W., Luisman, T., Kluft, C., Moerland, M., & Malone, K. E. (2016). Comparison of Three Isolation Techniques for Human Peripheral Blood Mononuclear Cells: Cell Recovery and Viability, Population Composition, and Cell Functionality. *Biopreservation and Biobanking*, *14*(5), 410–415. https://doi.org/10.1089/bio.2015.0104

Grubb, P. (1993). Artiodactyla. In W. D. E. and R. D. M. (Ed.), *Mammal species of the world* (2nd ed., pp. 377–414).

Gudex, B., Walker, M., Fisher, P., & Spelman, R. (2014). Validation of a single-nucleotide polymorphism panel for parentage testing of farmed red deer. *Animal Genetics*, *45*(1), 142–143. https://doi.org/10.1111/age.12085

Guex, N., Peitsch, M. C., & Schwede, T. (2009). Automated comparative protein structure modeling with SWISS-MODEL and Swiss-PdbViewer: A historical perspective. *Electrophoresis*, *30*(SUPPL. 1), S162–S173. https://doi.org/10.1002/elps.200900140

Guha, S., Goyal, S. P., & Kashyap, V. K. (2007). Molecular phylogeny of musk deer: A genomic view with mitochondrial 16S rRNA and cytochrome b gene. *Molecular Phylogenetics and Evolution*, *42*(3), 585–597. https://doi.org/10.1016/J.YMPEV.2006.06.020

Guo, J., Shi, L., Gong, X., Jiang, M., Yin, Y., Zhang, X., … Eppig, J. J. (2016). Oocyte-dependent activation of MTOR in cumulus cells controls the development and survival of cumulus-oocyte complexes. *Journal of Cell Science*, *129*(16), 3091–3103. https://doi.org/10.1242/jcs.182642

Gustavsson, I., Rockborn, G. (1964). Chromosome abnormality in three cases of lymphatic leukaemia in cattle. *Nature*, *203*(1), 990.

Gustavsson, I. (1969). Cytogenetics, distribution and phenotypic effects of a translocation in Swedish cattle. *Hereditas*, *63*(1), 68–169.

Gustavsson, I. (1980). Chromosome aberrations and their influence on the reproductive performance of domestic animals – a review. *Z Tierzuchtg Zuchtgsbiol*, *97*(1), 176–195.

Hall, B. G. (2013). Building Phylogenetic Trees from Molecular Data with MEGA. *Molecular Biology and Evolution*, *30*(5), 1229–1235. https://doi.org/10.1093/molbev/mst012

Hall, T. A. (1999). BioEdit: A User-Friendly Biological Sequence Alignment Editor and Analysis Program for Windows. *Nucleic Acids Symposium Series*, *41*(1), 95–98. Retrieved from https://bioedit.software.informer.com/

Han, H., Lei, Q., Zhou, Y., Gao, J., Liu, W., Li, F., … Cao, D. (2015a). Association between BMP15 Gene Polymorphism and Reproduction Traits and Its Tissues Expression Characteristics in Chicken. *PloS One*, *10*(11), e0143298. https://doi.org/10.1371/journal.pone.0143298

Han, H., Lei, Q., Zhou, Y., Gao, J., Liu, W., Li, F., … Cao, D. (2015b). Association between BMP15 Gene Polymorphism and Reproduction Traits and Its Tissues Expression Characteristics in Chicken. *PloS One*, *10*(11), e0143298. https://doi.org/10.1371/journal.pone.0143298

Han, H., Lei, Q., Zhou, Y., Gao, J., Liu, W., Li, F., … Cao, D. (2015c). Association between BMP15 Gene Polymorphism and Reproduction Traits and Its Tissues Expression Characteristics in Chicken. *PloS One*, *10*(11), e0143298. https://doi.org/10.1371/journal.pone.0143298

Hanim Shabaan Mohammed Heikal, W. S. H. A. E. N. (2017). Genetic Improvement of Litter Size in Four Goat Breeds in Egypt Using Polymorphism in Bone Morphogenetic Protein 15 Gene. *Advances in Animal and Veterinary Sciences*, *95*(1), 107–130.

Hanrahan JP, Gregan SM, Mulsant P, Mullen M, Davis GH Powell R, G. S. (2004). Mutations in the genes for oocyte-derived growth factors GDF9 and BMP15 are associated with both increased ovulation rate and sterility in Cambridge and Belclare sheep (Ovisaries). *Biol. Reprod*, *70*, 900–909. https://doi.org/https://doi.org/10.1095/biolreprod.103.023093

Hanscombe, K. B., Morris, D. L., Noble, J. A., Dilthey, A. T., Tombleson, P., Kaufman, K. M., … Vyse, T. J. (2018). Genetic fine mapping of systemic lupus erythematosus MHC associations in Europeans and African Americans. *Human Molecular Genetics*, *27*(21), 3813–3824. https://doi.org/10.1093/hmg/ddy280

Hassanin, A., Delsuc, F., Ropiquet, A., Hammer, C., Jansen van Vuuren, B., Matthee, C., … Couloux, A. (2012). Pattern and timing of diversification of Cetartiodactyla (Mammalia, Laurasiatheria), as revealed by a comprehensive analysis of mitochondrial genomes. *Comptes Rendus Biologies*, *335*(1), 32–50. https://doi.org/10.1016/j.crvi.2011.11.002

Hathaipat Khongcharoensuk, Alongklod Tanomtong, I. P., & Praween Supanuam, S. S. and K. P. (2017). Karyotype and Idiogram of the Axis Deer (Axia axis , Cervidae) by Conventional Staining , GTG- ,. *Cytologia*, *82*(1), 91–98. https://doi.org/10.1508/cytologia.82.91

Hayashi, M. (2007). In Vivo Rodent Micronucleus Assay. In *Chromosomal Alterations* (pp. 257–270). https://doi.org/10.1007/978-3-540-71414-9_16

Hayashi, M. (2016). The micronucleus test-most widely used in vivo genotoxicity test. *Genes and Environment*, *38*(1), 4–9. https://doi.org/10.1186/s41021-016-0044-x

Hayes, H., Dutrillaux, B., & Popescu, P. (2000). *Preparation of Chromosome Spreads*. https://doi.org/10.1007/978-3-642-59711-4_1

Hayes, H., Dutrillaux, B., Popescu, P., & Bourgeois, C. (2000). *Chromosome Banding Techniques*. https://doi.org/10.1007/978-3-642-59711-4_2

Haynes, G. D., & Latch, E. K. (2012a). Identification of novel single nucleotide polymorphisms (SNPs) in deer (odocoileus spp.) using the BovineSNP50 Beadchip. *PLoS ONE*, *7*(5). https://doi.org/10.1371/journal.pone.0036536

Haynes, G. D., & Latch, E. K. (2012b). Identification of novel single nucleotide polymorphisms (SNPs) in deer (odocoileus spp.) using the BovineSNP50 Beadchip. *PLoS ONE*, *7*(5). https://doi.org/10.1371/journal.pone.0036536

Heckeberg, N. S., Erpenbeck, D., Wörheide, G., & Rössner, G. E. (2016). Systematic relationships of five newly sequenced cervid species. *PeerJ*, *4*, e2307. https://doi.org/10.7717/peerj.2307

Hedges, S., Duckworth, J. W., Timmins, R., Semiadi, G., & Dryden, G. (2015). *Rusa timorensis Blainville*, Javan Deer. *Rusa timorensis Blainville. The IUCN Red List of Threatened Species 2015: E.T41789A22156866*, *8235*. Retrieved from http://dx.doi.org/10.2305/IUCN.UK.2015-2.RLTS.T41789A22156866.en%5CnCopyright:

Hernández, N., Martínez-González, J. C., Parra-Bracamonte, G. M., Sifuentes-Rincón, A. M., López-Villalobos, N., Morris, S. T., … Meza-García, L. A. (2016). Association of polymorphisms in growth hormone and leptin candidate genes with live weight traits of Brahman cattle. *Genetics and Molecular Research*, *15*(3). https://doi.org/10.4238/gmr.15038449

Horváthová, T., Nakagawa, S., & Uller, T. (2012). Strategic female reproductive investment in response to male attractiveness in birds. *Proceedings. Biological Sciences*, *279*(1726), 163–170. https://doi.org/10.1098/rspb.2011.0663

Howe, B., Umrigar, A., & Tsien, F. (2014). Chromosome preparation from cultured cells. *Journal of Visualized Experiments*, (83), e50203. https://doi.org/10.3791/50203

Hua, R., Yu, S., Liu, M., & Li, H. (2018). A PCR-based method for RNA probes and applications in neuroscience. *Frontiers in Neuroscience*, *12*(MAY), 1–11. https://doi.org/10.3389/fnins.2018.00266

Huang, H., & Chen, J. (2017). Chromosome bandings. *Methods in Molecular Biology*, *1541*, 59–66. https://doi.org/10.1007/978-1-4939-6703-2_6

Huang, L., Wang, J., Nie, W., Su, W., & Yang, F. (2006). Tandem chromosome fusions in karyotypic evolution of Muntiacus: Evidence from M. feae and M. gongshanensis. *Chromosome Research*, *14*(6), 637–647. https://doi.org/10.1007/s10577-006-1073-2

Huang, Ling, Chi, J., Nie, W., Wang, J., & Yang, F. (2006). Phylogenomics of several deer species revealed by comparative chromosome painting with Chinese muntjac paints. *Genetica*, *127*(1–3), 25–33. https://doi.org/10.1007/s10709-005-2449-5

Iannuzzi, I. (1996). G- and R-banded promethaphase karyotypes in cattle (Bos taurus L.). *Chromosome Research*, *4*(1), 448–456.

Iannuzzi, L. (1996). G- and R-banded prometaphase karyotypes in cattle (Bos taurus L.). *Chromosome Research*, *4*(6), 448–456. https://doi.org/10.1007/BF02265052

Iannuzzi, L., Perucatti, A., Di Meo, G. P., Polimeno, F., Ciotola, F., Incarnato, D., … Vonghia, G. (2004). Chromosome fragility in two sheep flocks exposed to dioxins during pasturage. *Mutagenesis*, *19*(5), 355–359. https://doi.org/10.1093/mutage/geh041

Iannuzzi, Leopoldo. (2010). The genetic improvement of the water buffalo (Bubalus bubalis): The contribution of the cytogenetics. *Revista Veterinaria*, *21*(SUPPL.1), 66–71.

Iannuzzi, Leopoldo, Villagómez, D. A. F., & King, W. A. (2009). Preface. *Cytogenetic and Genome Research*, *126*(1–2), 5–6. https://doi.org/10.1159/000245901

Ioannidis, N. M., Rothstein, J. H., Pejaver, V., Middha, S., McDonnell, S. K., Baheti, S., … Sieh, W. (2016). REVEL: An Ensemble Method for Predicting the Pathogenicity of Rare Missense Variants. *American Journal of Human Genetics*, *99*(4), 877–885. https://doi.org/10.1016/j.ajhg.2016.08.016

Issa, É. C., Jorge, W., & Sereno, J. R. B. (2006). Cytogenetic and molecular analysis of the Pantaneiro cattle breed. *Pesquisa Agropecuaria Brasileira*, *41*(11), 1609–1615. https://doi.org/10.1590/S0100-204X2006001100006

Ittisoponpisan, S., Islam, S. A., Khanna, T., Alhuzimi, E., David, A., & Sternberg, M. J. E. (2019). Can Predicted Protein 3D Structures Provide Reliable Insights into whether Missense Variants Are Disease Associated? *Journal of Molecular Biology*, *431*(11), 2197–2212. https://doi.org/10.1016/j.jmb.2019.04.009

J. Van Durme, J. Delgado, F. Stricher, L. Serrano, J. Schymkowitz, F. R. (2011). A graphical interface for the FoldX force field. *Bioinformatics*, *27*, 1711–1712.

Jabbour, H., Hayssen, V., & Bruford, M. (1997a). Conservation of deer: contributions from molecular biology, evolutionary ecology, and reproductive physiology. *Journal of Zoology*, *243*(3), 461–484. https://doi.org/10.1111/j.1469-7998.1997.tb02795.x

Jabbour, H., Hayssen, V., & Bruford, M. (1997b). Conservation of deer: contributions from molecular biology, evolutionary ecology, and reproductive physiology. *Journal of Zoology*, *243*(3), 461–484. https://doi.org/10.1111/j.1469-7998.1997.tb02795.x

Jansson, T. (2014). Genes involved in ovulation rate and litter size in sheep. *Uppsala*. Retrieved from http://epsilon.slu.se

Jones, D. T., Taylor, W. R., & Thornton, J. M. (1992). The rapid generation of mutation data matrices from protein sequences. *Computer Applications in the Biosciences : CABIOS*, *8*(3), 275–282. Retrieved from http://www.ncbi.nlm.nih.gov/pubmed/1633570

Jonsson, H., & Peng, S. L. (2005). Forkhead transcription factors in immunology. *CMLS Cellular and Molecular Life Sciences*, *62*(4), 397–409. https://doi.org/10.1007/s00018-004-4365-8

Kallel, H., Zaïri, H., Rourou, S., Essafi, M., Barbouche, R., Dellagi, K., & Fathallah, D. M. (2002). Use of Taguchi's methods as a basis to optimize hybridoma cell line growth and antibody production in a spinner flask. *Cytotechnology*, *39*(1), 9–14. https://doi.org/10.1023/A:1022437514334

Katzeff, J. S., Phan, K., Purushothuman, S., Halliday, G. M., & Kim, W. S. (2019). Cross-examining candidate genes implicated in multiple system atrophy. *Acta Neuropathologica Communications*, *7*(1), 117. https://doi.org/10.1186/s40478-019-0769-4

Kearney, L. (2006). Multiplex-FISH (M-FISH): technique, developments and applications. *Cytogenetic and Genome Research*, *114*, 189–198.

Keehner, J. R., Wielgus, R. B., & Waits, L. P. (2007). Hybridization Between White-tailed Deer and Mule Deer in Northeastern Washington: Are Mountain Lions Protecting the Genetic Integrity of Mule Deer? *Felid Biology and Conservation*, 60. Retrieved from Keehner_et_al_2007_Hybridization_Between_White-tailed_Deer_&_Mule_Deer_in_Washington.pdf

Kirkpatrick, B. W., & Morris, C. A. (2015). A major gene for bovine ovulation rate. *PLoS ONE*, *10*(6), e0129025. https://doi.org/10.1371/journal.pone.0129025

Klinder, A., Markhoff, J., Jonitz‐Heincke, A., Sterna, P., Salamon, A., & Bader, R. (2019). Comparison of different cell culture plates for the enrichment of non‐adherent human mononuclear cells. *Experimental and Therapeutic Medicine*, 2004–2012. https://doi.org/10.3892/etm.2019.7204

Korkmaz Ağaoğlu, Ö., Saatci, M., Akyüz, B., Elmaz, Ö., Çolak, M., Balkan, B. M., & Zeytünlü, E. (2015). Melatonin receptor 1A gene RsaI and inhibin alpha subunit gene HaeII polymorphisms in Honamli and Hair goat breeds reared in Western Mediterranean region of Turkey. *Turkish Journal of Veterinary and Animal Sciences*, *39*, 23–28. https://doi.org/10.3906/vet-1409-31

Kovac, J. R., Pastuszak, A. W., & Lamb, D. J. (2013). The use of genomics, proteomics, and metabolomics in identifying biomarkers of male infertility. *Fertility and Sterility*, *99*(4). https://doi.org/10.1016/j.fertnstert.2013.01.111

Kowalska, A., Bozsaky, E., & Ambros, P. F. (2010). *Sequence-Based High Resolution Chromosomal Comparative Genomic Hybridization (CGH)*. https://doi.org/10.1007/978-1-60761-789-1_23

Krepelova, A., Simandlova, M., Vlckova, M., Kuthan, P., Vincent, A. L., & Liskova, P. (2016). Analysis of *FOXL2* detects three novel mutations and an atypical phenotype of blepharophimosis-ptosis-epicanthus inversus syndrome. *Clinical & Experimental Ophthalmology*, *44*(9), 757–762. https://doi.org/10.1111/ceo.12783

Kristensen, S. G., Andersen, K., Clement, C. A., Franks, S., Hardy, K., & Andersen, C. Y. (2014). Expression of TGF-beta superfamily growth factors, their receptors, the associated SMADs and antagonists in five isolated size-matched populations of pre-antral follicles from normal human ovaries. *MHR: Basic Science of Reproductive Medicine*, *20*(4), 293–308. https://doi.org/10.1093/molehr/gat089

Kulski, J. K., Shiina, T., Anzai, T., Kohara, S., & Inoko, H. (2002). Comparative genomic analysis of the MHC: the evolution of class I duplication blocks, diversity and complexity from shark to man. *Immunological Reviews*, *190*(1), 95–122. https://doi.org/imr19008 [pii]

Kumar, S., Stecher, G., Li, M., Knyaz, C., & Tamura, K. (2018). MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. *Molecular Biology and Evolution*, *35*(6), 1547–1549. https://doi.org/10.1093/molbev/msy096

Kuwayama, R., & Ozawa, T. (2000). Phylogenetic relationships among european red deer, wapiti, and sika deer inferred from mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution*, *15*(1), 115–123. https://doi.org/10.1006/mpev.1999.0731

Kydd, J., Marlin, D. J., Deaton, C. M., Saunders, K., Heaton, P., Kingston, D. A., … Smith, N. C. (2018). Application of the Comet Assay for Investigation of Oxidative DNA Damage in Equine Peripheral Blood Mononuclear Cells. *The Journal of Nutrition*. https://doi.org/10.1093/jn/134.8.2133s

Lai, P., Zhang, B., Wang, P., Chu, M., Song, W., & Cai, B. (2013). Polymorphism of the Melatonin Receptor Genes and its Relationship with Seasonal Reproduction in the Gulin Ma Goat Breed. *Reproduction in Domestic Animals*, *48*(5), 732–737. https://doi.org/10.1111/rda.12153

Larkin, M. A., Blackshields, G., Brown, N. P., Chenna, R., Mcgettigan, P. A., McWilliam, H., … Higgins, D. G. (2007). Clustal W and Clustal X version 2.0. *Bioinformatics*, *23*(21), 2947–2948. https://doi.org/10.1093/bioinformatics/btm404

Lassoued, N., Benkhlil, Z., Woloszyn, F., Rejeb, A., Aouina, M., Rekik, M., … Bedhiaf-Romdhani, S. (2017). FecX Bar a Novel BMP15 mutation responsible for prolificacy and female sterility in Tunisian Barbarine Sheep. *BMC Genetics*, *18*(1), 43. https://doi.org/10.1186/s12863-017-0510-x

Lawce, H. J. (2017). Chromosome stains. *The AGT Cytogenetics Laboratory Manual*, 213–300. https://doi.org/10.1002/9781119061199.ch6

Le, S. Q., & Gascuel, O. (2008). An Improved General Amino Acid Replacement Matrix. *Molecular Biology and Evolution*, *25*(7), 1307–1320. https://doi.org/10.1093/molbev/msn067

Lee, G. S., Kim, H. S., Hwang, W. S., & Hyun, S. H. (2008). Characterization of porcine growth differentiation factor-9 and its expression in oocyte maturation. *Molecular Reproduction and Development*, *75*(5), 707–714. https://doi.org/10.1002/mrd.20810

Lee, J. I., & Kim, I. H. (2007). Pregnancy loss in dairy cows: The contributing factors, the effects on reproductive performance and the economic impact. *Journal of Veterinary Science*, *8*(3), 283–288. https://doi.org/10.4142/jvs.2007.8.3.283

Lee, P. (2014, May 5). Sambar deer facing extinction in peninsula. *The Star Online*.

Leslie, D. M. (2011). *Rusa unicolor Kerr* (Artiodactyla: Cervidae). *Mammalian Species*, *43*(871), 1–30. https://doi.org/10.1644/871.1

Lister, A. M., Edwards, C. J., Nock, D. A. W., Bunce, M., van Pijlen, I. A., Bradley, D. G., … Barnes, I. (2005). The phylogenetic position of the 'giant deer' Megaloceros giganteus. *Nature*, *438*(7069), 850–853. https://doi.org/10.1038/nature04134

Liu, A., Lund, M. S., Boichard, D., Karaman, E., Fritz, S., Aamand, G. P., … Su, G. (2019). Improvement of genomic prediction by integrating additional single nucleotide polymorphisms selected from imputed whole genome sequencing data. *Heredity*. https://doi.org/10.1038/s41437-019-0246-7

Loudon, A. S., & Curlewis, J. D. (1988). Cycles of antler and testicular growth in an aseasonal tropical deer (*Axis axis Erxleben*). *Journal of Reproduction and Fertility*, *83*(2), 729–738. https://doi.org/10.1530/jrf.0.0830729

Luo, W., Pla-Roca, M., & Juncker, D. (2011). Taguchi Design-Based Optimization of Sandwich Immunoassay Microarrays for Detecting Breast Cancer Biomarkers. *Analytical Chemistry*, *83*(14), 5767–5774. https://doi.org/10.1021/ac103239f

Luzhna, L., Kathiria, P., & Kovalchuk, O. (2013). Micronuclei in genotoxicity assessment: From genetics to epigenetics and beyond. *Frontiers in Genetics*, *4*(JUL), 1–17. https://doi.org/10.3389/fgene.2013.00131

Maddox, J. F. (2005). *A presentation of the differences between the sheep and goat genetic maps A presentation of the di ff erences between*. *37*, 1–10.

Madeira, F., Park, Y. M., Lee, J., Buso, N., Gur, T., Madhusoodanan, N., … Lopez, R. (2019). The EMBL-EBI search and sequence analysis tools APIs in 2019. *Nucleic Acids Research*, *47*(W1), W636–W641. https://doi.org/10.1093/nar/gkz268

Mahre, M. B., Wahid, H., Rosnina, Y., & Jesse, F. F. A. (2015). Assessment of temperament in *Rusa timorensis Blainville* and its relationship to stress. *Journal of Animal Science*, *93*(3), 1276–1283. https://doi.org/10.2527/jas.2014-8080

Mäki, A., Salmi, P., Mikkonen, A., Kremp, A., & Tiirola, M. (2017). Sample Preservation, DNA or RNA extraction and data analysis for high-throughput phytoplankton community sequencing. *Frontiers in Microbiology*, *8*(SEP), 1–13. https://doi.org/10.3389/fmicb.2017.01848

Makowski, K., Matusiak, K., Borowski, S., Bielnicki, J., Tarazewicz, A., Maroszyńska, M., … Gutarowska, B. (2017). Optimization of a Culture Medium Using the Taguchi Approach for the Production of Microorganisms Active in Odorous Compound Removal. *Applied Sciences*, *7*(8), 756. https://doi.org/10.3390/app7080756

Makunin, A. I., Kichigin, I. G., Larkin, D. M., Brien, P. C. M. O., Ferguson-smith, M. A., Yang, F., … Trifonov, V. A. (2016). Contrasting origin of B chromosomes in two cervids (Siberian roe deer and grey brocket deer) unravelled by chromosome- specific DNA sequencing. *BMC Genomics*, 1–14. https://doi.org/10.1186/s12864-016-2933-6

Makunin, A. I., Kichigin, I. G., Larkin, D. M., O'Brien, P. C. M., Ferguson-Smith, M. A., Yang, F., … Trifonov, V. A. (2016). Contrasting origin of B chromosomes in two cervids (Siberian roe deer and grey brocket deer) unravelled by chromosome-specific DNA sequencing. *BMC Genomics*, *17*(1), 618. https://doi.org/10.1186/s12864-016-2933-6

Mardis, E. R. (2010). The $1,000 genome, the $100,000 analysis? *Genome Medicine*, *2*(11), 84. https://doi.org/10.1186/gm205

Martins, R. F., Fickel, J., Le, M., van Nguyen, T., Nguyen, H. M., Timmins, R., … Wilting, A. (2017). Phylogeography of red muntjacs reveals three distinct mitochondrial lineages. *BMC Evolutionary Biology*, *17*(1), 34. https://doi.org/10.1186/s12862-017-0888-0

Mary, N., Barasc, H., Ferchaud, S., Billon, Y., Meslier, F., Robelin, D., … Pinton, A. (2014). Meiotic recombination analyses of individual chromosomes in male domestic pigs (Sus scrofa domestica). *PLoS ONE*, *9*(6), e99123. https://doi.org/10.1371/journal.pone.0099123

Masuda, Y., Takahashi, H., Sato, S., Tomomori-Sato, C., Saraf, A., Washburn, M. P., … Hatakeyama, S. (2015). TRIM29 regulates the assembly of DNA repair proteins into damaged chromatin. *Nature Communications*, *6*, 1–13. https://doi.org/10.1038/ncomms8299

Mateos-Langerak, J., Bohn, M., de Leeuw, W., Giromus, O., Manders, E. M. M., Verschure, P. J., … Goetze, S. (2009). Spatially confined folding of chromatin in the interphase nucleus. *Proceedings of the National Academy of Sciences*, *106*(10), 3812–3817. https://doi.org/10.1073/pnas.0809501106

Matoušek, J. (1986). Genetics of reproduction in sheep. *Animal Reproduction Science*, *11*, 235–236. https://doi.org/10.1016/0378-4320(86)90125-9

Matsuda, K. (2017). PCR-Based Detection Methods for Single-Nucleotide Polymorphism or Mutation: Real-Time PCR and Its Substantial Contribution Toward Technological Refinement. In *Advances in Clinical Chemistry* (Vol. 80, pp. 45–72). https://doi.org/10.1016/bs.acc.2016.11.002

Mcneil, N., Montagna, C., Difilippantonio, M. J., & Ried, T. (2010). Comparative Cancer Cytogenetics. *Cancer*, (Cml), 1–22.

McNeil, N., & Ried, T. (2000). Novel molecular cytogenetic techniques for identifying complex chromosomal rearrangements: technology and applications in molecular medicine. *Expert Reviews in Molecular Medicine*, *2000*(September 2000), 1–14. https://doi.org/doi:10.1017/S1462399400001940

McPherson, J. D., Marra, M., Hillier, L., Waterston, R. H., Chinwalla, A., Wallis, J., … International Human Genome Mapping Consortium. (2001). A physical map of the human genome. *Nature*, *409*(6822), 934–941. https://doi.org/10.1038/35057157

McPherson, M. C., Robinson, C. M., Gehlen, L. P., & Delany, M. E. (2014). Comparative cytogenomics of poultry: Mapping of single gene and repeat loci in the Japanese quail (Coturnix japonica). *Chromosome Research*, *22*(1), 71–83. https://doi.org/10.1007/s10577-014-9411-2

Messer, L. A., Wang, L., Tuggle, C. K., Yerle, M., Chardon, P., Pomp, D., … Rothschild, M. F. (1997). Mapping of the melatonin receptor 1a (MTNR1A) gene in pigs, sheep, and cattle. *Mammalian Genome*, *8*(5), 368–370. https://doi.org/10.1007/s003359900444

Meuwissen, T., Hayes, B., & Goddard, M. (2016). Genomic selection: A paradigm shift in animal breeding. *Animal Frontiers*, *6*(1), 6–14. https://doi.org/10.2527/af.2016-0002

Min, L., Nie, M., Zhang, A., Wen, J., Noel, S. D., Lee, V., … Kaiser, U. B. (2016). Computational Analysis of Missense Variants of G Protein-Coupled Receptors Involved in the Neuroendocrine Regulation of Reproduction. *Neuroendocrinology*, *103*(3–4), 230–239. https://doi.org/10.1159/000435884

Mirzaghaderi, G., & Marzangi, K. (2015). *IdeoKar* : an ideogram constructing and karyotype analyzing software. *Caryologia*, *68*(1), 31–35. https://doi.org/10.1080/00087114.2014.998526

Moradband, F., Rahimi, G., & Gholizadeh, M. (2011). Association of polymorphisms in fecundity genes of GDF9, BMP15 and BMP15-1B with litter size in iranian Baluchi sheep. *Asian-Australasian Journal of Animal Sciences*, *24*(9), 1179–1183. https://doi.org/10.5713/ajas.2011.10453

Morgan-Richards, M., Smissen, R. D., Shepherd, L. D., Wallis, G. P., Hayward, J. J., Chan, C. H., … Chapman, H. M. (2009). A review of genetic analyses of hybridisation in New Zealand. *Journal of the Royal Society of New Zealand*, *39*(1), 15–34. https://doi.org/10.1080/03014220909510561

Morita, T., MacGregor, J. T., & Hayashi, M. (2011). Micronucleus assays in rodent tissues other than bone marrow. *Mutagenesis*, *26*(1), 223–230. https://doi.org/10.1093/mutage/geq066

Muir, P. D., Semiadi, G., Asher, G. W., Broad, T. E., Tate, M. L., & Barry, T. N. (1993). Sambar deer (Cervus unicolor) x red deer (C. elaphus) interspecies hybrids. *The Journal of Heredity*, *88*(5), 366–372.

Mullen, M. P., & Hanrahan, J. P. (2014). Direct Evidence on the Contribution of a Missense Mutation in GDF9 to Variation in Ovulation Rate of Finnsheep. *PLoS ONE*, *9*(4), e95251. https://doi.org/10.1371/journal.pone.0095251

Nagdy, H., Mahmoud, K. G. M., Kandiel, M. M. M., Helmy, N. A., Ibrahim, S. S., Nawito, M. F., & Othman, O. E. (2018). PCR-RFLP of bone morphogenetic protein 15 (BMP15/FecX) gene as a candidate for prolificacy in sheep. *International Journal of Veterinary Science and Medicine*, *6*(Suppl), S68–S72. https://doi.org/10.1016/j.ijvsm.2018.01.001

Naha, B. C., Prakesh, C., & Boro, P. (2016). Review Article Application of Cytogenetic Techniques in Livestock. *International Journal of Science and Nature*, *7*(1), 30–33.

Nakaya, Masataka, Tanabe, Hideyuki, Takamatsu, Shingo, Hosokawa, Misaki and Mitani, T. (2017). Visualization of the spatial arrangement of nuclear organization using three-dimensional fluorescence *in situ* hybridization in early mouse embryos: A new "EASI-FISH chamber glass" for mammalian embryos. *Journal of Reproduction and Development*, *63*(2), 167–174. https://doi.org/10.1262/jrd.2016-172

Nani, J. P., Rezende, F. M., & Peñagaricano, F. (2019). Predicting male fertility in dairy cattle using markers with large effect and functional annotation data. *BMC Genomics*, *20*(1), 258. https://doi.org/10.1186/s12864-019-5644-y

Nicholson, L. B. (2016). The immune system. *Essays in Biochemistry*, *60*(3), 275–301. https://doi.org/10.1042/EBC20160017

Nicol, L., Bishop, S. C., Pong-Wong, R., Bendixen, C., Holm, L. E., Rhind, S. M., & McNeilly, A. S. (2009). Homozygosity for a single base-pair mutation in the oocyte-specific GDF9 gene results in sterility in Thoka sheep. *Reproduction*, *138*(6), 921–933. https://doi.org/10.1530/REP-09-0193

Norling, A., Hirschberg, A. L., Rodriguez-Wallberg, K. A., Iwarsson, E., Wedell, A., & Barbaro, M. (2014). Identification of a duplication within the GDF9 gene and novel candidate genes for primary ovarian insufficiency (POI) by a customized high-resolution array comparative genomic hybridization platform. *Human Reproduction*, *29*(8), 1818–1827. https://doi.org/10.1093/humrep/deu149

Notter, D. (2008). Genetic Aspects of Reproduction in Sheep. *Reproduction in Domestic Animals*, *43*, 122–128. https://doi.org/10.1111/j.1439-0531.2008.01151.x

O Khalifa, N., F. Khater, H., A. Fahmy, H., E.I.Radwan, M., & S.A. Afify, J. (2014). Genotyping and Phylogenetic Analysis of Cystic Echinococcosis Isolated from Camels and Humans in Egypt. *American Journal of Epidemiology and Infectious Disease*, *2*(3), 74–82. https://doi.org/10.12691/ajeid-2-3-2

Oecd. (2014). *OECD Test Guideline 487*. (September), 1–26. Retrieved from https://ntp.niehs.nih.gov/iccvam/suppdocs/feddocs/oecd/oecd-tg487-2014-508.pdf

Olano-Marin, J., Plis, K., Sönnichsen, L., Borowik, T., Niedziałkowska, M., & Jędrzejewska, B. (2014). Weak population structure in European roe Deer (Capreolus capreolus) and evidence of introgressive hybridization with Siberian roe deer (C. Pygargus) in Northeastern Poland. *PLoS ONE*, *9*(10). https://doi.org/10.1371/journal.pone.0109147

Olivieri, C., Marota, I., Rizzi, E., Ermini, L., Fusco, L., Pietrelli, A., … Luciani, S. (2014). Positioning the red deer (Cervus elaphus) hunted by the Tyrolean Iceman into a mitochondrial DNA phylogeny. *PLoS ONE*, *9*(7). https://doi.org/10.1371/journal.pone.0100136

P.W. Rose, A. Prlić, A. Altunkaya, C. Bi, A.R. Bradley, C.H.Christie, et al. (2017). The RCSB protein data bank: integrative view of protein, gene and 3D structural information. *Nucleic Acids Research*, *45*, D271–D281.

P, S. (2000). The Sequence Manipulation Suite: JavaScript programs for analyzing and formatting protein and DNA sequences. *BioTechniques*, *28*, 1102–1104.

Pandey, R. V., Pabinger, S., Kriegner, A., & Weinhäusel, A. (2016). ClinQC: A tool for quality control and cleaning of Sanger and NGS data in clinical research. *BMC Bioinformatics*, *17*(1). https://doi.org/10.1186/s12859-016-0915-y

Pauciullo, A., Knorr, C., Perucatti, A., Iannuzzi, A., Iannuzzi, L., & Erhardt, G. (2016). Characterization of a very rare case of living ewe-buck hybrid using classical and molecular cytogenetics. *Scientific Reports*, *6*(1), 34781. https://doi.org/10.1038/srep34781

Peng, J., Li, Q., Wigglesworth, K., Rangarajan, A., Kattamuri, C., Peterson, R. T., … Matzuk, M. M. (2013). Growth differentiation factor 9:bone morphogenetic protein 15 heterodimers are potent regulators of ovarian functions. *Proceedings of the National Academy of Sciences of the United States of America*, *110*(8), E776–E785. https://doi.org/10.1073/pnas.1218020110

Perelman, P. L., Beklemisheva, V. R., Yudkin, D. V., Petrina, T. N., Rozhnov, V. V., Nie, W., & Graphodatsky, A. S. (2012). Comparative Chromosome Painting in Carnivora and Pholidota. *Cytogenetic and Genome Research*, *137*(2–4), 174–193. https://doi.org/10.1159/000341389

Perkins, A. T., & Bickel, S. E. (2017). Using Fluorescence In Situ Hybridization (FISH) to Monitor the State of Arm Cohesion in Prometaphase and Metaphase I Drosophila Oocytes. *Journal of Visualized Experiments*, (130). https://doi.org/10.3791/56802

Petrey, D., Chen, T. S., Deng, L., Garzon, J. I., Hwang, H., Lasso, G., … Honig, B. (2015, June 1). Template-based prediction of protein function. *Current Opinion in Structural Biology*, Vol. 32, pp. 33–38. https://doi.org/10.1016/j.sbi.2015.01.007

Pires, D. E. V., Ascher, D. B., & Blundell, T. L. (2014). DUET: A server for predicting effects of mutations on protein stability using an integrated computational approach. *Nucleic Acids Research*, *42*(W1). https://doi.org/10.1093/nar/gku411

Pūraitė, I., Paulauskas, A., & Sruoga, A. (2013). Analysis of genetic diversity of roe deer (Capreolus capreolus L.) in Lithuania using RAPD and allozyme systems. *Biologija*, *59*(1), 29–38. Retrieved from http://www.lmaleidykla.lt/ojs/index.php/biologija/article/view/2649%5Cnhttp://www.lmaleidykla.lt/ojs/index.php/biologija/article/download/2649/1485

Qafary, M., Gharanfoli, M., & Qafari, S. M. (2018). Taking Advantage of Taguchi Design Method to Optimize Medium Culture Conditions for Producing Recombinant Follicle Stimulating Hormone. *Journal of Biometrics & Biostatistics*, *09*(04), 1–4. https://doi.org/10.4172/2155-6180.1000409

Qanbari, S., Osfoori, R., & Nasab, M. P. E. (2007, April 1). A preliminary study of marker data applicability in gene introgression program for Afshari sheep breed. *Biotechnology*, Vol. 6, pp. 513–519. https://doi.org/10.3923/biotech.2007.513.519

Qin, N., Liu, Q., Zhang, Y. Y., Fan, X. C., Xu, X. X., Lv, Z. C., … Xu, R. F. (2015). Association of novel polymorphisms of forkhead box L2 and growth differentiation factor-9 genes with egg production traits in local Chinese Dagu hens. *Poultry Science*, *94*(1), 88–95. https://doi.org/10.3382/ps/peu023

Qu, X., Swanson, R., Day, R., & Tsai, J. (2009). A Guide to Template Based Structure Prediction. *Current Protein & Peptide Science*, *10*(3), 270–285. https://doi.org/10.2174/138920309788452182

Rachmawati, A. (2012). Motilitas dan viabilitas semen rusa timor (Cervus timorensis) menggunakan pengencer yang berbeda pada suhu 5. *Jurnal Ilmu-Ilmu Peternakan*, *20*(2), 1–9.

Ramesh, T., Kalle, R., Sankar, K., Qureshi, Q., & Downs, C. T. (2013). Aspects of breeding biology of chital (*Axis axis Erxleben*) and sambar (*Rusa unicolor Kerr*) in the Western Ghats. *Acta Ethologica*, *16*(3), 147–155. https://doi.org/10.1007/s10211-013-0145-5

Ramírez, O., Tomàs, A., Barragan, C., Noguera, J. L., Amills, M., & Varona, L. (2009). Pig melatonin receptor 1a (MTNR1A) genotype is associated with seasonal variation of sow litter size. *Animal Reproduction Science*, *115*(1–4), 317–322. https://doi.org/10.1016/J.ANIREPROSCI.2008.12.013

Raudsepp, T., & Chowdhary, B. P. (2016). Chromosome Aberrations and Fertility Disorders in Domestic Animals. *Annual Review of Animal Biosciences*, *4*(1), 15–43. https://doi.org/10.1146/annurev-animal-021815-111239

Rauw, W. M., & Gomez-Raya, L. (2015). Genotype by environment interaction and breeding for robustness in livestock. *Frontiers in Genetics*, *6*(OCT), 1–15. https://doi.org/10.3389/fgene.2015.00310

Reavey, C. E., Warnock, N. D., Vogel, H., & Cotter, S. C. (2014). Trade-offs between personal immunity and reproduction in the burying beetle, Nicrophorus vespilloides. *Behavioral Ecology*, *25*(2), 415–423. https://doi.org/10.1093/beheco/art127

Reeb, J., Hecht, M., Mahlich, Y., Bromberg, Y., & Rost, B. (2016). Predicted Molecular Effects of Sequence Variants Link to System Level of Disease. *PLoS Computational Biology*, *12*(8), 1–14. https://doi.org/10.1371/journal.pcbi.1005047

Remmert, M., Biegert, A., Hauser, A., & Söding, J. (2012). HHblits: lightning-fast iterative protein sequence searching by HMM-HMM alignment. *Nature Methods*, *9*(2), 173–175. https://doi.org/10.1038/nmeth.1818

Rexroad, C., Vallet, J., Matukumalli, L. K., Reecy, J., Bickhart, D., Blackburn, H., … Coleman, L. (2019). Genome to phenome: Improving animal health, production, and well-being - A new USDA blueprint for animal genome research 2018-2027. *Frontiers in Genetics*, *10*(MAY), 1–29. https://doi.org/10.3389/fgene.2019.00327

Rogers, M. F., Shihab, H. A., Mort, M., Cooper, D. N., Gaunt, T. R., & Campbell, C. (2018). FATHMM-XF: accurate prediction of pathogenic point mutations via extended features. *Bioinformatics*, *34*(3), 511–513. https://doi.org/10.1093/bioinformatics/btx536

Rønne, M., Rønne, I., & Rønne, M. (1989). Chromosome preparation and high resolution banding techniques. A review. *Journal of Dairy Science*, *72*(5), 1363–1377. https://doi.org/10.3168/jds.S0022-0302(89)79243-2

Rothkamm K., Barnard S., Moquet J., Ellender M., R. Z. & B.-R. S. (2015). DNA damage foci: meaning and significance. *Environmental and Molecular Mutagenesis*, *56*, 491–504.

Ruchika D., Likhite, A. A., Zanwar, D. R., & Majumdar, G. (2007). JOURNAL OF SOILS AND CROPS. *Journal of Soils and Crops*, *17*(2), 320–325. Retrieved from https://www.cabdirect.org/cabdirect/abstract/20083005374

Russell, Tracey, Lisovski, S., Olsson, M., Brown, G., Spindler, R., Lane, A., … Madsen, T. (2018). MHC diversity and female age underpin reproductive success in an Australian icon; the Tasmanian Devil. *Scientific Reports*, *8*(1), 4175. https://doi.org/10.1038/s41598-018-20934-9

Russell, Ty, Cullingham, C., Kommadath, A., Stothard, P., Herbst, A., & Coltman, D. (2019). Development of a Novel Mule Deer Genomic Assembly and Species-Diagnostic SNP Panel for Assessing Introgression in Mule Deer, White-Tailed Deer, and Their Interspecific Hybrids. *G3: Genes|Genomes|Genetics*, *9*(March), g3.200838.2018. https://doi.org/10.1534/g3.118.200838

Rymešová, D., Králová, T., Promerová, M., Bryja, J., Tomášek, O., Svobodová, J., … Albrecht, T. (2017). Mate choice for major histocompatibility complex complementarity in a strictly monogamous bird, the grey partridge (Perdix perdix). *Frontiers in Zoology*, *14*(1), 1–10. https://doi.org/10.1186/s12983-017-0194-0

Saavedra, J. T., Schwartzman, J. A., & Gilmore, M. S. (2017). Current Protocols in Molecular Biology: Mapping Transposon Insertions in Bacterial Genomes by Arbitrarily Primed PCR. *Current Protocols in Molecular Biology*, *118*, 15.15.1-15.15.15. https://doi.org/10.1002/cpmb.38

Sabury, C. M., Bhattarai, E. K., Taylor, J. F., Viswanathan, G. G., Cooper, S. M., Davis, D. S., … Seabury, C. M., Bhattarai, E. K., Taylor, J. F., Viswanathan, G. G., Cooper S. M., Davis D. S., Dowd S.E., L. M. L. and S. P. M. (2011). Genome-wide polymorphism and comparative analyses in the whitetailed deer (Odocoileus virginianus): a model for conservation genomics. *Plos One*, *6:*(1), 15811. https://doi.org/http://dx.doi.org/10.1371/journal.pone.0015811

Sadegh-Nasseri, S., & Kim, A. (2015). MHC Class II Auto-Antigen Presentation is Unconventional. *Frontiers in Immunology*, *6*, 372. https://doi.org/10.3389/fimmu.2015.00372

Salisu, I. B, Olawale, A. S, Jabbar, B, Koloko, B. L, Abdurrahaman, S. L, Amin, A. B, and Ali, Q. (2018). Molecular markers and their Potentials in Animal Breeding and Genetics. *Nigerian J. Anim. Sci*, *20*(3), 29–48.

Salviano, M. B., Cursino, M. S., Zanetti, E. dos S., Abril, V. V., & Duarte, J. M. B. (2017). Intraspecific chromosome polymorphisms can lead to reproductive isolation and speciation: An example in red brocket deer (Mazama americana). *Biology of Reproduction*, *96*(6), 1279–1287. https://doi.org/10.1093/biolre/iox041

Saxena, V. K., Jha, B. K., Meena, A. S., & Naqvi, S. M. K. (2014). Sequence analysis and identification of new variations in the coding sequence of melatonin receptor gene (MTNR1A) of Indian Chokla sheep breed. *Meta Gene*, *2*, 450–458. https://doi.org/10.1016/j.mgene.2014.05.005

Scaramuzzi, R., & Martin, G. (2008). The Importance of Interactions Among Nutrition, Seasonality and Socio-sexual Factors in the Development of Hormone-free Methods for Controlling Fertility. *Reproduction in Domestic Animals*, *43*, 129–136. https://doi.org/10.1111/j.1439-0531.2008.01152.x

Schaller, G. B., & Vrba, E. S. (1996). Description of the Giant Muntjac (Megamuntiacus vuquangensis) in Laos. *Journal of Mammalogy*, *77*(3), 675. https://doi.org/10.2307/1382672

Scherthan, H., & Loidl, J. (2010). *FISH as a Tool to Investigate Chromosome Behavior in Budding Yeast*. https://doi.org/10.1007/978-1-60761-789-1_28

Schwarz, J. M., Rödelsperger, C., Schuelke, M., & Seelow, D. (2010). MutationTaster evaluates disease-causing potential of sequence alterations. *Nature Methods*, *7*(8), 575–576. https://doi.org/10.1038/nmeth0810-575

Sepil, I., Lachish, S., & Sheldon, B. C. (2013). Mhc-linked survival and lifetime reproductive success in a wild population of great tits. *Molecular Ecology*, *22*(2), 384–396. https://doi.org/10.1111/mec.12123

Serakinci, N., & Kølvraa, S. (2009). Molecular Cytogenetic Applications in Diagnostics and Research : An Overview. *Fluorescence In Situ Hybridization (FISH) – Application Guide*, 3–21.

Serdyńska-Szuster, M., Jędrzejczak, P., Ożegowska, K. E., Hołysz, H., Pawelczyk, L., & Jagodziński, P. P. (2016). Effect of growth differentiation factor-9 C447T and G546A polymorphisms on the outcomes of in vitro fertilization. *Molecular Medicine Reports*, *13*(5), 4437–4442. https://doi.org/10.3892/mmr.2016.5060

Shemetun, O. V., Talan, O. A., Demchenko, O. M., Kurinnyi, D. A., Papuga, M. S., & Pilinska, M. A. (2018). Frequency of Spontaneous and Radiation-Induced Chromosomal Aberrations in Peripheral Blood Lymphocytes of Individuals of Different Ages. *Cytology and Genetics*, *52*(6), 461–466. https://doi.org/10.3103/S0095452718060117

Sigurdardóttir, S., Lundén, A., & Andersson, L. (2009). Restriction fragment length polymorphism of DQ and DR class II genes of the bovine major histocompatibility complex. *Animal Genetics*, *19*(2), 133–150. https://doi.org/10.1111/j.1365-2052.1988.tb00799.x

Sim, N. L., Kumar, P., Hu, J., Henikoff, S., Schneider, G., & Ng, P. C. (2012). SIFT web server: Predicting effects of amino acid substitutions on proteins. *Nucleic Acids Research*, *40*(W1), W452–W457. https://doi.org/10.1093/nar/gks539

Slota, M., Maluszynski, M., & Szarejko, I. (2016). Bioinformatics-based assessment of the relevance of candidate genes for mutation discovery. In *Biotechnologies for Plant Mutation Breeding: Protocols* (pp. 263–280). https://doi.org/10.1007/978-3-319-45021-6_17

Smith, S. L., Carden, R. F., Coad, B., Birkitt, T., & Pemberton, J. M. (2014). A survey of the hybridisation status of Cervus deer species on the island of Ireland. *Conservation Genetics*, *15*(4), 823–835. https://doi.org/10.1007/s10592-014-0582-3

Smith, S. L., Senn, H. V, Megan, S. P., Heap, E., & Pemberton, J. M. (2018). *Introgression of exotic Cervus (nippon and canadensis) into red deer (Cervus elaphus) populations in Scotland and the English Lake District*. (May 2017), 2122–2134. https://doi.org/10.1002/ece3.3767

Smith, S., Mang, T., De Bellocq, J. G., Schaschl, H., Zeitlhofer, C., Hackländer, K., & Suchentrunk, F. (2010). Homozygosity at a class II MHC locus depresses female reproductive ability in European brown hares. *Molecular Ecology*, *19*(19), 4131–4143. https://doi.org/10.1111/j.1365-294X.2010.04765.x

Snibson, K. J., Maddox, J. F., Fabb, S. A., & Brandon, M. R. (1998). Allelic variation of ovine MHC class II DQA1 and DQA2 genes. *Animal Genetics*, *29*(5), 356–362. https://doi.org/10.1046/j.1365-2052.1998.295351.x

Sohn, S. H., Cho, E. J., Son, W. J., & Lee, C. Y. (2007). Diagnosis of bovine freemartinism by fluorescence in situ hybridization on interphase nuclei using a bovine Y chromosome-specific DNA probe. *Theriogenology*, *68*(7), 1003–1011. https://doi.org/10.1016/j.theriogenology.2007.06.022

Solari, S., & Baker, R. J. (2007). Mammal species of the world: a taxonomic and geographic reference. *Journal of Mammalogy*, *88*(3), 824–830. https://doi.org/10.1644/06-MAMM-R-422.1

Somody, J. C., MacKinnon, S. S., & Windemuth, A. (2017, December 1). Structural coverage of the proteome for pharmaceutical applications. *Drug Discovery Today*, Vol. 22, pp. 1792–1799. https://doi.org/10.1016/j.drudis.2017.08.004

Soto, M., García-Santisteban, I., Krenning, L., Medema, R. H., & Raaijmakers, J. A. (2018). Chromosomes trapped in micronuclei are liable to segregation errors. *Journal of Cell Science*, *131*(13). https://doi.org/10.1242/jcs.214742

Speicher, M. R., & Carter, N. P. (2005). The new cytogenetics: blurring the boundaries with molecular biology. *Nature Reviews. Genetics*, *6*(10), 782–792. https://doi.org/10.1038/nrg1692

Spiridonova, L. N., Valchuk, O. P., Red'kin, Y. A., Saitoh, T., & Kryukov, A. P. (2017). Phylogeography and demographic history of Siberian rubythroat Luscinia calliope. *Russian Journal of Genetics*, *53*(8), 885–902. https://doi.org/10.1134/S1022795417080105

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Y.-K. Y. (2005). Protein database searches using compositionally adjusted substitution matrices. *FEBS J.*, *272*, 5101–5109.

Stomornjak-Vukadin, M., Kurtovic-Basic, I., Mehinovic, L., & Konjhodzic, R. (2015). Combined use of cytogenetic and molecular methods in prenatal diagnostics of chromosomal abnormalities. *Acta Informatica Medica : AIM :*

Journal of the Society for Medical Informatics of Bosnia & Herzegovina : Casopis Drustva Za Medicinsku Informatiku BiH, *23*(2), 68–72. https://doi.org/10.5455/aim.2015.23.68-72

Studer, R. A., Dessailly, B. H., & Orengo, C. A. (2013). Residue mutations and their impact on protein structure and function: Detecting beneficial and pathogenic changes. *Biochemical Journal*, *449*(3), 581–594. https://doi.org/10.1042/BJ20121221

Sun, L. P., Song, Y. P., Du, Q. Z., Song, L. W., Tian, Y. Z., Zhang, S. L., … Yang, L. G. (2014). Polymorphisms in the bone morphogenetic protein 15 gene and their effect on sperm quality traits in Chinese Holstein bulls. *Genetics and Molecular Research*, *13*(1), 1805–1812. https://doi.org/10.4238/2014.March.17.8

Supakorn, C. (2009). The Important Candidate Genes in Goats - A Review. *Journal of Science and Technology*, *6*(1), 17–36. Retrieved from http://wjst.wu.ac.th/index.php/wjst/article/view/70

Suzy S. Stubblefield. Robert J. Warren and Brian R. Murphy. (1986). Hybridization of Free-Ranging White-Tailed and Mule Deer in Texas. *Journal of Wildlife Management*, *50*(4), 688–690. https://doi.org/10.2307/3800982

Sylwia Salamon, Joanna Nowacka-Woszuk, and M. S. (2015). Polymorphism of the CTNNB1 and FOXL2 Genes is not Associated with Canine XX Testicular/Ovotesticular Disorder of Sex Development. *FoliaBiologica(Kraków)*, *63*(1), 57–62. https://doi.org/10.3409/fb63

Takeshima, S., Chen, S., Miki, M., Kado, M., & Aida, Y. (2008). *Distribution and origin of bovine major histocompatibility complex class II DQA1 genes in Japan*. 195–205. https://doi.org/10.1111/j.1399-0039.2008.01092.x

Talebi, R., Ahmadi, A., Afraz, F., Sarry, J., Woloszyn, F., & Fabre, S. (2018). Detection of single nucleotide polymorphisms at major prolificacy genes in the Mehraban sheep and association with litter size. *Annals of Animal Science*, *18*(3), 685–698. https://doi.org/10.2478/aoas-2018-0014

Tambasco, D. D., Paz, C. C. P., Tambasco-Studart, M., Pereira, A. P., Alencar, M. M., Freitas, A. R., … Regitano, L. C. A. (2003). Candidate genes for growth traits in beef cattle crosses Bos taurus x Bos indicus. *Journal of Animal Breeding and Genetics*, *120*(1), 51–56. https://doi.org/10.1046/j.1439-0388.2003.00371.x

Tate, M. L., Mathias, H. C., Fennessy, P. F., Dodds, K. G., Penty, J. M., & Hill, D. F. (1995). A new gene mapping resource: Interspecies hybrids between Pere David's deer (Elaphurus davidianus) and red deer (Cervus elaphus). *Genetics*, *139*(3), 1383–1391.

Teng, S., Srivastava, A. K., Schwartz, C. E., Alexov, E., & Wang, L. (2010). Structural assessment of the effects of Amino Acid Substitutions on protein stability and protein-protein interaction. *International Journal of Computational Biology and Drug Design*, *3*(4), 334–349. https://doi.org/10.1504/IJCBDD.2010.038396

Tety Hartatik, Slamet Diah Volkandari, M. P. R. and S. (2012). Polymorphism leu/val of growth hormone gene identified from limousin cross local cattle in Indonesia. *The 3rd International Conference on Sustainable Future for Human Security SUSTAIN*, 105–108. https://doi.org/10.1016/j.proenv.2013.02.017

Teyssier, J., Migaud, M., Debus, N., Maton, C., Tillard, E., Malpaux, B., … Bodin, L. (2011). Expression of seasonality in Merinos d'Arles ewes of different genotypes at the MT1 melatonin receptor gene. *Animal*, *5*(03), 329–336. https://doi.org/10.1017/S1751731110001813

Thanakiatkrai, P., & Welch, L. (2012). Using the Taguchi method for rapid quantitative PCR optimization with SYBR Green I. *International Journal of Legal Medicine*, *126*(1), 161–165. https://doi.org/10.1007/s00414-011-0558-5

Thornton, P. K. (2010). Livestock production: Recent trends, future prospects. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *365*(1554), 2853–2867. https://doi.org/10.1098/rstb.2010.0134

Tobergte, D. R., & Curtis, S. (2013). Fluorescence in situ Hybridization (FISH). In *Journal of Chemical Information and Modeling* (Vol. 53). https://doi.org/10.1017/CBO9781107415324.004

Tran, A. N., Taylan, F., Zachariadis, V., Ivanov Öfverholm, I., Lindstrand, A., Vezzi, F., … Barbany, G. (2018). High-resolution detection of chromosomal rearrangements in leukemias through mate pair whole genome sequencing. *PLOS ONE*, *13*(3), e0193928. https://doi.org/10.1371/journal.pone.0193928

Treiber, M. L., Taft, D. H., Korf, I., Mills, D. A., & Lemay, D. G. (2020). Pre-and post-sequencing recommendations for functional annotation of human fecal metagenomes. *BMC Bioinformatics*, *21*(1). https://doi.org/10.1186/s12859-020-3416-y

Trumble, B. C., Blackwell, A. D., Stieglitz, J., Thompson, M. E., Suarez, I. M., Kaplan, H., & Gurven, M. (2016). Associations between male testosterone and immune function in a pathogenically stressed forager-horticultural population. *American Journal of Physical Anthropology*, *161*(3), 494–505. https://doi.org/10.1002/ajpa.23054

Udroiu, I., & Sgura, A. (2017). Cytogenetic tests for animal production: state of the art and perspectives. *Animal Genetics*, *48*(5), 505–515. https://doi.org/10.1111/age.12581

Uhlenhaut, N. H., & Treier, M. (2006). Foxl2 function in ovarian development. *Molecular Genetics and Metabolism*, *88*(3), 225–234. https://doi.org/10.1016/j.ymgme.2006.03.005

Valeri, M. P., Tomazella, I. M., & Duarte, J. M. B. (2018). Intrapopulation chromosomal polymorphism in mazama gouazoubira (Cetartiodactyla; Cervidae): The emergence of a new species? *Cytogenetic and Genome Research*, *154*(3), 147–152. https://doi.org/10.1159/000488377

Viana, J. M. S., Piepho, H.-P., Silva, F. F. e, Viana, J. M. S., Piepho, H.-P., & Silva, F. F. e. (2016). Quantitative genetics theory for genomic selection and efficiency of breeding value prediction in open-pollinated populations. *Scientia Agricola*, *73*(3), 243–251. https://doi.org/10.1590/0103-9016-2014-0383

Vidyadaran, M. K., Jaafar, M., & Ibrahim, J. (1993). The Deer Industry in Malaysia. *The Animal Industry in Malaysia*, pp. 111–119.

von Gall, C., Stehle, J. H., & Weaver, D. R. (2002). Mammalian melatonin receptors: molecular biology and signal transduction. *Cell and Tissue Research*, *309*(1), 151–162. https://doi.org/10.1007/s00441-002-0581-4

Von Zglinicki, T. (2002). Oxidative stress shortens telomeres. *Trends in Biochemical Sciences*, *27*(7), 339–344. https://doi.org/10.1016/S0968-0004(02)02110-2

Vozdova M., Ruiz-Herrera A., Fernandez J., Cernohorska H., Frohlich J., Sebestova H., K. S. & R. J. (2016). Meiotic behaviour of evolutionary sex-autosome translocations in Bovidae. *Chromosome Research*, *24*, 325 –38.

W.M.Z. Wan Somarny, A.R. Roziatul Erin, A.H.M.S. Suhaimi, M. O. N., & and R. Mohd Hifzan. (2013). A study of major prolificacy genes in Malin and Dorper sheep in Malaysia. *Journal of Tropical Agriculture and Food Science*, *41*(2), 265–272.

Wang, D.-D., Zhang, G.-R., Wei, K.-J., Ji, W., Gardner, J. P. A., Yang, R.-B., & Chen, K.-C. (2015). Molecular identification and expression of the Foxl2 gene during gonadal sex differentiation in northern snakehead Channa argus. *Fish Physiology and Biochemistry*, *41*(6), 1419–1433. https://doi.org/10.1007/s10695-015-0096-z

Wang, R. N., Green, J., Wang, Z., Deng, Y., Qiao, M., Peabody, M., … Shi, L. L. (2014). Bone Morphogenetic Protein (BMP) signaling in development and human diseases. *Genes & Diseases*, *1*(1), 87–105. https://doi.org/10.1016/j.gendis.2014.07.005

Wang, Z., & Moult, J. (2003). Three-dimensional structural location and molecular functional effects of missense SNPs in the T cell receptor V? domain. *Proteins: Structure, Function, and Genetics*, *53*(3), 748–757. https://doi.org/10.1002/prot.10522

Weise, A., Gross, M., Hinreiner, S., Witthuhn, V., Mkrtchyan, H., & Liehr, T. (2010). POD-FISH: a new technique for parental origin determination based on copy number variation polymorphism. *Methods Mol Biol*, *659*, 291–298. https://doi.org/10.1007/978-1-60761-789-1_22

Wigby, S., Suarez, S. S., Lazzaro, B. P., Pizzari, T., & Wolfner, M. F. (2019). Sperm success and immunity. In *Current Topics in Developmental Biology* (Vol. 135, pp. 287–313). https://doi.org/10.1016/bs.ctdb.2019.04.002

Williams, S. G., & Lovell, S. C. (2009). The effect of sequence evolution on protein structural divergence. *Molecular Biology and Evolution*, *26*(5), 1055–1065. https://doi.org/10.1093/molbev/msp020

Wnuk, M., Bugno, M., & Slota, E. (2008). Application of primed in situ DNA synthesis (PRINS) with telomere human commercial kit in molecular cytogenetics of Equus caballus and Sus scrofa scrofa. *Folia Histochemica et Cytobiologica*, *46*(1), 85–88. https://doi.org/10.2478/v10042-008-0012-9

Wu, H. L., Tong, C. C., Li, E., & Luo, T. L. (2012). Insight into gene evolution within Cervidae and Bovidae through genetic variation in MHC-DQA in the black muntjac (Muntiacus crinifrons). *Genetics and Molecular Research : GMR*, *11*(3), 2888–2898. https://doi.org/10.4238/2012.May.15.13

Yahaya, M. S., Salisi, M. S., Isa, N. M. M., Haron, A. W., & Peter, I. D. (2019). Application of Veterinary Cytogenetics in Domestic Animals: A Review. *Annual Research & Review in Biology*, *33*(1), 1–16. https://doi.org/10.9734/arrb/2019/v33i130112

Yamakawa, R. H., Saito, P. K., Gelmini, G. F., da Silva, J. S., Bicalho, M. da G., & Borelli, S. D. (2017). MICA diversity and linkage disequilibrium with HLA-B alleles in renal-transplant candidates in southern Brazil. *PLOS ONE*, *12*(4), e0176072. https://doi.org/10.1371/journal.pone.0176072

Yamamoto, N., Christenson, L. K., McAllister, J. M., & Strauss, J. F. (2002). Growth Differentiation Factor-9 Inhibits 3′5′-Adenosine Monophosphate-Stimulated Steroidogenesis in Human Granulosa and Theca Cells. *The Journal of Clinical Endocrinology & Metabolism*, *87*(6), 2849–2856. https://doi.org/10.1210/jcem.87.6.8551

Yang, F. F., Huo, L. J., Yang, L. G., Riaz, H., Xiong, L. R., Chen, J. G., … Xiong, J. J. (2014). Association between melatonin receptor 1A (MTNR1A) gene single-nucleotide polymorphisms and the velvet antler yield of Sika deer. *Molecular Biology Reports*, *41*(4), 1901–1906. https://doi.org/10.1007/s11033-013-2883-x

Yang, F., Müller, S., Just, R., Ferguson-Smith, M. A., & Wienberg, J. (1997). Comparative chromosome painting in mammals: Human and the Indian muntjac (Muntiacus muntjak vaginalis). *Genomics*, *39*(3), 396–401. https://doi.org/10.1006/geno.1996.4497

Yang, Q. L., Kong, J. J., Wang, D. W., Zhao, S. G., & Gun, S. B. (2013). Swine leukocyte antigen-DQA gene variation and its association with piglet diarrhea in large white, landrace and duroc. *Asian-Australasian Journal of Animal Sciences*, *26*(8), 1065–1071. https://doi.org/10.5713/ajas.2013.13067

Yin, T., & König, S. (2019). Genome-wide associations and detection of potential candidate genes for direct genetic and maternal genetic effects influencing dairy cattle body weight at different ages. *Genetics Selection Evolution*, *51*(1). https://doi.org/10.1186/s12711-018-0444-4

Zakaria, M. A., Zamri-Saad, M., Hasliza, A. H., & Wahid, H. (2016). Growth and Reproductive Performances of Farmed Timorensis Deer, Cervus timorensis. *Pertanika Journal of Tropical Agricultural Science*, *39*(1), 79–86.

Zhang, L. P., Gan, Q. F., Zhang, X. H., Li, H. D., Hou, G. Y., Li, J. Y., … Xu, S. Z. (2009). Detecting a deletion in the coding region of the bovine bone morphogenetic protein 15 gene (BMP15). *Journal of Applied Genetics*, *50*(2), 145–148. https://doi.org/10.1007/BF03195665

Zhang, W.-Q., & Zhang, M.-H. (2012). Phylogeny and evolution of Cervidae based on complete mitochondrial genomes. *Genetics and Molecular Research : GMR*, *11*(1), 628–635. https://doi.org/10.4238/2012.March.14.6

Zhao, D., Liu, S., Guo, Z., & Li, R. (2016). [Application of eight-probe fluorescence in situ hybridization and R-banding karyotype analysis for the diagnosis of acute lymphoblastic leukemia]. *Zhonghua Yi Xue Yi Chuan Xue Za Zhi = Zhonghua Yixue Yichuanxue Zazhi = Chinese Journal of Medical Genetics*, *33*(1), 9–12. https://doi.org/10.3760/cma.j.issn.1003-9406.2016.01.003

Zheng, J.-S., Sun, C.-Z., Zhang, S.-N., Hou, X.-L., & Bonnema, G. (2016). Cytogenetic Diversity of Simple Sequences Repeats in Morphotypes of Brassica rapa ssp. chinensis. *Frontiers in Plant Science*, *7*, 1049. https://doi.org/10.3389/fpls.2016.01049

Zheng Zhang, Scott Schwartz, Lukas Wagner, and W. M. (2000). A greedy algorithm for aligning DNA sequences. *Journal of Computational Biology*, *7*(1–2), 203–214.

Zhu, F., Cui, Q. Q., & Hou, Z. C. (2016). SNP discovery and genotyping using Genotyping-by-Sequencing in Pekin ducks. *Scientific Reports*, *6*, 1–5. https://doi.org/10.1038/srep36223

Zhu G.Q, Wang Q.I, KangY.G, L. Y. . and C. B. Y. (2013). Polymorphisms in GDF9 Gene and Its Relationship with Litter Size in Five Breeds of Black Goats. *Iranian Journal of Animal Science*, *3*(3), 625–628.

Zhu, Y., Wan, Q.-H., Zhang, H.-M., & Fang, S.-G. (2019). Reproductive Strategy Inferred from Major Histocompatibility Complex-Based Inter-Individual, Sperm-Egg, and Mother-Fetus Recognitions in Giant Pandas (Ailuropoda melanoleuca). *Cells*, *8*(3), 257. https://doi.org/10.3390/cells8030257

Zidi, A., Sànchez, A., Obexer-Ruff, G., & Amills, M. (2008). Sequence analysis of goat major histocompatibility complex class I genes. *Journal of Dairy Science*, *91*(2), 814–817. https://doi.org/10.3168/jds.2007-0342

Zuo, B., Qian, H., Wang, Z., Wang, X., Nisa, N., Bayier, A., … Wang, F. (2013). A Study on <italic>BMPR-IB</italic> Genes of Bayanbulak Sheep. *Asian-Australasian Journal of Animal Sciences*, *26*(1), 36–42. https://doi.org/10.5713/ajas.2012.12238