# THE MODERN CHALLENGES AND OPPORTUNITIES FOR IMPROVING THE GENETIC DIVERSITY OF TOMATOES

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**Abstract.** *This article designated modern climatic and genetic factors as causes of the intensification of genetic erosion in tomatoes (Solanum lycopersicum L). The possibility of expanding the genetic diversity of tomatoes through the use of mutant genes in breeding that control a wide range of economically valuable traits is being considered. The potential of mutant forms as a source of resistance to abiotic stress factors (high and low temperatures, drought) for use in breeding as donors is demonstrated. A description is provided of the phenotypic expression of mutant genes controlling plant habit and architecture, which determine the expression of various fruit traits, including resistance to the most common diseases. The possibility of using certain mutant genes to expand the range of recombinational variability in $F_2$ populations and to obtain transgressive tomato forms with a completely new combination of mutant marker and economically valuable traits is demonstrated.*

**Keywords:** Tomato (*Solanum lycopersicum* L.), climatic and genetic factors, mutant genes, selection, genetic diversity

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## 1. Introduction

The tomato (*Solanum lycopersicum* L.) is one of the most widely cultivated vegetable crops in the world (approximately 5 million hectares) [1]. Its high share in the structure of gross vegetable production in various countries is due to its ecological adaptability and the nutritional value of its fruits, which contain sugars, organic acids, mineral salts, vitamin C, carotenoids, lycopene, fats, carbohydrates, fiber, and others [22]. These qualities facilitate its use in both fresh and processed forms.

However, global and local climate change on the one hand, and one-sided breeding aimed at creating high-yielding, uniform, transportable tomato varieties and hybrids that better meet general standards on the other, have led to the intensification of its genetic erosion. Farmers and larger producers have also contributed to this in their pursuit of high yields, they have ceased to grow local varieties with superior flavor, leading to their loss as carriers of valuable traits

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characteristic of the ecological niche of the Republic of Moldova. The rapid evolution of pathogens and pests has also contributed to this. All these factors, identified as modern challenges (Figure 1), led to a deficit in the genetic diversity f the tomatoes cultivated gene pool, a decrease in the adaptability of modern varieties and hybrids, and their vulnerability to biotic, abiotic, and other stress factors, which ultimately affected crop yields and, in particular, their quality and, especially, the quality of the produce.

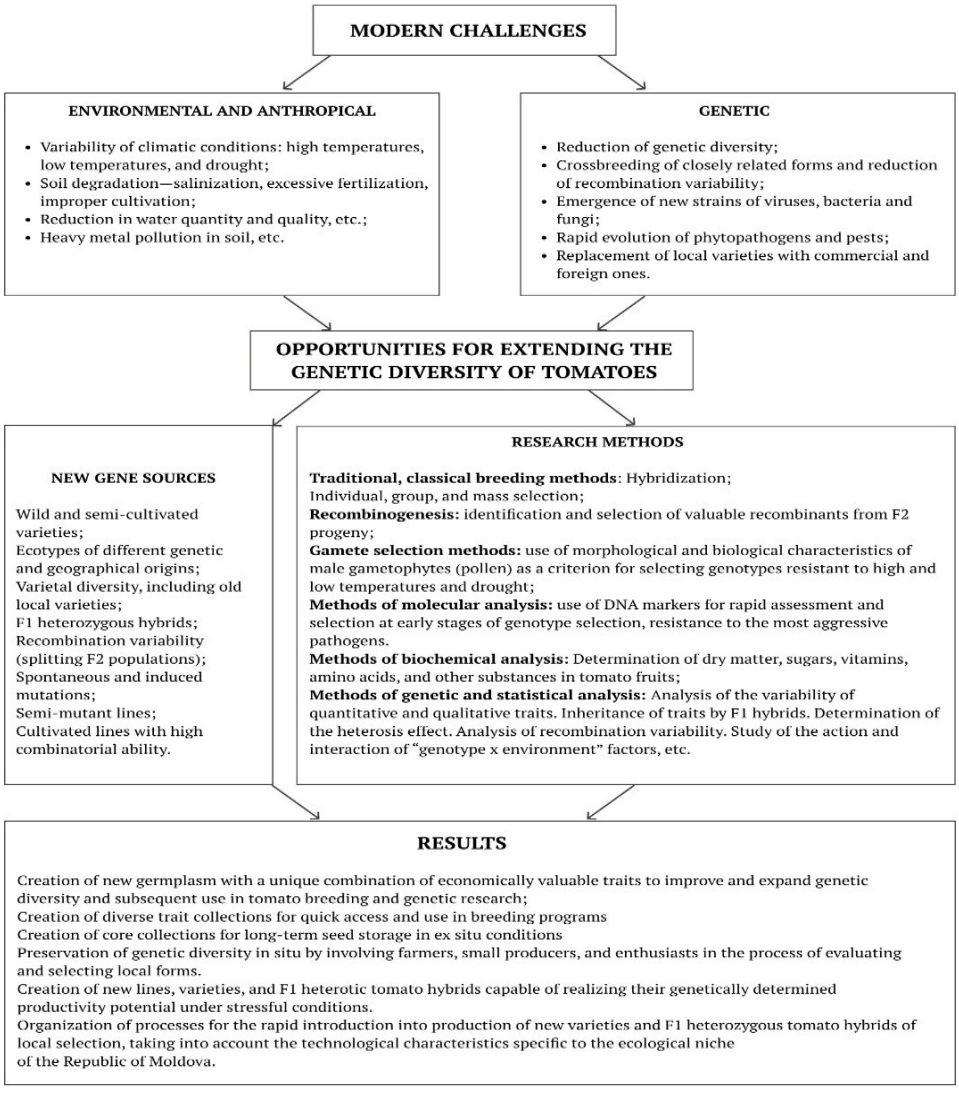


**Figure 1.** Climatic and genetic factors increasing tomato erosion and opportunities to improve its genetic diversity

The increasing deficit of tomato genetic diversity indicates that the search for opportunities to improve and expand it is becoming a strategic direction for modern research. This requires a reorientation of fundamental research and applied breeding toward the search for, identification of, and incorporation into the breeding process of sources of new germplasm with higher genetic diversity. These may include wild and semi-cultivated tomato varieties, landraces, as well as hybrid populations artificially created with their participation.

Of particular interest in this regard are spontaneously occurring and artificially induced mutations [22, 17, 19]. The availability of a large number of easily identifiable tomato mutant marker genes it possible to address a wide and diverse range of research questions. These include, first and foremost, genome mapping [18]; localization of quantitative traits [3]; identification of the characteristics of the heterosis effect [8]; study of recombinational variability in $F_2$-$F_3$ hybrid populations [9, 11, 16]; study of biochemical and physiological processes of plant development [6, 18]; and others. There are examples of their effective use in practical breeding to obtain new varieties with a beneficial combination of economically valuable traits [9, 10, 16].

A comprehensive approach to evaluating and identifying sources of new germplasm, combined with the use of classical breeding methods alongside gametic technologies, can also contribute to improving the genetic diversity of the tomato. According to Pfahler (1982), the male gametophyte of the tomato is more sensitive to environmental conditions and changes than the female gametophyte, which is covered by thick layers of somatic tissues [15]. This has been confirmed in the works of other authors who use male gametophyte traits as criteria for evaluating and selecting genotypes resistant to adverse environmental factors, not only in tomatoes but also in other agricultural crops [4, 5, 12]. High sensitivity and the presence of a large amount of pollen allow for the rapid testing of extensive collections and the identification of genotypes resistant to one or several stress factors at once [10].

Hybridization plays a key role in expanding genetic diversity as one of the most important methods of classical breeding. It allows us to harness heredity as the greatest force that drives morphological development. Interspecific and intergeneric crosses are particularly effective in this regard, facilitating the production of plant forms with entirely new combinations of valuable traits [22]. The combined use of classical breeding and pollen analysis methods allows for working with large hybrid populations using a streamlined approach and identifying genotypes that combine economically valuable traits with resistance to various abiotic stress factors [10].

Farmers can also contribute to expanding the genetic diversity of tomatoes by selecting, under production conditions, the most valuable varieties that are less susceptible to current local challenges, differ in fruit characteristics, and possess

high flavor qualities. Selection, conservation, and active cultivation of these varieties represent one potential approach to enriching the gene pool of local varieties with ecotypes capable of realizing their genetically determined productivity potential under the conditions of the Republic of Moldova.

As we can see, there are quite a few opportunities to overcome the negative impact of climatic and genetic factors on the intensification of tomato erosion. Proper organization and their combined use will allow for the intensification of the search, identification, and selection of the most valuable genotypes that combine economically valuable traits with resistance to abiotic and biotic stress factors, thereby contributing to the expansion of tomato genetic diversity.

The aim of the research was to comprehensively study the genetic potential of mutant marker genes of tomato for their effective use in practical breeding, improving varietal diversity and replenishing collections with genes controlling a wide range of economically valuable traits

## 2. Materials and Methods

The experimental material consisted of 125 mutant tomato lines carrying 187 mutant marker genes, more than 50% of which are of practical value for addressing current challenges in practical breeding.

**2.1. Phenotypic expression of mutant genes**.

The nature of expression and the degree of phenotypic expression of the mutant genes were determined in accordance with the tomato gene nomenclature [22, 20].

Studied the nature and characteristics of the expression of marker genes controlling plant habit, architecture, and fruit traits (shape, color, taste).

**2.2. Screening of mutant tomato lines for resistance to abiotic stress factors.**

Testing for resistance to abiotic stress factors (high and low temperatures, drought) was conducted based on male gametophyte (pollen) traits using artificially simulated stress conditions *in vitro* [10]. Fresh pollen collected from the flowers of each mutant sample served as a control, it was germinated on an artificial nutrient medium (15% sucrose and 0.006% boric acid) under *in vitro* conditions (3 hours) at a temperature of 25°C. Pollen viability-germination (*p, %*) and pollen tube length (*l, μm*) were determined.

Resistance to high (45°C) and low (6°C) temperatures, as well as drought (simulated by high sucrose concentration), was assessed based on the ability of pollen from experimental samples to germinate (pollen germination resistance), and the ability of germinated grains to form pollen tubes (resistance based on tube length) of a length sufficient for fertilization (three pollen grain diameters) [7] under the influence of these stressors. For each sample and in each experimental treatment, 500 pollen grains were evaluated in 3 replicates. Pollen preparations were examined under a microscope (Zeiss model, 7×20). The resistance of each genotype was determined by the ratio of the

indices of the studied pollen traits in the experimental variants (E) to the control (C), expressed as a percentage (%).

### 2.3. The expression of morpho biological and economically valuable traits in homozygous and heterozygous offspring.

The morphological, biological, and economically valuable traits, including yield and fruit quality, were assessed in accordance with UPOV recommendations (*Solanum lycopersicum* L.) [21] and standard methods [14]. Hybridization was carried out according to schemes specifically developed by us. More than 50 $F_1$ hybrid combinations were obtained. The nature of expression and the degree of phenotypic expression of traits controlled by mutant genes in the $F_1$ and $F_2$ progeny populations were determined following the gene nomenclature [22]. Statistical analysis of the raw data was performed using the computer software programs Excel and Statistica 7.

## 3. Results and Discussions

The success of breeding new tomato lines, varieties, and hybrids depends directly on the availability of thoroughly studied donor plants with the desired traits in collections. However, concepts for organizing such collections remain undeveloped, a situation observed not only in local collections but also in global ones [23]. According to the author, of the one million samples collected in global collections, less than 1% have phenotypic characteristics. This creates enormous difficulties for breeders, as they must repeatedly review large amounts of material in search of sources of the desired traits. Consequently, a comprehensive study of available genetic resources not only for immediate use but also for supplementing existing and creating new trait collections – is a top priority. In this regard, we conducted an assessment of the genetic potential of mutant tomato forms, aimed at identifying genes that control a wide range of traits at different stages of ontogenesis, including resistance to abiotic and biotic stress factors, for the subsequent expansion of existing and creation of new traits collections.

### 3.1. The potential of mutant tomato varieties for resistance to abiotic stress factors, as determined by male gametophyte (pollen) characteristics.

Testing of an extensive collection of materials revealed significant heterogeneity among mutant forms in terms of the level and type of pollen resistance to high and low temperatures and drought.

First and foremost, marked differences were observed between genotypes within the collection regarding indicators of traits characterizing the quality of freshly collected pollen (control). Depending on their genotypic characteristics, the "viability-germination" trait varied widely (from 1.5% to 78.2%). Regarding the ability of germinated pollen grains to form pollen tubes of a certain length under *in vitro* conditions, the variation among them was even greater (from 11 μm to 150 μm). This

indicates that the same plant cultivation conditions had different effects on pollen quality, highlighting the genotype-specific characteristics of each.

The differences between mutant forms were more pronounced in terms of their pollen's response to high and low temperatures and drought. Pollen response was inconsistent, even within a single genotype, as measured by two different traits:

"pollen germination resistance" and "resistance to pollen tube length". The genotype-specific response of pollen to the effects of various factors, both individually and in combination, allowed for their classification into groups based on the type and level of resistance of each genotype to a specific stress factor (Figure 2).

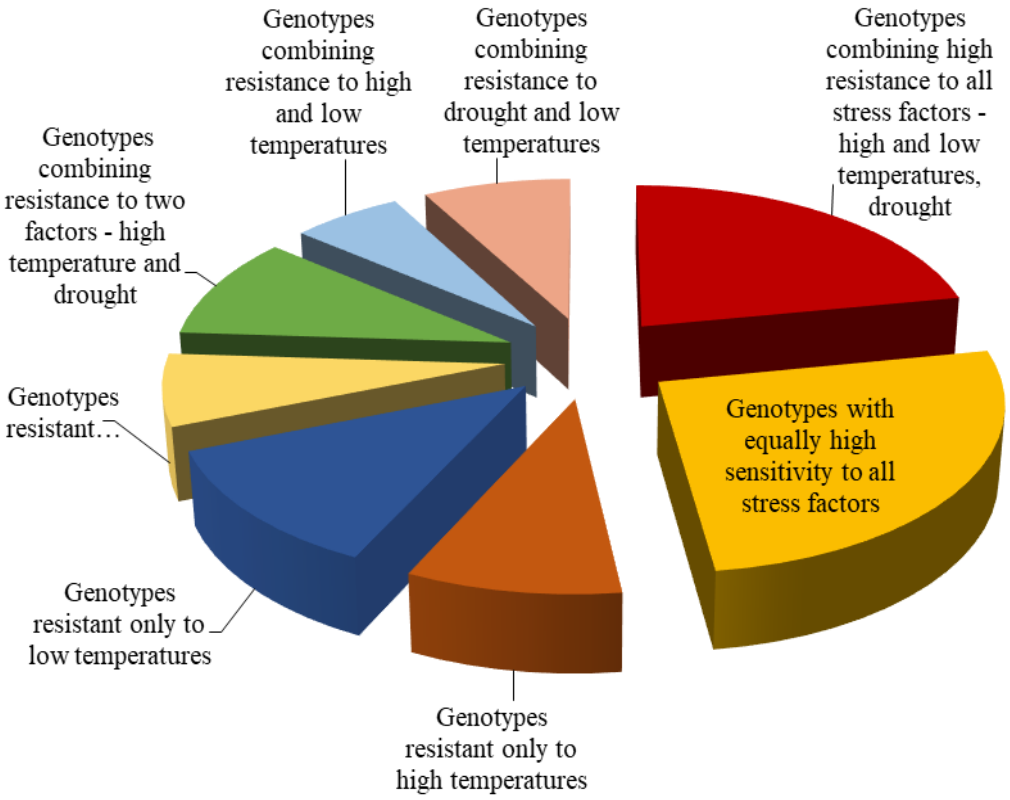


**Figure 2.** Characteristics of mutant tomato forms by type and level of resistance to high and low temperatures and drought

Twenty-two mutant forms were identified whose pollen germinated rapidly and with high efficiency (54.6%–97.8%), while also forming long pollen tubes (58 µm–150 µm) under the influence of all three negative factors. This indicates the high resilience of their male gametes, which are capable of germinating and forming long pollen tubes under conditions that significantly from optimal ones.

In contrast, another group of mutant forms (26 genotypes) exhibited pollen that was highly sensitive to all three stress factors. Both pollen germination rates and pollen tube lengths were very low in this group, ranging from 0.4% to 9.7% and 1.0 μm to 20.4 μm, respectively. They were classified into the group of unstable genotypes (Figure 2).
The third, fourth, and fifth groups comprised mutant forms (28 genotypes) whose pollen exhibited high resistance to only one of the stress factors studied, but was highly sensitive to the other two. Conversely, mutant forms (Group 6) were identified whose pollen germinated well, simultaneously forming very long pollen tubes under the influence of high temperature and drought, but exhibited high sensitivity to the low-temperature factor. A similar pollen response is also characteristic of the mutant forms distributed in groups 7 and 8 (Figure 2).
This is undoubtedly a unique gene pool of particular value for use as a source of resistance to abiotic stress factors in the male gametophyte during the breeding of new tomato varieties and hybrids, as well as for expanding existing genetic collections and establishing new trait-based genetic collections.

### 3.2. Genetic diversity of mutant genes that determine the growth habit and architecture of tomato plants.

Plant habit is a key indicator for any variety or hybrid, determining its intended use and agronomic suitability.
An evaluation and analysis of the potential of mutant forms based on the phenotypic expression of genes affecting plant habit revealed a high degree of diversity, but only a few of them have practical value.
This diversity is mainly related to plant size, which is controlled by the genes *bls*, *d, dd, dmp, dmd, sd, ssp, sp, sp*$^{+}$ and *sp*$^{\pm}$. Morphological differences between them are determined both by the intensity of lateral shoot formation (*ls*) and the degree of their branching (*atn, bu, br, cg, bip*).
A special group within the collection consists of forms with mutant genes *ssp, br*, *com, sd, d, dd* and *bls,* which increase the plant's compactness. They exhibit a distinctive phenotype caused by mutational changes in the genome (Figure 3). These are compact varieties with short internodes the plants are stunted in growth. Twenty-four forms have been identified, which are grouped by a series of mutant genes exhibiting similar phenotypic manifestations.
The clear phenotypic expression of mutant marker genes under various growing conditions (open field, greenhouse) made it possible to include some of them in hybridizations (Mo 113, Mo 443, Mo 500, Mo 504, Mo 632, Mo 755, and Mo 791). Crossbreeding them with lines from our own breeding program and known

**Figure 3.** Some varieties of mutant tomato plants with a bush-type growth habit

varieties (L111, L1185, Fakel, Zagadka, Barnaulsky Konservny) and subsequent analysis of heterozygous $F_1$ progeny and segregating $F_2$ populations demonstrated the effectiveness of their use. Eleven $F_2$ populations from different hybrid combinations were analyzed. High recombination and transgressive variability was established for marker traits. The pronounced phenotypic expression of traits such as compactness, dwarfism, limited growth, and leaf surface characteristics allowed for the evaluation of extensive hybrid populations at early stages of ontogenesis (in the seedling phase). This made it possible to accelerate the research by conducting it on small plots and to identify a wide variety of forms with genetically determined traits.

The targeted use of some of these has made it possible to accelerate the breeding process and, in a short period of time, create more than 20 lines and a number of ornamental varieties – Prichindel, Cireaska, MiracolMak, Dimetra and Ilika. These are intended for cultivation on balconies, loggias, and terraces, and are homologated in the Republic of Moldova [2].

At the same time, the collection was found to contain genes controlling indeterminate *(sp$^+$),* determinate *(sp),* and superdeterminate *(ssp)* plant growth types. Of particular interest are plant varieties with a semi-determinate *(sp$^\pm$)* growth type (Mo 147, Mo 341, Mo 432, Mo 446, Mo 544, Mo 620, Mo 723, La 1159, La 2529, La 2921, La 3179), which are widely sought after in breeding for heterosis to create early-maturing $F_1$ tomato hybrids.

Such a high degree of diversity among mutant genes that control plant growth patterns opens up broad opportunities for their versatile use in breeding to develop tomato varieties and hybrids intended for cultivation both in the field and in greenhouses.

However, a significant factor reducing the efficiency of tomato cultivation in protected ground conditions is the excessive formation of lateral shoots, the removal of which requires considerable labor and financial costs. The creation of varieties and hybrids with low suckering potential, short internodes, and a longer fruiting period may help solve this problem.

This is possible by incorporating the *ls* (*lateral suppressor*) and *br* (*brachytic*) genes into the breeding program. However, their direct use is complicated by their

linkage to traits of the reproductive system (small fruit size, partial sterility). We were able to partially overcome these difficulties using a specially designed crossing scheme that included mutant lines (Mo 341, Mo 835, Mo 443, La 2529, La 3179), semi-mutant forms (111, 11069, 1751), and cultivated-type lines (L28, L186, L187, L828, L556). Analysis of $F_1$ hybrids showed 100% dominance of the tillering ability of the cultivated parental forms in all combinations. In contrast, in the segregating $F_2$ populations, high recombination variability was observed for the *ls* and *br* genes, confirming the conclusions of other authors regarding the role of mutant genes in activating genetic recombination and broadening the spectrum of intrapopulation variability, which facilitates the selection of new forms with beneficial combinations of economically valuable traits in the $F_2$–$F_3$ generations [22, 9, 16].

The complex nature of the expression of the traits “internode length” and “number of lateral shoots per stem” in $F_2$ inbred populations necessitated their classification into a cluster complex based on breeding value in combination with other traits (flower structure, fruit weight, shape, and color). This allowed us to identify more than 50 recombinant forms with a completely new combination of mutant marker and economically valuable traits. Some of them (23 lines) already demonstrate stable expression of traits in the $F_3$–$F_4$ generations. Eight of these have a semi-determinate growth habit and are characterized by early fruit ripening (94…109 days). Most of these lines are distinguished by weak tillering ability, short internodes, and uniform inflorescences, including in fruit color, shape, and weight. Some genotype variants with different levels of tillering ability are clearly shown in Figure 4.

**Figure 4.** Varieties of tomato genotypes based on the pattern of lateral shoot (stepson) formation and internode length: **1** – plants with short internodes but intense lateral shoot formation; **2** – short internodes, single reduced lateral shoots; **3** – short internodes and absence of lateral shoots; **4** – long internodes and absence of lateral shoots

The rich genetic potential of the collection of tomato mutant forms, particularly in terms of genes influencing plant habit and architecture, and the potential for their effective use in breeding to develop varieties and hybrids with novel and beneficial combinations of economically valuable traits demonstrates the potential for their use in creating trait collections and expanding genetic diversity.

### 3.3. Mutant genes controlling various fruit traits and their significance for expanding the genetic diversity of tomatoes.

Genes controlling fruit traits (color, taste, shape, fruit weight, fruit surface structure, pericarp thickness, number of seed chambers, etc.) play a special role in enriching the tomato's cultivated gene pool.

An assessment of the potential of mutant forms based on the nature of their expression and the degree of phenotypic expression of the genes they carry revealed a high degree of diversity, including unique combinations of genes that influence different fruit traits.

A total of 32 gene carriers controlling unusual fruit coloration were identified: *Abg, dg, gs, gf, r, t, y, sh, o, B, Del.* Marked differences between mutant forms carrying the same genes were established based on the nature of expression and the intensity of coloration in the ripening fruit, depending on their combination with other genes within the same genome (Figure 5).

**Figure 5.** Characteristics of fruit coloration in the mutant tomato lines Mo 922, Mo 120, and Mo 632, which carry the *t (tangerine)* gene, under different combinations of this gene with other genes in their genomes

*Fruit coloration* is determined by several genes, with the *R*-red flesh being dominant over the *r*-yellow, the *Y*-yellow skin over the *y*-colorless, and the *P*-smooth, shiny, hairless skin over the *p*-dull, hairy surface. The recessive *t* gene is responsible for orange fruit color. Most mutants in the collection (93 forms) carry the dominant *RTY* genes and have red flesh and yellow skin. Mutants with the double recessive genotype *rrtt* have orange-colored fruits. The homozygous

genotypes *RRTT, rrTT*, and *RRtt* have red, yellow, and orange fruits, respectively. Fruit color is also influenced by the *B* gene. Some authors believe that the *B, $B^c$*, and $B^{og}$ genes, which control lycopene and *β-carotene* content, simultaneously influence the color, taste, and marketability of the fruit [22, 9]. The *B* gene causes an increased *β-carotene* content in the fruit only in the presence of the dominant *R* gene. Therefore, the *RRTTBB* genotype produces *β-orange* or pink fruits, whereas the $RRTTB^+B^+$ genotype produces red ones. Yellow-fruited tomatoes have the genotype $rrTTB^+B^+$. In some mutant forms, the yellow flesh of the fruit may be determined by recessive *atat* genes.

Mutant forms carrying the *hp, hp-1* and *Ip* genes have also been described and isolated, these are of interest for the development of varieties characterized by high levels of carotenoids, ascorbic acid (vitamin C), and dry matter. According to available information [13], genes of the *high pigment* series increase the content of lycopene in fruits by 35–45%, *β-carotene* by 80–90%, and vitamin C by 20–50%, making their use essential in tomato breeding for taste qualities.

The *gs* gene also imparts a distinctive coloration to the fruit. Tomatoes with this gene have a striped surface on both green and ripe fruit. The *gs* gene is easily transmitted, especially to large-fruited plants from its carriers. The coloration of the radial stripes on ripe fruits varies: golden on pink fruits; pink-red on orange fruits; and yellow or orange on red fruits (Figure 6).

**Figure 6.** Expression patterns of traits controlled by the *gs* gene.

The presence of the *Del* and *sh* genes in the tomato genome gives the fruit flesh a reddish-orange color, which is associated with a decrease in lycopene content and an increase in *β-carotene*.

Varieties with the *Abg* and *gf* genes, which influence the chlorophyll content in the fruit, have higher levels of lycopene and *β-carotene*. This gives them a dark hue, the intensity of which depends on their interaction with other genes (Fig. 7).

A number of other genes may also influence fruit color, but those whose combination can ensure high levels of vitamin C, *β-carotene* (provitamin A), and, overall, high processing and taste qualities of the fruit are of particular value for breeding. Of the genotypes shown in Figures 6 and 7, five are the result of our own breeding program using the *gs, Del*, and *gf* genes in crosses.

**Figure 7.** Characteristics of trait expression in genotypes with the *Del, sh, Abg* and *gf* genes

The appearance of the fruit is most appealing when the fruit ripens simultaneously and uniformly across its entire surface. Mutant forms with the *u* gene, which is recessive to the *U* gene that controls the presence of a green spot at the base of the fruit, exhibit uniform coloring. Sometimes the green spot remains even on ripe fruits, which leads to a decrease in product quality. The proportion of mutant tomato forms with a green spot at the base of the fruit in the collection is quite high, at 53.6%.

One of the most important characteristics that largely determines the direction and intended use of the product is the shape of the fruit. In contrast to the commonly accepted round fruit shape, the mutant collection includes genotypes with flat, ellipsoidal, pear-shaped, heart-shaped, oval, cylindrical, and other shapes. The high diversity of the collection is due to the presence of forms with different fruit surfaces (ranging from smooth to highly ribbed) (Figure 8). In some forms, the fruit surface is smooth, but the apical part is elongated into a more or less pointed tip. The nature of the manifestation and the degree of phenotypic expression of these and a number of other traits are controlled by the presence in the collection of a large number of the genes $O^l$, *o, obl, el, f, bk, n* and *n-2*.

**Figure 8.** Varieties of mutations in the shape and surface of the fruit with the *n, n-2, bk, el* and *f* genes

Mutant genes *rin, nor* and *alc* are of particular value for breeding, as their presence in the tomato genome prevents fruit overripening (Figure 9). These genes contribute to increased total yield and affect the viscosity of fruit juice, which is twice as high in varieties and hybrids containing these genes compared to conventional ones, ensuring high marketability [9].
By using them in crosses with inbred lines with high combinatorial potential, we were able to obtain more than 24 combinations of $F_1$ hybrids.

**Figure 9.** Phenotypic expression of traits controlled by the *nor, rin* and *alc* genes

Most of these exhibited high heterosis in terms of yield and fruit quality. Some ($F_1$ Ingstar and $F_1$ Rozamak) successfully passed state testing and were homologated in the Republic of Moldova [2]. A number of others are currently undergoing competitive testing. However, to improve the efficiency of breeding $F_1$ heterotic hybrids involving these genes, it is recommended to use earlier-maturing varieties and lines with high taste qualities and large fruits as one of the parental forms (preferably the maternal parent).The intermediate inheritance of these traits by $F_1$ hybrids balances the negative influence of the parent with mutant genes. In such combinations, the first-generation offspring typically exhibit heterosis in terms of overall productivity and fruit quality.
The genes that control the degree of pubescence in various parts of the tomato plant including the fruits namely $W^{om}$, *Ln, p, Vi* confer exceptional ornamental value and special significance on the plants.
The phenotypic expression of these genes is observed from the cotyledon leaf to the mature fruit, which is covered with a light fluff down (Figure 10). Mature fruits have a beautiful, presentable appearance and excellent taste, due to their high content of dry matter, sugars, and vitamin C. The fruits are intensely red with dense flesh, multi-chambered, and have seeds that form only in the apical portion of the fruit. As the fruit grows and develops, the pubescence on it decreases and becomes slightly visible in mature fruit (Figure 10).
Carriers of the $W^{om}$ and *Ln* genes (Mo 835 and Mo 341) have been incorporated into the breeding program. Direct and reciprocal hybrids (16 combinations) were obtained from crosses with homozygous lines (L8/234, L33/241, L1033) and

cultivated-type lines (L187, L556, L828) with high combinatorial ability, which are currently undergoing genetic and biochemical studies for their effective use in practical breeding and replenishment of collections with useful genes.

**Figure 10.** The nature of fetal phenotypic expression at different stages of development, controlled by the *Ln* and $W^{om}$ genes

A high degree of heterogeneity was observed among the mutant forms, as evidenced by *fruit weight, pericarp thickness, and the number of seed chambers.* Fruit weight is a complex polygenic trait that varies depending on environmental conditions [22]. Significant differences in fruit weight were observed among the mutant forms: 24.6% of the forms had large and very large fruits (100…300 g); very small fruits (0.4…20 g) were observed in 17.8%; the remaining 57.6% of mutant tomato forms had fruit weights ranging from 30 to 100 grams.

Pericarp thickness and the number of seed chambers are traits that directly determine fruit quality and marketability. The collection describes a large number of mutant genes controlling pericarp thickness, shape and seed chamber structure – *Gr, bs, bs-2, el, ck, fie, Ip, lo, loc, Ol, ptb, ss*, and others. The phenotypic expression of some of these is shown in Figure 11.

**Figure 11.** Some varieties classified by characteristics such as number, shape, color, and structure of the seed chambers, which are controlled by the *Lc, Ip, lo, loc,* $O^{l,}$ *bs-2* genes

### 3.4. Genetic sources of resistance to certain diseases.

The presence of genes controlling resistance to pathogens may help address problems associated with the rapid evolution of pathogens. From the total number of tomato mutant forms studied, 14 genotypes were identified that carry genes controlling resistance to *Mi – Meloidogyne incognita*; *Tm, $Tm^{2a}$, Tm-2* – to *Tomato mosaic virus*; *F* – to *Fusarium; Ve* – to *Verticillium*; *Cf, Cf-2, Cf-3, Cf-4* to *Cladosporium*. The genomes of these mutant forms contain, in various combinations, genes that simultaneously control resistance to a particular pathogen, different fruit traits, and plant growth type (primarily indeterminate and semi-determinate). They can be used to enrich working and long-term collections with valuable genes.

## C**onclusions**

(1). It is shown that the genetic potential of mutant forms, which carry a large number of marker genes controlling important economically valuable traits in tomatoes, represents a unique source of new germplasm for enhancing genetic diversity through the creation of new breeding materials, lines, varieties, and hybrids of tomato, as well as for supplementing existing and creating new trait collections.
(2). A high degree of heterogeneity was observed among mutant tomato lines in terms of resistance to abiotic stress factors (high and low temperatures, drought). Genotypes with different levels and types of resistance, as determined by characteristics of the male gametophyte of the tomato, have been identified; under conditions of climate change, these are of particular value for use in breeding programs as sources of resistance.
3). It was found that mutant genes, when combined with cultivated tomato lines, stimulate genetic recombination processes, leading to an expansion of the spectrum of intrapopulation transgressive variation and the emergence of new forms with unique combinations of mutant marker and economically traits, thereby contributing to the enrichment of the tomato crop gene pool and the expansion of its genetic diversity.

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