

# Mobilization of genetic diversity of the genus *Malus* on the basis of information technologies for the breeding of varieties with complex resistance to fungal pathogens

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**Abstract.** Breeding renewal of the southern assortment of apple trees for the Russian fruit growing industry based on the accelerated process of creating domestic genotypes with a complex increased resistance to the main fungal pathogens of the culture (*Venturia inaequalis* (Cooke) Wint., *Podosphaera leucotricha* (Ell. & Ev.) E.S. Salmon, *Phyllosticta mali* Pr. et. Del., *Phyllosticta briardi* Sacc.) is due to the systematic use of modern methods, innovative breeding techniques and improved techniques. The purpose of the study is to develop and create a database of representatives of the genus *Malus* Mill., which is promising for use in the production and accelerated breeding of new domestic genetic resources for the southern region of Russia. During the research work, Russian modern and generally accepted programs and methods of breeding, variety study for fruit plants were used. The formed database "Main economically valuable, morphological and molecular-genetic characters of representatives of the genus *Malus* Mill. with resistance to the main fungal pathogens in the south of Russia"; filed an application for its patent. Using the data of the obtained information system will significantly speed up the solution of practical selection problems and reduce the costs of organizing the breeding process.

## 1 Introduction

The breeding of an apple tree (*Malus × domestica* Borkh.) For most economically significant traits (resistance to fungal diseases, early maturity, yield, fruit quality, etc.) is a rather difficult task due to the polygenic nature of these traits and indicators [1]. The apple tree is susceptible to diseases that are caused by various pathogens, for example, fungi, bacteria, viruses, mycoplasmas and nematodes. It was found that apple varieties are affected by more than 70 infectious diseases, most of which are caused by pathogenic fungi that cause significant damage to the plant, represented in the form of rotting of fruits, root system, leaves, the

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appearance of spots on fruits and leaves [2-4]. To successfully combat the main diseases of the apple tree culture, an integrated systematic approach is required based on the creation of immune and resistant varieties, biological control of diseases, reasonable and targeted use of fungicides, the choice of a suitable site for laying a garden and control over the ecological situation [5]. Frequent use of fungicides, while significantly increasing production costs, at the same time has a negative impact on human health and the environment. Apple varieties with immunity and resistance to scab require significantly less fungicides for cultivation, which can reduce costs and reduce the negative impact of chemical treatments on the environment [6]. Genetic resistance to scab (*V. inaequalis*) in apple is primarily determined by 20 genes (*Rvi*), most of which were identified in wild specimens and a number of local varieties and forms of the genus *Malus* [7-10]. Currently, the fundamental and integral part of the breeding process includes both the use of existing domestic and international databases and the creation of new ones. To date, a fairly large amount of information has been accumulated on apple breeding, which must be evaluated, summarized, analyzed, systematized and made available to breeders around the world. Usually, databases include information on the origin, ploidy, phenotypic data, basic quality indicators of fetuses, key traits and allelic composition of molecular markers [11, 12]. Modern databases are considered a reliable tool that contributes to the effective management of genetic resources, makes it possible to assess the existing breeding potential of a plant, select and search for the necessary genotypes according to the key parameters for the breeder [13-15]. In 2007, the AppleBreed Data Base was announced, the innovative concept of which provides information on the location and method of conservation of genetic resources, on genotyped loci and phenotypic manifestations of traits [16]. This idea was developed in the course of research, including the assessment of genetic diversity and phenotypic traits, both varieties and hybrid material, collected in the FruitBreedomics database [13, 14]. There are also more narrowly targeted databases, for example, containing information on the allelic composition of the self-incompatibility gene [17]. The relevance of these studies is due to the strengthening and improvement of the efficiency of management of the genus *Malus* in order to accelerate the selection and creation of new generation genotypes for the most important and key parameters, economically significant and adaptive indicators and traits for use in further breeding research and industrial horticulture. The aim of the study is to develop and create a database of representatives of the genus *Malus* Mill., which is promising for use in the production and accelerated selection of new domestic genetic resources for the southern region of Russia.

## 2 Materials and methods

The objects of research are apple genotypes (*Malus* × *domestica* Borkh.), different in ploidy and ecological-genetic origin. The location of the collection of the general resources of the apple tree NCFSCHVW is the experimental production farm "Centralnoye" (city of Krasnodar). Experimental plantations of apple trees (on the M9 rootstock, planting in 2000-2015, according to schemes of 5×1.5 m and 5×2 m) are located in the Kuban zone, the central subzone of horticulture of the North Caucasian region of the Russian Federation. To create a database ("The main economically valuable, morphological and molecular-genetic characters of representatives of the genus *Malus* Mill. with resistance to the main fungal pathogens of southern Russia") summarized, systematized and analyzed long-term phenotypic data (for the period 2002–2020) on 33 collection specimens of apple, which are at the time of full fruiting at the present time. The study was carried out with the financial support of the Kuban Science Foundation in the framework of the scientific project No. IFR – 20.1/92. Research work was carried out according to breeding programs and methods: "Program of the North Caucasus Center for the selection of fruit, berry, flower and ornamental crops and grapes for

the period up to 2030"; "Modern methodological aspects of the breeding process organization in horticulture and viticulture"; "Program and methodology of variety studies of fruit, berry and nut crops"; UPOV method for apple trees RTG/0014/2; software product in Microsoft Access format.

### 3 Results and discussion

For targeted inclusion in the breeding process for the accelerated creation of domestic competitive varieties of leading fruit crops, the role of conservation, mobilization and optimal practical use of the apple tree gene pool is enormous, including the creation of electronic databases. The creation of a database that unites the most valuable samples of the gene pool of fruit crops, including apple trees, is the most important stage in variety study. The developed information system includes a software product for the formation of a database of general resources, representatives of the genus *Malus* Mill. (complex interspecific varieties, forms and hybrids of apple trees of domestic and foreign selection). By creating and improving the software product - a database of genetic resources of representatives of *Malus* Mill. the development of this information system was carried out in the Microsoft Access format. The choice of the format is due to the fact that Microsoft Access is a relational database management system (RDMS) with a fairly wide range of functionality, which includes communication with external databases and tables, related queries, contains all the necessary functions and tools to compose any queries related to to databases, including: fetching data from a table, grouping results, searching and sorting by specified criteria, importing data from an external source, distributed queries to combine results from several tables, etc.

At present, the database "Main economically valuable, morphological and molecular-genetic characters of representatives of the genus *Malus* Mill. with resistance to the main fungal pathogens of the south of Russia ", which includes varieties with high stable resistance to scab, powdery mildew, phylostictosis in the cultivation region, including: foreign selection - Florina, Piotosh, John Downie, York Imperial, Feri, Gertruda and others, regional - Favorite Dutovoy (NCFSCHVW, VNIISPK and SEBS breeding), Talida (NCFSCHVW), Carmen, Lyubava, Orpheus, Nocturne, Taina, Soyuz, Rodnichok, Talisman (NCFSCHVW, VNIISPK), Flooring (MESIPI) resistant and immune to scab, with adaptability to the complex of abiostressors of the region. The genetic resources database includes characteristics for 33 representatives of the genus *Malus* Mill., promising for breeding for complex resistance to fungal pathogens; consists of three tables:

- "Genotype" (name of the sample, ploidy, origin, DNA passport, the presence of alleles of the S self-incompatibility gene, economically valuable genes);
- «DHS» (assessment of distinctness, homogeneity and stability - characteristic of the sample by 57 morphological characteristics) (Figure 1);
- "Varieties" (description of the original breeding valuable material of the apple tree, which includes: name, synonyms, IPI, catalog number, taxonomy, origin (parental forms), variety authors, originator, variety status, country of origin, phenology, description of the tree, fruits, main economic characteristics (early maturity, low growth and compactness of the crown, type of fruiting, rate of increase in yield, stability of fruiting, resistance to the main fungal pathogens (scab, powdery mildew, phylostictosis), frost resistance, resistance to spring frosts, drought resistance, etc.), data of cytological analysis , features and advantages of the sample).



**Fig. 1.** Form of the table "DHS" of the database "Main economically valuable, morphological and molecular genetic characteristics of representatives of the genus *Malus* Mill. with resistance to the main fungal pathogens of the south of Russia"

The capabilities of the software platform include searching for samples in the database by a number of parameters, displaying a general list of samples and displaying detailed information for each variety separately (Figure 2). To enter data into the "DHS" table, a special form has been implemented that supports data entry using drop-down lists that make it easier to fill in the data. The table and form of the DHS contain a complex of 57 morphological characters according to the international UPOV methodology. In the form we have realized, they are divided into the characteristics of the tree and growth, leaf blade and petiole, flower and fruit, phenological and productive. For ease of use, these sections in the form are highlighted with different color markers and corresponding images. This database in the table "DHS" contains information about 33 samples of apple trees.

The table "Varieties" contains a lot of textual information, therefore, for the convenience of filling it out, a corresponding form has been created, which includes 10 fields for entering information: variety, synonyms (IPI catalog number), taxonomy, country of origin, origin, phenology, tree, fruits, features, advantages. The table contains information on 33 apple tree specimens.

Код	Сорт	Дерево_сита_роста	Дерево_тип	Дерево_форма_кроны	Дерево_тип_плодоношения	Прирост_прошлого_года_топшана	Прирост_прошлого_года_длина_листья
1	Юрий	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	топшан (7)	средней длины (5)
2	Салт	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	топшан (7)	средней длины (5)
3	Талда	слаборослое (3)	ветвистое (2)	вертикальная (1)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
4	Рассвет	среднерослое (5)	ветвистое (2)	вертикальная (1)	на кольчатках и прутиках (2)	топшан (7)	средней длины (5)
5	Красный венгер	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
6	Виктория	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
7	Зарянка	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
8	Гербурда	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
9	Дюк Дуин	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
10	Милорад Павла	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
11	Белый	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
12	Венгос	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
13	Темновидное	слаборослое (3)	ветвистое (2)	свисающая (3)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
14	Фрея	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
15	Разное белое	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
16	Спартак	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
17	Василик	среднерослое (5)	ветвистое (2)	вертикальная (1)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
18	Житозеленое	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
19	Мелитопольное	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
20	Золотое летнее	слаборослое (3)	ветвистое (2)	вертикальная (1)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
21	Кармен	среднерослое (5)	ветвистое (2)	вертикальная (1)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
22	Лейба	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
23	Лобанов Длитель	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
24	Никола	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	топшан (7)	средней длины (5)
25	Рислинг красный	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
26	Татарское	среднерослое (5)	ветвистое (2)	вертикальная (1)	на кольчатках и прутиках (2)	топшан (7)	короткие (3)
27	Таня Любим	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
28	Фей	среднерослое (5)	ветвистое (2)	вертикальная (1)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
29	Флорана	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	средней топшаны (5)	средней длины (5)
30	Флорина	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	топшан (7)	средней длины (5)
31	Риданок	среднерослое (5)	ветвистое (2)	раскидистая (2)	на кольчатках и прутиках (2)	топшан (7)	средней длины (5)
32	Натюр	среднерослое (5)	ветвистое (2)	вертикальная (1)	на кольчатках и прутиках (2)	топшан (7)	средней длины (5)

**Fig. 2.** Table "DHS" of the database "Main economically valuable, morphological and molecular genetic characters of representatives of the genus *Malus* Mill. with resistance to the main fungal pathogens of the south of Russia"

Microsoft Access is available on the software market in the Russian Federation, has a user-friendly interface and can be used by researchers with minimal knowledge of

information technology. Unlike published catalogs, this is a powerful and flexible tool that allows you to quickly and efficiently transform based on the needs and requests of the user.

## 4 Conclusion

Thus, the most effective solution to the breeding priorities of the apple tree is due to the mobilization of the genetic potential of the genus *Malus* Mill., the search, isolation and active targeted use of new sources of key traits, as well as the improvement, development and application, along with a complex of selection methods, information technologies. The database "Main economically valuable, morphological and molecular-genetic characters of representatives of the genus *Malus* Mill. with resistance to the main fungal pathogens of the south of Russia" and an application for its patent was filed. *Malus* Mill. Genetic Resources Database. in Microsoft Access format is of practical importance for use in the gardening industry of southern Russia and accelerated selection of apple trees for resistance to the main fungal pathogens (scab, powdery mildew, phyllostictosis) and their complex for creating promising domestic varieties of a new generation. The results of fundamental research obtained during the implementation of the regional project will significantly speed up the solution of practical breeding problems in the south of Russia, contributing to a reduction in the period for creating a domestic variety with a complex of valuable traits, as well as a serious reduction in the costs of organizing the entire long-term breeding process.

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