STATE SCIENTIFIC INSTITUTION

INSTITUTE OF GENETICS AND CYTOLOGY OF THE NATIONAL ACADEMY OF SCIENCES OF BELARUS

APPLIED DEVELOPMENTS

BIOTECHNOLOGIES FOR HEALTH CARE | BIOTECHNOLOGIES FOR SPORTS | BIOTECHNOLOGIES FOR ANIMAL BREEDING | BIOTECHNOLOGIES FOR FISH BREEDING | BIOTECHNOLOGIES FOR ENVIRONMENTAL PROTECTION | BIOTECHNOLOGIES FOR PLANT BREEDING

MEDICAL GENETICS

ACCREDITED ACTIVITIES

LABORAORY OF HUMAN GENETICS
Irma Mosse, Professor, PhD
I.Mosse@igc.by
Tel.: +375 17 395 51 80

DETECTION OF GENETIC PREDISPOSITION TO MULTIFACTORIAL DISEASES. PHARMACOGENETICS

DNA testing is an essential step of personalized and preventive medicine.

Developed DNA testing technologies: genetic predisposition of a person to multifactorial diseases: cardiovascular pathologies, venous thrombosis, type 2 diabetes, osteoporosis, carbohydrate-fat metabolism disorders, metabolic syndrome (obesity + hypertension + diabetes mellitus), rupture and tension of ligaments and tendons.

PCR method is used for testing. The genes associated with regulation of blood pressure, maintenance of water-salt homeostasis, blood clotting, metabolism of fats and carbohydrates, folic acid metabolism, regulation of cholesterol concentration, and etc. are tested.

Determining the genetic causes of pregnancy loss is in most demand. When an obstetrician-gynecologist detects a high risk of pregnancy non-carrying, appropriate therapy is prescribed and this contributes to the normal course of pregnancy and successful delivery.

Pharmacogenetic testing for hypersensitivity or resistance to Warfarin and Clopidogrel is carried out, which allows to choose the correct medication dosage and avoid complications (sometimes lethal).

Detected genetic predisposition allows to:

- Take prophylactic measures or diagnose multifactorial diseases at an early stage;
- Choose correct methods of treatment;
- Consider an individual response to medication, which increases the treatment efficacy and reduces the risk of complications.

The obtained results have been integrated for use in the Republican Scientific and Practical Centre «CARDIOLOGY», the City Center for Osteoporosis Prevention and a number of city and regional hospitals of the Republic of Belarus.

The instruction for use «DNA testing of genetic predisposition to thrombophilia of various origin» of April 13, 2012 approved by the Ministry of Health of the Republic of Belarus.

Patent «Method for determining genetic risk of myocardial infarction» of October 28, 2014.

International Certificate of the Reference Institute of Bioanalytics (Bonn, Germany) of April 8, 2017.

GENETIC LABORATORY DIAGNOSTICS
Tel.: +375 17 385 9739, +375 33 380 5040
http: genpasport.igc.by

MEDICAL GENETICS

LABORATORY OF CYTOPLASMIC HEREDITY
Larisa Sivitskaya, PhD
cytoplasmic@mail.ru
Tel.: +375 17 268 64 20

DETECTION OF GENETIC REASONS FOR NON-CORONAROGENIC HEART DISEASES

Non-coronarogenic heart diseases are associated with a high risk of sudden cardiac death. This includes hereditary cardiomyopathy and channelopathy accompanied by heartbeat arrhythmia. The cause of this hereditary disease group - pathogenic mutations in the genes of contractile, nuclear and cytoskeletal proteins, as well as structural proteins of ion channels and cell-cell contacts, transmembrane carriers.

A modern technology to determine the genetic cause of non-coronarogenic heart disease development using the NGS method (Next Generation Sequencing) has been developed. Such genetic diagnosis is of particular importance for the verification of primary channelopathies and cardiomyopathies, including at the preclinical stages of the disease development in asymptomatic carriers. It is very important for the families of patients with an established genetic cause of heart disease development. Identification of mutations' carriage in asymptomatic relatives is necessary to predict the disease outcome, to take measures for effective primary prophylaxis and to choose optimal treatment methods.

LABORATORY OF CYTOPLASMIC HEREDITY
Inessa Goloenko, PhD
cytoplasmic@mail.ru
Tel.: +375 17 268 64 20

DNA TESTING TO IDENTIFY A RISK OF DRUG-INDUCED AKATHISIA AND PARKINSONISM

The DNA technology to diagnose a high genetic risk of extrapyramidal complications arising in the treatment of various mental disorders with antipsychotic spectrum drugs has been developed.

The use of antipsychotic drugs is often (from 20% to 80% of cases) aggravated by motor complications, including acute akathisia and parkinsonism, which can be associated with the carriage of frequently occurring among the Belarusian population C allele (frequency - up to 80%) of the 2nd dopamine receptor gene DRD2 and deletions in the genes of enzymes GST-M1 (the frequency - up to 46%) and GST-T1 (the frequency - up to 20%) responsible for the performance of the glutathione xenobiotic detoxification system.

The DNA technology allows for the selection or replacement of medications and doses with the lowest risk of side-effects and complications in the form of extrapyramidal disorders.

LABORATORY FOR MODELLING OF GENETIC PROCESSESS
Natalya Chakova, PhD
N.Chakova@igc.by
Cell phone: +375 29 392 55 34

MOLECULAR GENETIC DIAGNOSIS OF HYPERTROPHIC CARDIOMYOPATHY

The technology for accurate verification of the hypertrophic cardiomyopathy diagnosis with the aim of timely and pathogenetically targeted treatment has been developed.

The use of this technology is proposed for DNA testing to identify mutations that cause the hypertrophic cardiomyopathy development. Hypertrophic cardiomyopathy is a common genetically conditioned disease (1:500 people) with an autosomal dominant type of inheritance. The risk of transmitting the disease to children is 50%. Clinical symptoms of hypertrophic cardiomyopathy can manifest at any age. This disease is characterized by clinical and genetic heterogeneity and a high risk of sudden cardiac death, which may be the first and the only manifestation of hypertrophic cardiomyopathy. The risk of sudden cardiac death increases with certain mutations.

DNA testing is recommended for:

- Patients with hypertrophic cardiomyopathy diagnosed by a doctor to determine the genetic cause of a disease, to verify the diagnosis and exclude the presence of hypertrophic cardiomyopathy phenocopy (Danone, Pompe, Fabry, Noonan; Friedreich's ataxia, Familial Amyloidosis, Wolff-Parkinson-White syndrome, and etc.) with a view of prescribing timely and pathogenetically targeted treatment or its adjustment. Upon detection of a pathogenic mutation, it is possible to conduct pre-natal genetic diagnosis (intra-uterine) during natural pregnancy or preimplantation diagnosis in case of in vitro fertilization, which will prevent the birth of a sick child;
- Close relatives of a patient with hypertrophic cardiomyopathy with no symptoms of hypertrophic cardiomyopathy at the present time to determine whether they are mutation carriers or not. The detected mutation allows for an early (pre-clinical) diagnosis of hypertrophic cardiomyopathy. When a mutation is detected in an asymptomatic relative, he/she needs to undergo regular medical observation to detect the disease at an early stage, avoid heavy physical exertion, follow dietary pattern, and etc., not to provoke early disease development;
- Close relatives of a patient with an established diagnosis of hypertrophic cardiomyopathy who died from a sudden cardiac death.

MEDICAL GENETICS

ACCREDITED ACTIVITIES

LABORAORY OF HUMAN GENETICS
Irma Mosse, Professor, PhD
I.Mosse@igc.by
Tel.: +375 17 395 51 80

DETERMINING GENETIC REASONS FOR NON-CARRYING OF PREGNANCY

A technology to assess the risk of pregnancy non-carrying based on genetic markers associated, inter alia, with an increased tendency to thrombosis has been developed.

Annually, every fifth wanted pregnancy ends with a spontaneous abortion (according to the data of the Ministry of Health of the Russian Federation). Recently, hereditary thrombophilia, which is characterized by an increased tendency to intravascular thrombosis, has become a major cause of miscarriages. DNA testing is the only way to determine the hereditary predisposition to thrombophilia. The genetic risk of thrombophilia is often realized only under additional conditions, in particular during pregnancy. Thus, clinical and biochemical tests before pregnancy do not show any abnormalities, but in the course of the pregnancy microthrombs are formed in the placenta, blocking the umbilical cord, and a spontaneous miscarriage or termination of pregnancy occurs (missed miscarriage).

Molecular genetic testing allows to detect risk factors of pregnancy abnormalities in each particular case. In the genotypes of 90.7% of women with habitual miscarriages we examined, from 3 to 6 risk factors of pregnancy non-carrying were identified and more than one third of patients (35%) had five of such factors in the genotype.

Modern medical science has the means and methods to correct the adverse manifestations of hereditary information. In case of a high pregnancy loss risk, the gynecologist prescribes medications that correct the effects of unfavorable variants of genes, which ensures the normal course of pregnancy. Our survey of 1000 patients with established genetic causes resulting in noncarrying of pregnancy showed successful birth of children in 86.6% of cases, provided that they had been receiving appropriate medications.

International Certificate of the Reference Institute of Bioanalytics (Bonn, Germany) of April 8, 2017.

GENETIC LABORATORY DIAGNOSTICS
Tel.: +375 17 385 97 39, +375 33 380 50 40
http: genpasport.igc.by

MEDICAL GENETICS

LABORATORY OF MOLECULAR GENOME STABILITY BASES
Nadezhda Ryabokon, PhD
ldgmo@igc.by
Cell phone: +375 33 622 17 88

DNA FRAGMENTATION ANALYSIS IN MALE SPERM BY THE DNA-COMET ASSAY

A method to diagnose genetically conditioned forms of male infertility has been developed. The development was carried out jointly with the Republican Scientific and Practical Centre «Mother and Child». An alkaline version of the DNA-comet assay (gel electrophoresis of single cells) was used as a basis allowing to detect a wide range of DNA damages recorded as DNA fragments and with a high probability can cause low male fertility.

DNA fragmentation is one of the main genetic causes of low male fertility. Sperm DNA fragmentation analysis is recommended as one of the ways to diagnose genetically conditioned causes of low male fertility.

Based on the analysis results, medical workers prescribe therapeutic treatment where necessary. After the course of treatment, the number of DNA damages significantly reduces (by 50% on average), which indicates the improved reproductive health of patients.

No contra-indications to the method use.

Indications to the study:

- Idiopathic infertility.
- Noncarrying of pregnancy.
- Unsuccessful attempts of artificial insemination.
- Preparation for the Assisted Reproductive Technologies (ART) use.
- Freezing of sperm for long-term storage and donation.
- Deviations in seminogram.
- Risk factors in conception planning:

  - Age of a man over 45 years;
  - Acute and chronic inflammatory diseases of a male urogenital system;
  - Acute and chronic diseases of a general nature (extragenital);
  - Smoking, alcohol ingestion, drug administration, chemo- and radiotherapy, exposure to harmful chemicals, elevated environmental temperatures.

Instruction for use «***Method to diagnose genetically conditioned forms of male infertility***» (approved by the Ministry of Health of the Republic of Belarus in 2016; Registration No. 196/1115).

MEDICAL GENETICS

LABORATORY OF CYTOPLASMIC HEREDITY
Nina Danilenko, PhD; Marina Sinyavskaya, PhD
cytoplasmic@mail.ru
Tel.: +375 17 268 64 20

DETERMINING GENETIC REASONS FOR SENSORINEURAL HEARING LOSS

A DNA technology to determine the carriage of adverse mutations associated with sensorineural hearing loss to prevent the disease progression with age has been developed.

Carriage of a 35delG mutation causing congenital or early hearing loss in more than 50% of cases and of a 12SrRNA gene mutation (mitochondrial gene of a small rRNA subunit) transmitted matrilineally and associated with deafness that developed after taking ototoxic antibiotics are analyzed. Identifying of A1555G mutation carriers will prevent hearing loss after taking (even in cases of one-time use) certain antibiotics.

Carriers of the most common 35delG mutation have normal hearing and only if two carriers enter into the marriage, they can have deaf children. If there have been cases of deaf children in families and it has been established that a person with normal hearing is a mutation carrier in such a family, it is recommended to undergo a genetic examination of his/her future partner to exclude the birth of hard-of-hearing children or to be ready for their birth.

DNA DIAGNOSIS OF GILBERT'S SYNDROME

A DNA technology that allows to determine the carriage of an unfavorable mutation in the promoter region of the UGT1A1 gene associated with Gilbert's syndrome with a view of choosing correct therapeutic methods has been developed.

Gilbert's syndrome is an autosomal recessive disorder associated with the low activity of a bilirubin glucuronosyltransferase enzyme caused in the promoter region of the UGT1A1 gene by a mutation.

Patients with Gilbert's syndrome should have an individual pharmacogenetic approach to the treatment of various diseases. It is extremely important to consider the likelihood of side-effects that many antiviral drugs can cause.

MEDICAL GENETICS

LABORATORY OF CYTOPLASMIC HEREDITY
Nina Danilenko, PhD; Marina Sinyavskaya, PhD
cytoplasmic@mail.ru
Tel.: +375 17 268 64 20

DNA DIAGNOSIS OF HEREDITARY HEMOCHROMATOSIS

A DNA technology that allows to determine the carriage of adverse mutations associated with hereditary hemochromatosis to make a correct therapeutic choice has been developed.

The technique allows to identify the most common single nucleotide substitutions in the 2nd and 4th exons of the HFE gene (H63D and C282Y correspondingly). Mutations in the HFE gene determine the development of the so-called type 1 hemochromatosis (classical hemochromatosis). This is the most common monogenic disease worldwide.

If a mutant genotype by the HFE gene and chronic Hepatitis C are combined, a risk of fibrosis and cirrhosis of the liver increases, while adverse processes occur in patients at a younger age.

MITOCHONDRIAL DISEASES: LEBER'S HEREDITARY OPTIC NEUROPATHY (LHON); MELAS SYNDROME

DNA technologies to detect mutations in mitochondrial DNA in connection with the development of Leber's hereditary optic neuropathy (LHON) and MELAS Syndrome have been developed.

DNA testing allows to identify the cause of a developing disease, which is especially important in case of mytochondrial diseases, and to choose right therapeutic methods, alleviating the patient's condition whenever possible.

In case of Leber's syndrome (LHON), a hereditary defect is localized in mitochondrial DNA and is passed to descendants on the mother's side exclusively. In 95% of cases, the cause of a disease lies in three mitochondrial mutations in the genes controlling respiratory complex 1 subunits: ND1, ND4 and ND6. LHON is characterized by a rapid and usually painless loss of focal vision. In most cases, it develops in the 15-30 age group and mainly in males.

MELAS Syndrome is one of the most common mitochondrial diseases. Typical signs of the disease: myopathy, encephalopathy, lactate acidosis and stroke-like episodes. One of the most striking signs is physical intolerance manifesting as muscle pain, muscle weakness, fatigability, deterioration of the general condition, and hypotrophy. The disease mainly manifests itself in the 12-16 age group.

SPORTS GENETICS

ACCREDITED ACTIVITY

LABORATORY OF HUMAN GENETICS
Irma Mosse, Professor, PhD
I.Mosse@igc.by
Tel.: +375 17 395 51 80

SELECTION & PROFILING OF ATHLETES. ARE YOU PLANNING A SPORTING FUTURE FOR YOUR CHILD?

«DNA testing system for athletes» and «Selection and profiling programmes for athletes in different kinds of sports (cyclic, speed-strength, game, complex coordination sports) (no foreign analogues known)» have been developed.

One of the most promising directions in sports genetics is to study how sporting achievements and the genes responsible for functional development and control required for sporting perfection are related.

Integration of molecular genetic methods into sports significantly increases the prognostic potential in sports selection and professional orientation. DNA testing allows to design an individual training regimen, adjust the biomedical support to an athlete, ensure rational use of public funds and contribute to the enhanced sports prestige of the country.

Already at birth, you can design the child's DNA Certificate, which includes information on individual genetic characteristics of an organism and allows you to choose the most suitable sports specialization for your child (sprinter, stayer or team player), determine the load type with no harm to your child's health.

Selecting pupils for children's and young people's sports schools based on genetic analysis, allows you to avoid disappointment, make no harm to health of young people in the course of intensive trainings and significantly reduce training costs for promising athletes in the particular sport.

International Certificate of the Reference Institute of Bioanalytics (Bonn, Germany) of April 8, 2017.

GENETIC LABORATORY DIAGNOSTICS
Tel.: +375 17 385 97 39; Cell phone: +375 33 380 50 40
http: genpasport.igc.by

SPORTS GENETICS

ACCREDITED ACTIVITY

LABORATORY OF HUMAN GENETICS
Irma Mosse, Professor, PhD
I.Mosse@igc.by
Tel.: +375 17 395 51 80

BIOMEDICAL SUPPORT CORRECTION FOR HIGHLY QUALIFIED ATHLETS

Technologies for testing by a complex of genes that have a significant impact on the state of the locomotor apparatus, endurance, speed, strength, adaptation to hypoxia and the ability to recover after physical loads have been developed. Polymorphic variants of genes that regulate angiogenesis, vasomotor control, energy metabolism, erythropoiesis, myoglobin synthesis, etc. are identified. The genes responsible for predisposition to cardiovascular disorders (including sudden death syndrome) in conditions of high physical loads, varicose veins in hockey and football players, brain injuries in boxers, bone fractures, rupture and tension of ligaments and tendons are detected.

DNA testing of athletes provides valuable support to doctors and team coaches not only in selecting the most promising athletes, but also in correct biomedical support needed to achieve outstanding sports results.

Modern medical science is equipped with the tools and techniques allowing to correct adverse manifestations of hereditary information. Detected genetic predisposition to dangerous pathologies allows for their prevention or early diagnosis and correct treatment methods to choose.

Based on genetic testing, it is also possible to assess individual drug sensitivity of a person important to know when choosing medication and its correct dosage.

DNA Certificates are designed for athletes indicating variants of genes needed for high sporting results to achieve, as well as occupational pathology risk genes. Only in this case each athlete can be provided with the conditions necessary for full realization of his/her genetic potential.

The results were integrated into the State Institution «Republican Center for Sports Medicine», the Republican Scientific and Practical Sports Center at the Sports and Tourism Ministry of the Republic of Belarus, the Republican Centers for Olympic Training in Rhythmic Gymnastics and Ice Sports, the Belarusian Biathlon, Archery and Fire Rescue Sport Federations, the Center for Professional Advancement of Management Personnel and Specialists «High School of Coaches», and etc.

GENETIC LABORATORY DIAGNOSTICS
Tel.: +375 17 385 97 39, Cell phone: +375 33 380 50 40
http: genpasport.igc.by

CATTLE BREEDING

ACCREDITED ACTIVITY

LABORATORY OF ANIMAL GENETICS
Mariya Mikhailova, Associate Professor, PhD
M.Mikhailova@igc.by
Tel.: +375 17 399 32 05

IDENTIFICATION OF HEREDITARY DISEASE CARRIERS MARKER-ASSISTED SELECTION BY AGRONOMIC CHARACTERS

The methods to identify important for breeding fertility haplotypes in cattle - HCD, HH0, HH1, HH2, HH3, HH4, HH5, HHB, HHC, and HHD, influencing a pregnancy degree and/or associated with embryonic and early post-embryonic death have been developed.

Developed DNA technologies assisting in identification of mutation carriers associated with:

- Hereditary immunodeficiency (BLAD syndrome);
- Early abortion in cattle (DUMPS);
- Complex vertebral malformation (CVM);
- Blood clotting factor deficiency (FXID);
- Bone deformity - brachyspina (BY);
- Urea biosynthesis disorder - citrullinemia (BC).

The decision to exclude male carriers of hidden mutations from the breeding process was scientifically grounded due to the need to eliminate the further spread of mutant alleles in the population and reduce the economic loss caused by losses in reproduction.

Using the methods developed at the Institute, we provide assistance to specialists in genetic assessment of milk production and quality characters, fixation of useful alleles, development of homozygous specialized animal lines.

Methodological recommendations «DNA technology for identification of a genetic defect in Holstein breed cattle that determines brachyspina syndrome (BY)» (approved and recommended for publication by the Science and Technology Council of the Directorate-General for the Intensified Animal Breeding and Veterinary Medicine of the Ministry of Agriculture and Food of the Republic of Belarus (Protocol No. 1 of March 1, 2016).

Methodological recommendations «DNA technology for detecting mutations causing the development of a DUMPS hereditary disease - early abortion of cattle embryos» (approved and recommended for publication by the Science and Technology Council of the Directorate-General for the Intensified Animal Breeding and Veterinary Medicine of the Ministry of Agriculture and Food of the Republic of Belarus (Protocol No. 1 of March 1, 2016).

Methodological recommendations «DNA technology for the detection of complex spinal anomalies (CVM) and leukocyte adhesion deficiency (BLAD) in cattle using multiplex real-time PCR» (approved and recommended for publication by the Science and Technology Council of the Directorate-General for the Intensified Animal Breeding and Veterinary Medicine of the Ministry of Agriculture and Food of the Republic of Belarus (Protocol No. 11 of March 18, 2014).

PIG BREEDING

ACCREDITED ACTIVITY

LABORATORY OF ANIMAL GENETICS
Mariya Mikhailova, Associate Professor, PhD
M.Mikhailova@igc. by
Tel.: +375 17 399 32 05

MARKER-ASSISTED SELECTION BY AGRONOMIC CHARACTERS

The methods developed at the Institute are used for:

- Instant diagnosis of pig fertility (HRM technologies by ESR-1 estrogen receptor genes and PRLR prolactin receptor);
- Genotyping of pigs of meat breeds by hormonal genes (pPit-1,pGH, pGHR, pGHRH, pIGF-1, pIGF-1R, pIGF-2);
- Genotyping of pigs for the presence of genes associated with prolificacy (pPRLR and pESR).

The use of these technologies allows to identify preferential genotypes to improve meat and fattening qualities in pigs to accelerate the breeding process.

DNA testing of animals prevents the inclusion of hidden mutations' carriers in the breeding process and thereby the economic loss caused by the lack of young animals with high producing potential reduces. It allows to entrench beneficial alleles, evaluate productivity and meat quality characters and develop homozygous specialized animal lines.

According to the Law of the Republic of Belarus «On pedigree work in animal breeding» of May 20, 2013 No. 24-3, Article 31. Genetic examination, all pedigree animals used for reproduction must be tested on a mandatory basis for their origin verification and the presence of genetic defects that determine the development of hereditary diseases. In case the origin has not been verified or genetically conditioned diseases have been identified, such animals should be excluded from the breeding process.

Methodological recommendations «DNA technology for detecting single nucleotide A3072G polymorphism in the gene of insulinoid growth factor (IGF2), intron 3 in pigs (SUS SCROFA) using sequencing method» (approved and recommended for publication by the Science and Technology Council of the Directorate-General for the Intensified Animal Breeding and Veterinary Medicine of the Ministry of Agriculture and Food of the Republic of Belarus (Protocol No. 2 of March 1, 2016).

GENETIC EXAMINATION

ACCREDITED ACTIVITY

LABORATORY OF ANIMAL GENETICS
Mariya Mikhailova, Associate Professor, PhD
M.Mikhailova@igc. by
Tel.: +375 17 399 32 05

GENETIC EXAMINATION OF CATTLE AND PIGS WITH DNA CERTIFICATE ISSUANCE

In the Republic of Belarus, control over the origin verification of pedigree animals is a prerequisite for breeding work.

According to the Law of the Republic of Belarus «On pedigree work in animal breeding» of May 20, 2013 No. 24-3, Article 31. Genetic examination, all pedigree animals used for reproduction must be tested on a mandatory basis for their origin verification and the presence of genetic defects that determine the development of hereditary diseases. In case the origin has not been verified or genetically conditioned diseases have been identified, such animals should be excluded from the breeding process.

We carry out molecular genetic examination to verify the origin of cattle and pigs using a microsatellite marker panel recommended by the International Society for Animal Genetics (ISAG)*. A DNA Certificate issued verifies the animal's origin with an accuracy of 99.9%.

At the request of a customer, a DNA Certificate is supplemented with data on the animal carriage of genetically conditioned diseases (BLAD, CVM, DUMPS, FXID, BC, BY, cattle leukemia provirus, immunodeficiency virus, stress sensitivity, colibacillosis), as well as data on the carriage of genes associated with productivity and quality characters.

**The Institute of Genetics and Cytology, NAS of Belarus, is a member of the International Society for Animal Genetics (ISAG), which provides a quality standard of work comparable to that of the world in its part of:*

- *Determining of genes responsible for agronomic characters and hereditary diseases of animals;*
- *Molecular genetic verification of the animal's origin, their species and breed belonging.*

GENETIC EXAMINATION

ACCREDITED ACTIVITY

LABORATORY OF GENETIC AND CELL ENGINEERING
Valentina Lemesh, PhD, Associate Professor; Marina Bogdanova, PhD
M.Bogdanova@igc.by
Tel.: +375 17 284 19 07

GENETIC EXAMINATION OF THE STURGEON FAMILY AND PRODUCTS FROM THEM

We identify the species belonging of the sturgeon family and products from them using molecular-genetic analysis and issuing a DNA Certificate for legal export, import and re-export of black caviar.

We check genetic purity of sturgeon species broodstocks selecting elite producers by sturgeon types for reproduction purposes, to obtain stocking material and introduce it into natural habitats.

We design individual DNA Certificates for sturgeon species producers to conduct breeding programs aimed at the increased fish productivity in sturgeon breeding.

Genetic examination involves documenting the genotypes of the examined individuals in the form of a DNA Certificate containing information on the mitochondrial haplotype and allelic composition of certain nuclear genome loci.

Certificate of May 23, 2016 No. 1341607925 «Information Referral System ''Use of molecular-genetic analysis for identification of species (population) belonging to the sturgeon family and products from them''».

We provide DNA testing services for the specialists of sturgeon farms and husbandries, environmental organizations and agencies, enterprises, companies and private entrepreneurs engaged in growing and processing of sturgeon fish and products from them, as well as for customs authorities, export, import and re-export of sturgeon species products across the border when checking sturgeon products' compliance with CITES requirements.

We conclude agreements to carry out research activities.

RAPID TEST METHODS

LABORATORY OF ANIMAL GENETICS
Mariya Mikhailova, Associate Professor, PhD
M.Mikhailova@igc. by
Tel.: +375 17 399 32 05

RAPID DIAGNOSTICS AND TEST SYSTEMS IN BREEDING OF CATTLE AND PIGS

We provide genetic testing services, conclude contracts for research and development works, using:

Methods of rapid diagnostics using HRM technology by the genes of estrogen receptor *ESR-1* and prolactin receptor *PRLR* (pig fertility markers).

Methods used for genotyping pigs of meat breeds by hormonal genes (*pPit-1, pGH, pGHR, pGHRH, pIGF-1, pIGF-1R, pIGF-2*) and multifetation genes (*pPRLR and pESR*).

Test systems for determining genotypes and the East European virus subtype of Porcine Reproductive and Respiratory Syndrome (Invention Patent of the Republic of Belarus No. 18950 with effect from December 21, 2011);

Test systems for determining the proviral DNA of a bovine leukemia virus (Invention Patent of the Republic of Belarus No. 21277 with effect from October 28, 2013);

Test systems for conducting DNA typing by the genes *ECR F18/FUT1 and MUC4* associated with resistance to colibacteriosis in piglets.

Highly sensitive methods for gene diagnostics of retroviral infections of farm animals (pigs, cattle) have been developed.

Using the PCR (polymerase chain reaction) method, we simultaneously determine the genotypes and subtypes of a Porcine Reproductive and Respiratory Syndrome virus: West European genotype, North American genotype, East European subtype. The proposed method allows to identify most of the endemic variants of the PRRS virus circulating on pig farms in the territory of the Republic of Belarus.

Blood serum and pathological material are used for analysis.

Whole blood is used to identify the proviral DNA of a bovine leukemia virus.

RAPID TEST METHODS

ACCREDITED ACTIVITY

NATIONAL COORDINATION BIOSAFETY CENTRE
Galina Mozgova, PhD
ldgmo@igc.by, biosafety.by
Tel.: +375 17 284 02 97, Cell Phone: +375 44 784 16 91

RAPID TEST METHOD FOR DETECTING RAW MATERIAL COMPONENTS IN FOOD PRODUCTS AND FEEDS

Species verification in meat components that make up raw materials, food products and feeds allows to identify a source of animal protein, adulterated products and plant components in the food products of animal origin.

Both raw and heat-treated meat products (animal body parts, minced meat and sausage products), raw materials and ingredients for food products, dry and canned feeds for birds and animals, compound feedstuff, and etc. are used as test objects.

PCR specific method optimal for heat-treated products is used for analysis.

Why is accurate verification of meat species composition needed?

- Contamination of expensive meat varieties with cheaper analogues (e.g. beef-horse meat, turkey-chicken, detecting the contamination of meat with soybeans and other plant components);
- Health problems (possible allergies);
- Personal preferences in food choices (e.g. vegetarianism);
- Accurate labelling.

Species verification in meat components is performed at the Accredited Laboratory included in the Register of Test Laboratories of the Customs Union. Test Protocols are recognized in all countries of the Customs Union.

State standard of the Republic of Belarus: GOST 31719-2012. The standard was prepared based on the application of GOST R 52723-2007 and adopted by the Interstate Council for Standardization, Metrology and Certification (Protocol of October 1, 2012 No. 51).

AQUICULTURE

LABORATORY FOR GENETIC PROCESSES MODELLING
Alexander Slukvin, PhD
a.slukvin@igc.by
Tel.: +375 17 284 21 90

ARTIFICIAL REPRODUCTION TECHNOLOGY FOR THE EUROPEAN CATFISH (*Silurus glanis L.*)

The developed technology allows to minimize and make technologies in the artificial reproduction of the European catfish Silurus glanis L. more cost-effective with the increased yield of two- and four-week fish juveniles by 25%.

The following techniques are excluded from the technological process:
- Removal of mucilage from eggs;
- Incubation of eggs in special devices;
- Washing off larvae from eggs;
- Transfer of larvae from the apparatus into trays for growing.

The technology makes it possible to use basins, cages and trays held by incubation facilities as efficiently and rationally as possible upon reaching the body weight of 0.1-1.0 g by juvenile fishes.

REPRODUCTION AND GROWING BIOTECHNOLOGY FOR THE NARROW-CLAWED CRAYFISH FINGELINGS (*Astacus leptodactylus Esch.*) IN GROUND PONDS AND PLASTIC TRAYS

Biotechnology of a semi-intensive type, including technological methods for growing narrow-clawed crayfish fingerlings in conditions of pond ecosystems and incubation facilities, which allows to increase the survival rate of juvenile crayfish by 30-50% as compared to natural conditions.

The developed biotechnology is destined for fish husbandries, firms of all ownership forms, individual entrepreneurs wishing to create crayfish farms.

AQUICULTURE

LABORATORY FOR GENETIC PROCESSES MODELLING

Alexander Slukvin, PhD
a.slukvin@igc.by

Tel.: +375 17 284 21 90

STIMULATION TECHNIQUE FOR EGG OVULATION IN THE FEMALE TENCH (*Tinca tinca L.*) REMOVED FROM DIFFERENT ECOSYSTEMS FOR ARTIFICIAL REPRODUCTION

The technique allows to differentiate hormonal injections to tench producers caught in different aquatic ecosystems (ponds, lakes, reservoirs, rivers) to receive quality ovulated eggs and sperm during the tench artificial reproduction.

We render services to the specialists of fish breeding plants, fish hatcheries and fish farms, firms and individual entrepreneurs involved in the cultivation of fish stocking material for the needs of pond farms and reservoir tenants.

PROFIBAKT - A BIOLOGICALLY ACTIVE DRUG BASED ON MICROORGANISMS - PROTEASE PRODUCERS

The drug is destined for removal of mucilage from eggs (fertilized eggs) in the course of artificial reproduction: perch, pike, carp, European catfish, tench, and sterlet before placing them into incubatory apparatus of Weiss type.

Exposure to fertilized eggs' treatment depends on the fish species and ranges from 2 to 9 minutes. The survival rate of fish embryos is 12-18.5% higher as compared to the traditional methods used for mucilage removal (milk, silt, tannin, talc, clay).

The drug cost is 3.2 times lower as compared to its foreign analogues («Alcalase» of Merk producer).

PROFIBAKT Trademark Certificate in Belarus No. 28898, registration date: January 6, 2009.

BIODIVERSITY CONSERVATION

LABORATORY OF ANIMAL GENETICS
Mariya Mikhailova, PhD, Associate Professor
M.Mikhailova@igc. by
Tel.: +375 17 399 32 05

EUROPEAN BISON (*Bison Bonasus*) GENOTYPING USING MULTILOCUS MICROSATELLITE ANALYSIS

Using the developed technology, the gene pool of natural populations of the European bison is assessed to conserve genetic diversity, rehabilitate and restore species numbers.

A DNA Certificate of the European bison has been developed by 12 STR-loci based on the international base panel and by the gene loci of the main histocompatibility complex *DRB3* and *DQB* responsible for the immunity development. Identification of individuals carrying unique allelic variants of *DRB3* and *DQB* genes of the main histocompatibility complex contributes to the enhanced genetic diversity and the involvement of unique genes and alleles in the breeding process allowing to increase species viability.

In order to combat poaching, specific molecular markers have been selected that allow identifying biological material with a high degree of certainty through verifying its species belonging (European bison, European roe deer, red deer, wild boar).

We provide genetic testing services to environmental institutions and hunting farms.

We conclude contracts to perform research and development activities.

BIODIVERSITY CONSERVATION

ACCREDITED ACTIVITY

LABORATORY OF GENETIC AND CELL ENGINEERING
Valentina Lemesh, PhD, Associate Professor; Marina Bogdanova, PhD
M.Bogdanova@igc.by
Tel.: +375 17 284 19 07

DNA DIAGNOSTICS OF HEREDIARY COMPANION ANIMAL DISEASES *(Canis familiaris, Felis catus)*

Early diagnostics and detected predisposition to hereditary diseases allows to choose effective treatment policy and makes it possible to exclude carrier animals from breeding work, select pairs for breeding and get healthy offspring.

DNA testing makes it possible to obtain qualitative data on the health status of pure-bred populations of home dogs and cats.

Detect hereditary diseases in cats *(Felis catus)*:
- Polycystic kidney disease;
- Spinal muscular atrophy;
- Hypertrophic cardiomyopathy;
- Progressive late retinal atrophy;
- Progressive early retinal atrophy.

We establish kinship, blood type, compatibility of animals before crossing.

We carry out a test for hair color and its length inheritance.

Detect hereditary diseases in dogs *(Canis familiaris)*:
- Hereditary cataract;
- Progressive retinal atrophy;
- Primary lens dislocation;
- Central core myopathy;
- Cystinuria;
- Cyclic neutropenia (Gray Collie Syndrome);
- Drug sensitivity;
- Episodic Falling Syndrome in Cavalier King Charles Spaniels.

GRAIN CROP BREEDING

LABORATORY OF PLANT CYTOGENOMICS
Nadezhda Dubovets, Corresponding Member, Elena Sycheva, PhD
N.I. Dubovets@igc.by
Tel.: +375 17 284 19 45

TECHNOLOGY TO DEVELOP RECOMBINANT TRITICALE FORMS WITH A COMPLEX OF AGRONOMIC CHARACTERS DETERMINED BY THE GENES LOCALIZED IN WHEAT D-GENOME CHROMOSOMES

The technology allows to obtain hexaploid triticale with D(A)- and D(B)-substitutions of chromosomes and select recombinant forms with a complex of agronomic characters determined by the genes localized in wheat D-genome chromosomes for use in breeding when developing new triticale varieties with given properties.

The technology for the chromosomal reconstruction of a triticale polygenome is based on the use of chromosome engineering approaches combined with phased DNA marking of the hybrid material. Including a preliminary (prior to screening for PCR markers) analysis of the genomic triticale structure using the method of molecular cytogenetic marking of genotypes (C-banding) into the technology allows targeted selection of primers to identify the alleles of target genes and significantly reduces the scope of a molecular genetic analysis.

Screening of the breeding material using DNA markers is carried out by the genes that determine short-stemming, resistance to pre-harvest germination, high baking qualities, and etc.

The technology constitutes an innovative approach to solving the main problems associated with triticale, such as the tendency to lodging and pre-harvest germination of grain and low baking qualities. The use of molecular cytogenetic and molecular genetic analysis in the selection of promising hybrid material makes it possible to reduce the time and improve the efficiency of the selection process.

Invention patent No. 13202 «Method to develop a three-species tetraploid hybrid of triticale and rye with inter-genome recombination of chromosomes» (registered with the State Register of Inventions of February 2, 2010).

Methodological recommendations «Technology of triticale marker selection for short-stemming» (approved at the Scientific Board Meeting of the Institute of Genetics and Cytology, Protocol of November 26, 2012 No. 10).

Methodological recommendations «DNA typing methods of genes that determine resistance to pre-harvest germination and high baking qualities of triticale grains» (approved at the Scientific Board Meeting of the Institute of Genetics and Cytology, Protocol of December 15, 2015 No. 15).

LABORATORY OF PLANT CYTOGENOMICS
Ivan Gordey, PhD, Professor; Igor Gordey, PhD
I.Gordei@igc.by
Tel.: +375 17 284 19 14

TECHNOLOGY TO DEVELOP WINTER RYE AUTOTETRAPLOIDS WITH A COMPLEX OF ECONOMIC TRAITS

The technology allows obtaining, selecting and identifying the initial breeding material of tetraploid winter rye with economic traits for inclusion in the breeding process to develop highly productive varieties of this crop.

The technology is based on the autopolyploidization with nitrous oxide of highly productive commercial diploid varieties of winter rye and heterotic F1 hybrids in combination with cytologic and molecular genetic analysis of experimental material. The use of cytologic analysis allows the selection of genomically balanced and stable autotetraploids, which are then subjected to DNA analysis using specific primers to economic traits' loci (secalins, short-stemmed, etc.) to choose promising breeding samples.

The developed technology is highly efficient - the yield of tetraploids averages up to 45% (in colchicination - 0.5-4.0% to compare). Use of cytologic analysis techniques and DNA markers in the selection allows for the increased efficiency and reduced time of the breeding process.

«Methodological recommendations for rye (Secale cereale L.) polyploidization (genome duplication) using nitrous oxide (N2O)» approved and recommended for publication by the Science and Technology Council, Plant Breeding Department of the Directorate-General for Plant Breeding of the Ministry of Agriculture and Food (Protocol of May 25, 2012 No. 11).

Methodological recommendations «DNA technology for identification and selection of tetraploid rye breeding material by a complex of economic traits' genes» (approved at the Scientific Board Meeting of the Institute of Genetics and Cytology of the National Academy of Sciences of Belarus, Protocol of December 22, 2016 No. 9).

GRAIN CROP BREEDING

LABORATORY OF PLANT CYTOGENOMICS
Ivan Gordey, Professor, PhD; Oleg Lyusikov
I.Gordei@igc.by
Tel.: +375 17 284 19 14

TECHNOLOGY TO DEVELOP RYE-WHEAT AMPHIDIPLOIDS ON THE RYE (SECALOTRITIKUM) CYTOPLASM WITH A COMPLEX OF ECONOMIC TRAITS

Genomic technology for developing stable, highly productive and stress-resistant forms of rye-wheat amphidiploids with the rye cytoplasm (Secalotriticum) is based on hybridization of tetraploid rye with hexaploid triticale and using the normalized meiosis effect in the conditions of rye-cytoplasm in F1 rye-triticale hybrids. The technology implementation is accompanied by molecular cytogenetic (C-banding) and molecular genetic marking of breeding samples, including genotyping by genes that determine shortness of stems and resistance to pre-harvest germination.

The technology for developing rye-wheat amphidiploids with the rye cytoplasm is an innovative approach to the problem of the expanded heteroplasmic triticale gene pool and allows to: achieve a more complete expression of the rye genome in the conditions of rye cytoplasm; enhance stress tolerance and environmental adaptability; expand the gene pool of triticale source material using the genetic potential of modern high-quality rye varieties.

Use of molecular cytogenetic methods for the analysis of a genomic structure of breeding samples and DNA markers in the selection makes it possible to reduce time needed for their development and increase the Secalotriticum breeding process effectiveness in terms of stability, productivity and sustainability.

Gordey I.A., Belko N.B., Lyusikov O.M. Secalotriticum (×Secalotriticum): genetic bases to develop and form a genome. - Minsk: Bel. navuka, 2011. - 214 p.

Protocol on conducting PCR in Secalotriticum (approved at the Scientific Board Meeting of the Institute of Genetics and Cytology, Protocol of February 2, 2017 No. 2).

GRAIN CROP BREEDING

LABORATORY OF MOLECULAR GENETICS
Oksana Urbanovich, PhD
O.Urbanovich@igc.by
Tel.: +375 17 294 91 80

DNA IDENTIFICATION OF WHEAT VARIETIES

DNA identification method for wheat varieties has been developed. It allows to quickly and efficiently determine varietal belonging and varietal purity of wheat batches. Grain from average sample batches is used for analysis.

Method of wheat varieties identification using a set of molecular genetic markers is applicable to:

- Conduct the breeding process and variety change in seed breeding;
- Settle disputes for cases of author's right protection to varieties;
- Verify varietal belonging of seed material in contentious cases;
- Control purity and homogeneity of seed material in the purchase and sale.

Methodological recommendations «Identification and certification of agricultural crop varieties (soft wheat, potato, tomato, flax and beet) using DNA markers». Institute of Genetics and Cytology, NAS of Belarus, Minsk, 2006. Approved by the Science and Technology Council, the Directorate-General for Plant Breeding of the Ministry of Agriculture and Food on November 23, 2007 No. 22; 28 p.

DEVELOPMENT OF PROMISING WHEAT FORMS WITH A COMPLEX OF ECONOMIC TRAITS

The developed method allows to identify wheat genes influencing grain hardness, quality of reserve glutenin seed proteins, premature seed germination, plant growth, photoperiod sensitivity, resistance to phytopathogens determined by 1BL.1RS translocation.

The method allows to:

- Select and produce initial breeding material with economic traits;
- Control the transfer of valuable for breeding gene alleles into the newly produced breeding material ;
- Develop genotypes with a complex of economic traits.

Methodological recommendations «Methods to identify wheat gene polymorphism (Triticum aestivum L.), controlling valuable breeding traits». Approved by the Science and Technology Council, the Directorate-General for Plant Breeding of the Ministry of Agriculture and Food. Protocol of April 20, 2016 No. 7.

GRAIN CROP BREEDING

LABORATORY OF CYTOPLASMIC HEREDITY
Oleg Davydenko, PhD
cytoplasmic@mail.ru
Tel.: +375 17 369 75 14

DEVELOPMENT OF PROMISING MALT BARLEY FORMS BY MOLECULAR MARKING. DNA IDENTIFICATION OF BARLEY VARIETIES

The developed method allows to differentiate variety samples by their intended purpose (feed/brewing) using microsatellite markers associated with brewing properties; identify, select and create original breeding material with economic brewing traits, including highly thermostable β-amylase; control the transfer of valuable breeding alleles into newly developed barley hybrids.

The developed DNA identification technology for barley varieties allows to quickly and efficiently determine varietal belonging and varietal purity of barley batches using a set of molecular genetic markers.

The given identification method of barley varieties is used to:
- Conduct targeted breeding and variety change in seed production;
- Settle disputes for cases of author's right protection to varieties;
- Verify varietal belonging of seed material in cases where suspicions of a mistake occurred arise;
- Cut the likelihood of fodder barley use instead of brewing one (falsification and impurity of batches);
- Monitor the purity and homogeneity of seed material.

Electronic information resource «Database of molecular markers for identification and certification of barley varieties». Registration Certificate of January 09, 2014 No. 1341403709.

METHOD TO ANALYZE CHLOROPLAST AND PLANT MITOCHONDRIA GENOMES USING NEXT-GENERATION SEQUENCING (NGS)

An algorithm to obtain full sequences of chloroplast and mitochondrial barley genomes (Hordeum sp.) has been developed, including:
- Isolation of chloroplast and mitochondria DNAs from the organelle fraction obtained by the differential centrifugation method;
- Sequencing of chloroplast and mitochondria genomes by NGS method using Illumina technology;
- Bioinformatic processing and analysis of NGS-sequencing data, whose products are complete sequences of chloroplast and mitochondria barley genomes in the FASTA format and VCF tables that include polymorphic loci of those genomes.

The method can be used for mixtures containing different ratios of chloroplast and mitochondria DNAs. The developers have applied this approach to obtain complete sequences of chloroplast and mitochondria genomes of wild and domesticated barley forms for the purpose of phylogenetic analysis. It can be used to address breeding and taxonomic challenges.

OIL PLANT BREEDING

LABORATORY OF CYTOPLASMIC HEREDITY
Oleg Davydenko, PhD
cytoplasmic@mail.ru
Tel.: +375 17 369 75 14

HYBRID SUNFLOWER BREEDING BASED ON CYTOPLASMIC MALE STERILITY

High-yielding early-ripe linear material was developed and sunflower hybrids adapted to the soil and climatic conditions of Belarus were zoned.

The low cost of domestic seed production and early maturity of the developed hybrids allow import substitution of imported seeds and oil meal (grist) and thus expanded cultivation areas under this crop in Belarus.

Created collections:

- Self-pollinated maternal lineages - sterility enhancers (8-9 inbreeding generation and their sterile analogues (BC 7-BC 8) with seed oil content (46-50%);
- Paternal pollen fertility restorer lines.

F1 sunflower hybrid POISK
Vegetation period: 105-110 days. Average plant height: 135-150 cm.
The seed yield over three years of competitive testing in Belarus constituted 34.8-48.8 dt/ha; the oil content of seeds 48.4-50.4%.
Mass of 1000 seeds: 59.3-63.9 g.
F1 hybrid POISK was zoned in Brest, Gomel, Grodno and Minsk Regions of Belarus in 2008. It is an early-ripe group standard in the State Variety Trial.
Breeder's Certificate No. 0002123 for the sunflower variety POISK.

F1 sunflower hybrid AGAT
High-yielding, high-oleic sunflower hybrid.
Vegetation period: 110-115 days. Average plant height: 125-135 cm.
The average seed yield over three years of competitive testing in Belarus constituted 43.8 dt/ha, the oil content of seeds 48-52.7%.
Mass of 1000 seeds: 55.0-58.0 g.
F1 hybrid AGAT was zoned in Grodno and Minsk Regions of Belarus in 2010.
Breeder's Certificate No. 0002267 for the sunflower variety AGAT.

F1 sunflower hybrid BELORUSSKIY RANNIY
Hybrid specifics - early ripening.
Vegetation period: 95-100 days. Average plant height: 120-125 cm.
The seed yield over three years of competitive testing in Belarus constituted 34.8–50.0 dt/ha, the oil content of seeds 44.0-49.7%
Mass of 1000 seeds: 46.0-64.7 g.
F1 hybrid BELORUSSKIY RANNIY was zoned in Brest, Gomel, Grodno and Minsk Regions of Belarus in 2014. It is an ultraearly group standard in the State Variety Trial.
Breeder's Certificate No. 0003753 for the sunflower variety BELORUSSKIY RANNIY.

OIL PLANT BREEDIN

LABORATORY OF GENETIC AND CELL ENGINEERING
Galina Mozgova, PhD
g.mozgova@igc.by
Tel.: +375 17 294 91 82

DNA IDENTIFICATION OF RAPE GENOTYPES WITH OPTIMAL FATTY ACID COMPOSITION FOR FOOD USE

A technology based on the use of DNA markers (dCAPS markers), which allows to determine the allelic state of FAE1.1, FAE1.2 and FAD3 genes controlling the synthesis of erucic and linolenic fatty acids in the rapeseed, has been developed.

The technology makes it possible to identify at any stage of rapeseed plant development the carriers of valuable agricultural traits, select plants with important for breeding traits, and thereby reduce the period needed to develop a variety.

Factors determining the competitive ability of the proposed technology:

- Possibility of direct identification of genes in the breeding material at an early stage of plant development allowing to reject the material undesirable for a breeder at the beginning of the growing season and exclude biochemical analysis of the fatty acid composition of oil in breeding samples after harvesting and grinding of seeds, significantly saving time and costs needed for the crop care, harvesting and post-harvest processing of the breeding material;
- Independent testing of genes located in A and C rape genomes allowing for a shorter period of time needed for the variety development;
- Low analysis cost as compared to the previously applied biochemical analysis of oil composition by the gas-liquid chromatography method and the detection of mutant alleles by SNaPshot.

Invention patent of the Republic of Belarus No. 20118 «Oligonucleotide primer pairs complementary to the FAD3 sequences of A and C genome genes of the tetraploid rape genome and a method to identify mutant alleles and FAD3 wild type alleles of A and C genome genes of the tetraploid rape genome».

Invention patent of the Republic of Belarus No. a20111648 «Method to identify homo- and heterozygous state of the FAE1.1 gene in the rapeseed using dCAPS markers».

OIL PLANT BREEDING

LABORATORY OF CYTOPLASMIC HEREDITY
Oleg Davydenko, PhD
cytoplasmic@mail.ru
Tel.: +375 17 369 75 14

DNA CERTIFICATION TECHNOLOGY FOR SOYBEAN VARIETIES AND MATERIAL SELECTION BY DOMINANT ALELES USING THE PROTEIN FRACTIONS OF PHOTOPERIODIC REACTION GENES AND LOCI ASSOCIATED WITH PROTEIN FRACTIONS

The developed DNA certification technology for soybean varieties and material selection by the alleles of E series photoperiodic reaction genes allows to protect author's rights to varieties and optimize the breeding process, that is, to develop varieties with desired properties.

Using DNA technology, an early-ripe soybean variety Ptich adapted to the soil and climatic conditions of the central agroclimatic zone of Belarus (53-54 ° north latitude) was developed.

Methodological recommendations «Technology assessment and selection of soybean breeding material by a set of economic traits».

Methodological recommendations «Individual selection methods in hybrid soybean populations» (2016).

Soybean variety PTICH
The variety obtained by individual breeding in the F4 hybrid combination McCall _ / _ Major. Vegetation period: 117 days.
Accumulated effective temperatures from germination to harvest ripeness: 2150 ° C. Plant height: 70-80 cm.
Mass of 1000 seeds: 200-220 g.
The variety is entered in the Register of Varieties of the Republic of Belarus.
According to the State Variety Testing results, the yield is at the level of the PRIPYAT standard.

Variety Certificate No. 0003752 for the soybean variety PTICH.
Patent No. 460 of the Republic of Belarus for the soybean variety PTICH.

Soybean variety PUSHCHANSKAYA
The variety was obtained by individual breeding in the F4 hybrid combination CH 1470-20-1/KG 20. Vegetation period: 118 days.
Accumulated effective temperatures from germination to harvest ripeness: 2350 ° C. Plant height: 80-90 cm.
Mass of 1000 seeds: 140-150 g.
The variety is entered in the Register of Varieties of the Republic of Belarus.
According to the State Variety Testing results, the yield is at the level of the PRIPYAT standard.

Variety Certificate No. 0004510 for the soybean variety PUSHCHANSKAYA.
Patent No. 494 of the Republic of Belarus for the soybean variety PUSHCHANSKAYA.

Methodological recommendations «Technology assessment and selection of soybean breeding material by a set of economic traits».
Methodological recommendations «Individual selection methods in hybrid soybean populations» (2016).

FRUIT CROP BREEDING

ACCREDITED ACTIVITY

LABORATORY OF MOLECULAR GENETICS
Oksana Urbanovich, PhD
O.Urbanovich@igc.by
Tel.: +375 17 284 91 80

DNA IDENTIFICATION AND FRUIT VARIETY VERIFICATION (CERTIFICATION)

Universal systems for DNA identification and certification of pomaceous and stone fruit crops grown in the Republic of Belarus, including apple, pear, plum, cherry, apricot and sweet cherry varieties have been developed.

The proposed DNA analysis methods using the developed sets of SSR markers allow to develop unique molecular-genetic profiles of fruit crops grown in the Republic of Belarus and carry out DNA identification of genotypes according to distinctness, uniformity and stability criteria.

DNA identification methods of pomaceous and stone fruit crops allow for the improved accuracy in establishing varietal typicality, clarifying pedigrees of varieties, identifying unique genotypes in collection gardens. The methods can be successfully used for the author's right protection of breeding institutions in the purchase and sale of planting material.

Advantages of the developed methods:
- Allow to identify varieties of pomaceous and stone fruit crops before tree fruit-bearing;
- High accuracy of analysis;
- Allow to establish varietal identity within a short period of time and at any stage of plant development;
- No similar methods.

Methodological recommendations for identification and certification of apple and pear varieties based on DNA markers. Approved by the Science and Technology Council of the Directorate-General for Plant Breeding of the Ministry of Agriculture and Food of the Republic of Belarus, Protocol of December 3, 2010 No. 11.

Invention patent of the Republic of Belarus No. 21664. A set of SSR molecular markers and a DNA identification method for sour cherry, cherry, home plum, diploid plum, and apricot varieties and their hybrids.

Based on the use of DNA markers, methods to identify the genes resistant to powdery mildew and scab in the genome of apple varieties and hybrids grown in Belarus, which are used in the breeding process to create the initial breeding material and hybrids with complex resistance to diseases and pests.

Methodological recommendations for the identification of apple scab resistance genes based on DNA markers. Approved by the Science and Technology Council of the Directorate-General for Plant Breeding of the Ministry of Agriculture and Food of the Republic of Belarus, Protocol of June 01, 2011 No. 5.

BERRY CROP BREEDING

LABORATORY OF MOLECULAR GENETICS
Oksana Urbanovich, PhD
O.Urbanovich@igc.by
Tel.: +375 17 284 91 80

DNA IDENTIFICATION AND ESTABLISHING VARIETAL IDENTITY (CERTIFICATION) OF BERRY CROPS
strawberry, black currant, red currant, garden gooseberry and ornamental representatives of the Ribes genus

The proposed method allows:
- Higher accuracy in establishing varietal uniformity;
- To verify variety lineages and identify unique genotypes in the collection gardens;
- It can be successfully applied to copyright protection of breeding institutions in the purchase and sale of planting material.

Advantages of the proposed method:
- High analysis accuracy;
- Possibility of establishing varietal identity within a short period of time and at any stage of plant development;
- No similar methods.

The methods are based on the use of highly informative SSR markers and allow for DNA identification and certification of berry varieties grown in the Republic of Belarus and DNA identification of genotypes in accordance with the distinctness, uniformity and stability criteria.

The developed methods allowed to design unique molecular genetic certificates for the following varieties:
- garden strawberries;
- black currant;
- red currant;
- gooseberry.

and the varieties included in the State Register of Varieties of the Republic of Belarus.

Invention patent application of May 11, 2018 No. a 20180093 and of May 22, 2018 No. a 20180102.

POTATO BREEDING

LABORATORY OF POTATO GENETICS
Alexander Ermishin, PhD
Ermishin@igc.by
Tel.: +375 17 369 83 26

POTATO PCR ASSESSMENT TECHNOLOGY BY THE COMPOSITION AND ALLELIC STATE OF DISEASE AND PEST RESISTANCE GENES TO OPTIMIZE PARENTAL FORMS' SELECTION FOR HYBRIDIZATION

The diploid potato breeding technology has been developed based on the use of DNA markers and involving the gene pool of wild potato species for an effective combination of highly efficient genes resistant to nematodes, viruses, cancer and late blight in the selection material to develop potato varieties with complex resistance to the most important pathogens based on this breeding material.

Identification methods for 9 potato genes resistant to nematodes, viruses, potato carcinoma and late blight using PCR analysis have been developed and the technology to assess potato for the presence and allelic state of these genes has been established allowing to optimize parental forms' selection for hybridization and further reduce the cost of breeding material testing.

Reduced cost of breeding material testing due to the reduced research cost and timing in diagnosing the presence of resistance genes and the increased efficiency of the best variety sample selection by reducing the size of hybrid populations needed to isolate breeding valuable genotypes determine the technology competitiveness in the domestic and global markets.

The technology will significantly improve the selection efficiency of valuable genotypes, reduce the cost of breeding material testing and optimize crossing programs to develop potato varieties with complex resistance to diseases and pests.

Invention patent of the Republic of Belarus No. 19566 «Breeding technology for the Salanum tuberosum potato».

Methodological recommendations «Evaluation of potato source material by the composition and allelic state of disease and pest resistant genes to optimize parental forms' selection for hybridization» of the Science and Technology Council of the Directorate-General for Plant Breeding of the Ministry of Agriculture and Food of the Republic of Belarus (Protocol of January 17, 2015 No. 17).

The transfer of test samples (elite seed material) to husbandries for propagation and sale under the terms and conditions of licensing and business contracts. Scientific and research work to develop new varieties. DNA typing of breeding material.

SWEET PEPPER BREEDING

LABORATORY OF ECOLOGICAL GENETICS AND BIOTECHNOLOGY
Alexander Kilchevsky, Academician; Olga Babak, PhD, Associate Professor
O.Babak@igc.by
Tel.: +375 17 284 19 46, +375 17 284 19 16

STRATIFIED SWEET PAPPER VARIETIES AND HYBRIDS «KASHTOUNY F_1», «CHYRVONY MAGNAT», «ALTYN», «CHERVONETS»

Determinate pepper varieties and hybrids for cultivation in unheated greenhouses and in the open ground adapted to weather and climatic conditions of the Republic of Belarus with high ecological stability, commercial yield, and disease resistant; can be used for fresh consumption and canning.

HYBRID F1 KASHTOUNY
Early ripe. The yield in the plastic greenhouse is 7.5-8.1 kg/m2, the bush is semi-spreading, 70-80 cm high. The fruits are oblongated, directed downwards. The fruit coloration is dark green at the stage of industrial ripeness and at the stage of biological ripeness is red.
Kashtouny Certificate No. 0003908.

CHYRVONY MAGNAT VARIETY
Mid-season. The yield in the plastic greenhouse is 6-8 kg/m2, the bush is semi-spreading, 60-70 cm high, fruit weight is 130-150 g, cuboidal, directed downwards, glossy. Wall thickness is 8-11 mm.
Chyrvony Magnat Certificate No. 0004592.

ALTYN VARIETY
Mid-season. The yield in the plastic greenhouse is 4.2-5.4 kg/m2. The fruit is cuboidal, large, 3-4 pockets; the fruit weight is 158-171g. The fruit coloration is yellow, cuboidal, with an abscission layer.
Altyn Certificate No. 0005058.

CHERVONETS VARIETY
Early ripe. Early yield is 1.5-2.0 kg/m2. Commercial yield is 5.0-8.0 kg/m2. The fruit is cuboidal, large, fruit weight is 150-180g. The fruit wall thickness: 10-12mm. The fruit coloration at the stage of biological ripeness is red.
Chervonets Certificate No. 0005063.

The designed DNA technologies make it possible to identify, select and create the source breeding material with economic properties to develop new varieties with desired properties. Receipt of additional net income due to higher yields relative to standards.

Scientific research activity to develop sweet pepper varieties and hybrids with longer fruit shelf life, resistant to abiotic and biotic stresses and with high carotenoid content.

DNA typing of breeding material.

Contractual seed selling.

TOMATO BREEDING

LABORATORY OF ECOLOGICAL GENETICS AND BIOTECHNOLOGY
Alexander Kilchevsky, Academician; Olga Babak, PhD, Associate Professor
O.Babak@igc.by
Tel.: +375 17 284 19 46, +375 17 284 19 16

STRATIFIED TOMATO VARIETIES AND HYBRIDS

SAPSAN F_1, CHIROK, BERKUT, BUBENCHIK F_1, AGENCHYK F_1, TAINIK F_1, CHERRY KORALL, STRELA, IRMA, TAMARA, STORADZH F_1, RUBIN F_1, AZART F_1, VITYAZ F_1, ALEKSHA

Tomato varieties and hybrids for plastic greenhouses and open ground adapted to weather and climatic conditions of the Republic of Belarus, high ecological stability, commercial yield, fruit shelf life and disease resistant.

High content of vitamin C, dry matter, sugars, carotenoids and lycopene. The designed technologies allow to identify, select and create the source breeding material with economic properties to develop new varieties with desired properties.

Additional net income (from 1.5 to 6 thousand rubles per hectare) due to higher yield with respect to standards. According to the state variety testing results, the noted commercial yield excess was by 0.3-0.7 kg/m2 in plastic unheated greenhouses and by 15-85 kg/ha in the open ground.

Sapsan Certificate No. 0002367.
Berkut Certificate No. 0002610.
Agenchyk Certificate No. 0003380.
Cherry Korall Certificate No. 00044072.
Irma Certificate No. 0003833.
Storadzh Certificate No. 0002365.
Azart Certificate No. 0004221.
Aleksha (Cherry) Certificate No. 0005057.
Chirok Certificate No. 0002615.
Bubenchik Certificate No. 0002617.
Tainik Certificate No. 0002619.
Strela Certificate No. 0003390.
Tamara Certificate No. 0002613.
Rubin Certificate No. 0003395.
Vityaz Certificate No. 0004232.

Methodological recommendations «DNA typing of fruit quality and tomato disease resistant genes» of the Ministry of Agriculture and Food of the Republic of Belarus.

Scientific research activity to develop tomato varieties and hybrids with longer fruit shelf life, resistant to abiotic and biotic stresses and with high carotenoid content.

DNA typing of breeding material.

Contractual seed selling.

TOMATO BREEDING

LABORATORY OF ECOLOGICAL GENETICS AND BIOTECHNOLOGY
Alexander Kilchevsky, Academician; Olga Babak, PhD, Associate Professor
O.Babak@igc.by
Tel.: +375 17 284-19-46, +375 17 284-19-16

STRATIFIED F_1 TOMATO HYBRIDS «POTENTSIAL», «NADZEYA», «KOMPROMISS»

Tomato hybrids for the open ground adapted to the weather and climatic conditions of the Republic of Belarus with high commercial yield and response to treatment with microbiological agents; recommended for use with microbiological agents in ecologically oriented agriculture.

Obtaining additional income due to increased commercial yield (up to 2 times) when treated with microbiological agents in relation to the standards.

Potentsial Variety Certificate No. 0003432.
Nadzeya Variety Certificate No. 0003431.
Kompromiss Variety Certificate No. 0003430.

Scientific research activity to develop tomato varieties and hybrids with the increased response to treatment with microbiological agents.

Contractual seed selling.

PROFIBAKT™-FITO

Bacterial agent recommended for:

- Cucumber root rot when grown in soil or on the mineral wool (hydroponics) in stationary and plastic greenhouses
- Root and bottom rot of protected soil tomato (mineral wool)
- Root rot of green crops in the conditions of flow hydroponics.

Cucumber protection efficiency - 60.8-63.3%, yield increase by 18-21%.
Tomato protection efficiency - 80%, yield increase by 8%.
Green crops protection efficiency - 70-81%.

PROFIBAKT™-FITO is based on a mixture of strains of rhizospheric bacteria Bacillus sp. BB58-3 (B. amyloliquefaciens group - B. subtilis) and Pseudomonas aurantiaca B-162/255.17. Agent's bacteria are antagonists for a number of plant causative agents of fungal and bacterial etiology. Selected combination of active strains in the agent's composition provides for the highly efficient biological protection and a balanced growth-stimulating effect on plants.

The agent is produced by demand of PLC «Bobruisk Plant of Biotechnology».

Form of cooperation: Trademark Licensing Agreement.

GENETIC ANALYSIS

ACCREDITED ACTIVITY

NATIONAL COORDINATION BIOSAFETY CENTRE
Galina Mozgova, PhD
ldgmo@igc.by, biosafety.by
Tel.: +375 17 284 02 97, Cell Phone: +375 44 784 16 91(Velcome)

DETECTION OF GENETICALLY MODIFIED INGREDIENTS (GMIs)

Detection of genetically modified ingredients (GMIs) in food raw materials and food products by real-time PCR.

Screening of authorized and unauthorized GM lines in the countries of the Customs Union.

It is held on the basis of the accredited Republican Center for Genome Biotechnology to implement legislative requirements for labelling of food products containing GMIs.

The GMI detection is carried out in the accredited laboratory included in the Register of Testing Laboratories of the Customs Union. Test Protocols are recognized in all countries of the Customs Union. Accreditation for compliance with STB ISO/IEC 17025 (Accreditation Certificate of December 7, 2009 BY/112 02.1.0.1599).

More than 10 years in the market of services, guaranteed quality, minimum order fulfillment time.

Naming of documents, Technical Normative Legal Acts establishing product requirements: Sanitary Regulations and Standards «Requirement for food raw materials and food products», Sanitary-hygienic standard «Safety and zero harm indicators of food raw materials and food products for a human» of June 21, 2013 No. 52; Technical Regulations of the Customs Union (CU TR 021/2011, CU TR 015/2011, etc.).

We provide commercial contract services and conclude research contracts.

We offer collaboration to legal entities and individual entrepreneurs on rendering of services in quality control of food and agricultural raw materials and food products.

REPUBLICAN DNA BANK

Alexander Kilchevsky, Academician
Elena Mikhakenko, PhD, Deputy Head of the Republican DNA Bank. DNAbank@tut.by, http://abs.igc.by
Tel.: +375 17 284 19 18

REPUBLICAN DNA BANK OF A HUMAN, PLANTS, ANIMALS AND MICROORGANISMS

In 2016, it acquired the National Heritage status
(Resolution of the Council of Ministers of the Republic of August 13, 2016 No. 629).

The establishment of the Republican DNA Bank commenced in 2013 pursuant to Paragraph 2 of the Instruction Protocol of the Prime Minister of the Republic of Belarus M.V. Myasnikovich of May 24, 2013 at the meeting on the biotech industry development in the Republic of Belarus.

The overarching objective of the Republican DNA Bank is the long-term storage, systematization, study and multiple utilization of DNA samples for the development of genomic biotechnologies in health care, sports, forensics, environmental protection, industry and agriculture.

The Bank structure includes the following sections:
- DNA Bank of a human;
- DNA Bank of animals;
- DNA Bank of plants;
- DNA bank of microorganisms;
- DNA bank of rare and endangered plant and animal species.

Sample collections are systematized according to a number of parameters (DNA of indigenous Belarusians, athletes, patients with multifactorial diseases, agricultural plants, rare and endangered plants and animals, reference samples of microorganisms for the food industry). For DNA samples' storage, the Institute is equipped with the storage facility with low-temperature refrigerating chambers and a cryopreservation system. The sample depositing procedure and the DNA sample record system have been established.

The Bank's scientific group conducts research (including DNA barcoding) and develops scientific and practical recommendations for their use, taking into account the specifics of scientific and/or practical problems in the field of biology, genetics, agricultural practice and biotechnological production, protection and sustainable use of biodiversity and medicine.

The Republican DNA Bank of a human, animals, plants and microorganisms renders services in long-term specialized storage of DNA samples and biological material of a human, animals, plants and microorganisms using cryopreservation technology.

GENETIC ANALYSIS

Shareable Core Facilities "GENOME"
Elena Guzenko, PhD, Tel.: +375 17 284 1941, E.Guzenko@igc.by
Olga Mazur, Tel.: +375 17 332 1613, genom@igc.by

SHAREABLE CORE FACILITIES «GENOME»

Areas of activity:
• Use of unique equipment for research in priority areas of science;
• Rendering services in molecular genetic analysis of DNA samples;
• Methodological assistance and consultations in various fields of genome technology application.

Equipment:

Genome Wide Sequencer MiSeq (Illumina, Inc, USA).
It allows to take on specialized tasks such as the study of target genome regions, metagenomics, small genomes', evaluation of gene groups' expression, amplicon sequencing and HLA typing. MiSeq reagents of new generation allow to achieve productivity of 15 billion bp and 25 million of separate readings, while the length of reading is 2x300 bp.

Genetic Analyzers 3500 (Applied Biosystems, Japan).
Destined for the nucleotide sequence detection of DNA fragments and for SSR, LOH, SNP, MLPA, FLP, t-RFLP analyses. It is possible to carry out de novo sequencing and resequencing of small genomes up to 1000 bp. The number of capillaries is 8. The number of dyes is 6. The ability to read tags: TAMRA, ROX, R6G, FAM, LIZ. Sequencing speed is 700 bp with an accuracy of 98.5% in less than 40 minutes.

QX200™ Droplet Digital PCR System
Designed for droplet digital PCR of nucleic acids for the single gene expression analysis, detection and evaluation of pathogens; determining the number of gene copies (CNV), determining the viral load, detecting of GMOs, work with microRNA, validating and quantifying of NGS libraries. In addition to working with Taq-man PCR, it is possible to use EvaGreen intercalating dye. ~ 20 000 drops formed from 20 µl reaction mixture are analyzed.

Shareable Core Facilities is also equipped with:
Amplifiers, amplifiers able to register real-time PCR products CFX96 (Bio-Rad, USA), robotic station for large-scale DNA isolation Freedom EVO 75 (TECAN, Switzerland), molecular scanner Pharos FX Plus Molecular Imager (BioRad, USA), NanoDrop 8000 Spectrophotometer (USA), water purification system PURELAB FLEX 3, PF3XXXXM1 (Elga. UK), ice generator IMS-30 (Teseus Lab. Czech Republic), PCR box, vortexes, centrifuges and other equipment needed for sample preparation (PCR, NGS, and etc.).

CONTENTS

State Scientific Institution

**INSTITUTE OF GENETICS AND CYTOLOGY
OF THE NATIONAL ACADEMY
OF SCIENCES OF BELARUS**

27, Akademicheskaya Street
220072 Minsk, Belarus
Tel.: +375 17 284 1856 (Reception)
Tel./Fax: +375 17 284 1917

www.igc.by