Digital Sequence information, Open Access, and Sustainable Benefit Sharing: Scientific Input to International Policy Decisions
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Our experience with DSI
Department of Animal Genetics and Conservation
Warsaw University of Life Sciences
Poland

Elzbieta Martyniuk & Zuzanna Nowak-Życzyńska
Introduction of the Department

Staff

• 17 Scientists
• 1 Secretariat
• 5 European bison projects
• 2 Laboratory animals
• 13 PhD students

Main areas of research

• Conservation breeding
• Molecular genetics
• Quantitative genetics
• Animal behaviour
Types of scientific questions and research areas

Material

- Wildlife species: (e.g. European bison, falcons, partridges, capercaillie)
- Dogs, including new breeds: Polish hounds, Polish hunting spaniel, Czechoslovakian wolfdog
- Sheep and chicken
- Animal origin products (honey, milk)

- Laboratory animals
- Various exotic species kept in ZOOs
Types of scientific questions and research areas

• Searching for new alleles / genetic forms conditioning health-related traits (wild species)
• Phylogenesis - identification of hybrids (falcons)
• Creating tools to identify a new breed (dogs)
• Identification of genetic background of diseases, including idiopathic diseases, mutations in known genes, and development of molecular tests (dogs)
  • Severe X-linked complex immunodeficiency in a domestic dog
  • Narcolepsy: prediction of functional partners genes, a molecular test to identify carriers
  • Identification of CLPTM1 gene mutation, conditioning cleft palate
  • C295G mutation of the T-box gene in a Polish hunting spaniel
Types of scientific questions and research areas

• Search for pathogens in products (milk, honey)

• Genetic Barcoding in fish species identification (sea bream - tilapia, bluefin and yellowfin tuna species)

• \textit{In silico} analysis in domestic dogs e.g. searching for candidate genes of the semi-vertebrate condition (lat. \textit{hemivertebræ}) based on functional association to the proteins (dogs)

• Detection of SNP (Single Nucleotide Polymorphisms) and INDEL (short Insertions and Deletions) variants for resistance / tolerance to Highly pathogenic avian influenza (chicken)
Use of sequence data in the daily work

• DNA isolation, amplification of selected genes / fragments
• Sequencing of selected regions
• Comparison with registered sequences in databases
• Registration of own records

• Bioinformatic research on HPAI - analysis of Hy-Line data
• In-silico studies of selected genes
Databases

Genetic diversity
• National Center for Biotechnology Information: https://www.ncbi.nlm.nih.gov/

Search for new alleles /genetic forms
• Ensembl Genome Browser: https://www.ensembl.org/index.html

Barcoding
• BARCODE OF LIFE DATA SYSTEM - BOLD Systems: http://www.boldsystems.org/
Lessons learned in the context of the Nagoya Protocol

• Native species / farm animals & pets: not relevant

• European bison from all over Europe:
  ✓ CH, CZ, DE, DK, ES, FR, NL, SE, SK, UK
  ✓ considered as reintroduced
  ✓ from semi free populations
  ✓ permission of the breeder only

• Transfer of biological material to Poland more difficult:
  ✓ Belarus, Ukraine, Russia
  ✓ material in European bison genebank „in deposit”
  ✓ only joint projects/activities
Final comments

• DSI databases are crucial for daily work
• Open access through logging in via institution IP
• Need to cite source of information

• Limited access to DSI databases
  ✓ Duplication of research
  ✓ Duplication of solutions (e.g. molecular tests), difficult to compare
  ✓ Difficulty to get reference sequences
https://smz.waw.pl/pestycydy-sa-zagrozeniem-dla-zdrowia-zubrow/