We are IntechOpen, the world's leading publisher of Open Access books Built by scientists, for scientists

6,100
Open access books available

149,000
International authors and editors

185M
Downloads

Our authors are among the

154
Countries delivered to

TOP 1%
most cited scientists

12.2%
Contributors from top 500 universities



WEB OF SCIENCE™

Selection of our books indexed in the Book Citation Index in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?
Contact book.department@intechopen.com

Numbers displayed above are based on latest data collected.
For more information visit www.intechopen.com



Chapter

New Perspectives in Grapevine (*Vitis* spp.) Breeding

Arif Atak

Abstract

Many grape varieties or genotypes of *Vitis* species are grown for different purposes in various parts of the world. However, despite a large number of cultivars, there is a demand for different grape cultivars due to changing consumer expectations. Grapevine breeding programs are carried out by scientists in different countries in order to meet these expectations. Breeding studies, which used to take a long time with traditional crossbreeding methods, have become studies that achieve the desired results in a much shorter time with the development of molecular methods and biotechnology. One of the most important developments in grapevine breeding is that the relevant gene regions in hybrid populations developed from breeding programs can be identified in a very short time. In recent years, the demand for cultivars that are more resistant or tolerant to biotic and abiotic stress conditions has increased, and for this purpose, there has been a significant increase in breeding studies on cultivars and rootstocks that are resistant or tolerant to different stress conditions. Considering the current breeding programs, genetically manipulated new cultivars with desired characteristics and interspecies hybrid cultivars will soon become the main study subjects of grapevine breeding programs.

Keywords: *Vitis* spp., breeding, molecular methods, tissue culture, biotic and abiotic stress

1. Introduction

Grapevine is one of the most widely grown crops in the world and covers about seven million hectares. According to the data of 2020, approximately 78 million tons of grapes are obtained from this area. The countries with the highest production, respectively, are China, Italy, Spain, France, and USA. Half of the world's total grape production is made in these five countries [1]. Grapevine cultivation is in high commercial demand on a global scale due to its high yield and different consumption patterns. In 2020, grapes were the world's 289th most traded product, with a total trade of $11B. Between 2019 and 2020 the exports of grapes grew by 2.27%, from $10.8B to $11B. Trade in grapes represent 0.066% of the total world trade. In 2020, the top exporters of grapes were Chile ($1.18B), China ($1.09B), United States ($1.02B), Peru ($1.01B), and Italy ($831M). In 2020, the top importers of grapes were United States ($1.36B), Germany ($943M), China ($817M), Netherlands ($816M), and United Kingdom ($812M). The countries with the highest import tariffs for grapes are

Turkmenistan (100%), India (73.9%), Iran (55%), and Turkey (54.6%) [2]. Grapes are the world's third most valuable horticultural crop (after potatoes and tomatoes). Cultivation of grapes for fruit and wine began at least 7000 years ago in the Near East, and over the millennia, thousands of cultivars have been developed and selected for different purposes. Nowadays, grapes are used to produce diverse consumer products including wine, table grapes, raisins, grape juice concentrate, and distillate for various industrial uses as well as making fortified wine and brandy. While wild Vitis species are very valuable to breeders, new cultivars developed from particular different breeding programs are important for grape growers to sell their quality products at high prices. With the rapid change in consumer preferences, different government policies, increased awareness of human/environmental health, global warming, and some other factors, it has become more important for researchers to better examine and understand the grapevine genome and, as a result, to develop new varieties that will meet all these expectations with the help of modern methods. Grapevine is not only an economically valuable species but also a highly preferred model for both cultivation and breeding studies due to its genetic characteristics [3]. In addition, for many countries, the culture of viticulture is a cultural heritage that has great meaning. For all these reasons, the grapevine plant (*Vitis* spp.) is among the most important plant species in which research and investment are made [4].

Grapevines (*Vitis* spp.) are members of the Vitaceae and include two subgenera, *Euvitis* (38 chromosomes) and *Muscadinia* (40 chromosomes), with about 60 species in total. The Vitaceae family is the most important agricultural species in the genus *Vitis*. Especially the varieties belonging to the *V. vinifera* species are the most widely cultivated species all over the world and dominate the markets. However, this species has some disadvantages of its own. Especially, the cultivars of this species are highly susceptible to biotic and abiotic stress factors. As a result of this susceptibility, there are significant quality losses [5].

In each country, grape production can be done for different purposes. Grapes are grown for wine, table, raisins, juice, jam, concentrate, seed oils, and other purposes. According to these different growing purposes, market demands, and expectations are changing rapidly and, in this case, the demand for new grape cultivars increases [6]. Controlled grape breeding is thought to start almost 200 years ago. Henri and Louis Bouschet de Bernard are believed to have begun generating hybrids between "Teinturier du cher" and "Aramon" cultivars in 1824 in southern France [7]. The birth of modern grape breeding is connected with the arrival of North American diseases (downy mildew, powdery mildew, and black rot) and insects (mainly phylloxera) to Europe. These diseases and pests caused substantial losses on the highly susceptible *V. vinifera* vines in European vineyards.

Several major progress in viticulture and grapevine breeding occurred as a result of the epidemics spreading through Europe in the late nineteenth and early twentieth centuries. Especially, the advent of rootstock breeding as an effective and immediate means to control phylloxera. Wild vines (*V. riparia* and *V. rupestris*) from North America were first imported to be used as rootstocks and provided *phylloxera* resistance [8].

Although, the cultivars obtained as a result of the hybridization of *V. labrusca, V. aestivalis* and *V. vinifera* species with each other and with *V. vinifera*, they started to be used for different purposes both in America and Europe in the following years. But the hybrids obtained from crosses made especially the hybrids obtained from crosses with wild species did not receive much demand in wine production due to their intense aromas [9].

First grapevine breeding studies started with wine grapes, and later on, at the end of the nineteenth century, also table grapes were included in these breeding studies. With the phylloxera pest affecting vines in the European continent, studies on rootstock breeding started at the same time (late nineteenth century). In the twentieth century, different institutions and organizations in the USA (such as the University, the private sector and the USDA) started breeding studies on table grapes and many new grape cultivars with superior characteristics were developed as a result of these studies. These cultivars, which were developed as a result of breeding programs in the USA and grown by grape growers, led to the development of the table grape industry all over the world. Afterwards, grape breeding programs started rapidly in different countries (Far East, South America, Europe, Turkey, Israel, Argentina, and many other countries) [10]. The main purpose of these breeding studies is to obtain new cultivars that will meet the expectations, taking into account the changing consumer demands, as soon as possible by using the opportunities provided by technology. Especially in recent years, demand for large berry, seedless and high-yielding cultivars that are resistant to different biotic and abiotic stress conditions for table grapes has increased and more emphasis has been given to these issues in breeding studies. Among the wine grapes, cultivars that are resistant to different biotic and abiotic stress conditions and have the desired wine quality criteria have also become prominent selection criteria in breeding studies. Most of the commonly grown *Vitis* species and cultivars are not resistant to biological agents (virus, bacteria, fungi, nematode, and others) that significantly affect yield and quality. The main causes of diseases that cause the most important losses in vineyards are viruses, fungi, and microorganisms such as fungi, oomycetes, and so on. A remarkable resistant cultivar has not yet been detected in economically important cultivars of *V. vinifera* [11]. Compared to other perennial plants, the number of viruses infecting grapevines is quite high [12]. Abiotic stress factors that are effective in grapevine include especially water availability, temperature, and light. In recent years, breeding studies have focused on these issues [13]. Most grapevine breeding programs were initially publicly funded (such as Universities and Research Institutes), but nowadays different private sector companies are also involved in these breeding programs. Since many of the new cultivars are protected by intellectual property rights, growers or organizations that want to grow them must first agree with the right holders. It is also seen that growers who want to grow these new cultivars have come together and created a new model in recent years. Because of this new "breeder club system", many countries and companies have started their own special breeding programs. Many grape varieties developed as a result of breeding studies are protected by strict breeder rights in many countries. Grape producers or companies that want to grow these varieties must first negotiate with the people or organizations that have the breeder's rights. In addition, in recent years, a system has started to spread for the cultivation of newly bred cultivars which have breeder's right in a limited area and with a club system to guarantee certain quality conditions. In addition to this, today companies, grower unions, or cooperatives sometimes cooperate with some government organizations for these breeding programs and try to jointly develop new grape varieties by financing their breeding programs. In recent years, especially in table grape breeding, this system is increasingly in demand and is spreading all over the world [14, 15]. It is among the important problems of breeding studies to reach correct results by analyzing many data obtained in the field, especially in grape breeding programs. After the integration of smart agriculture models into breeding studies, complex data that takes a lot of time can be obtained in a much shorter time and with high accuracy [16–18]. The challenges

are given by large field sizes with thousands of plants that need to be phenotyped today by laborious, manual, and subjective classification methods. For this purpose, scientists in Germany have developed systems that take images of different growth stages of plants and process them. The images taken in this system can be processed according to different scenarios and adapted for extreme conditions. These six different RGB images can be used in breeding studies with very high accuracy results in terms of applicability and transferability [19].

In this review, it is aimed to inform scientists from different fields who are interested in grapevine breeding by summarizing the remarkable techniques, methods, and developments in grape breeding studies carried out for different purposes in recent years.

2. New advances in grapevine breeding studies

2.1 Genomic and transgenic researches

Grapevine growing areas are increasing worldwide due to the understanding that grapes and grape products are beneficial for human health. Biotechnology research is increasingly playing a role in improving the yield and quality of grapes. Grapevine breeding and genetics researches increased after the 1950s and spread all over the world. Molecular markers have facilitated research in *Vitis* genetics. It is now possible to map the grapevine genome and to create unique DNA profiles for each genotype. The first plant linkage maps were based on visually scored morphological markers, isozymes, and DNA-based markers, which are virtually limited in number were used to create densely saturated maps. However, in recent years, much more information has been gained about the grapevine genome for breeding studies with much more sensitive SNP and genome sequencing applications. Nowadays, the results of different *Vitis* spp. genome sequencing has led to more innovative and targeted studies in grape breeding studies. Especially in parallel with the developments in biotechnology, it has become possible to obtain different transgenic vines with these innovative approaches. Significant progress has been made in the development of transgenic vines with the development of gene regions and markers associated with desired traits, the development of transformation systems, the use of genetic engineering against biotic and abiotic stress conditions, and the improvement of grape quality characteristics by identifying flavor and aroma components. Considering the results obtained from these studies; While some of them offer positive results for different *Vitis* species and varieties by providing direct application, it has been determined that some of them are far from increasing the quality conditions of the grapes as desired in breeding studies [10]. Very important progress has been made thanks to the Vitisgen1 and Vitisgen2 projects initiated with the participation of different institutions in the USA in order to determine different characteristics in the grapevine genome and to use these important characteristics related markers in breeding programs. The goals of these projects are to develop novel methods to improve production efficiency and profitability long-term throughout the table grape, raisin, and wine industry, such as through plant breeding and genomics. Also, they aimed to identify and address threats from diseases and insect pests, and develop novel methods to improve resistance to these pests and diseases. Projects (VitisGen1 and VitisGen2) are multidisciplinary, collaborative projects focused on decreasing the time, effort, and cost involved in developing the next generation of grapes. Incorporating cutting-edge

genomics technology and socioeconomic research into the traditional grape breeding process will speed up the ability to identify important genes related to consumer-valued traits like disease resistance, low-temperature tolerance, and enhanced fruit quality. Identifying these genes will help grape breeding programs from around the world to more rapidly develop new grape varieties that will appeal to a wide range of consumers, while also addressing grape grower and producer needs [20]. Genetic transformations offer many innovative solutions for grape breeding studies. They can be used successfully to transfer regions associated with particularly important traits to traditional varieties. However, researchers still lack the desired success rate in identifying high-throughput regeneration protocols. Positive results were obtained in the development of transgenic plants obtained by transferring different characteristics to some important grape cultivars [21, 22]. Embryogenic tissues are mostly preferred in transformation studies due to their morphogenetic competence. Various explant sources, such as leaves [23] and anthers [24] have been studied under inducing conditions to explore the possibilities of obtaining somatic embryos. In the initial transformation studies, leaf tissues of different *V. vinifera* cultivars [25] and different rootstocks [26–28] were studied, resulting in non-regenerating transgenic callus. Somatic embryogenesis has been used by different researchers in micro propagation and genetic transformation studies of various woody perennial plant species. However, in these studies, it has been reported that the efficiency of somatic embryo induction is generally very low and the success rate varies depending on the developmental stages of the explant [29]. Among the genetic transformation studies carried out with grapevines, the most successful results were obtained from Agrobacterium-mediated transformation coupled with proembryonic masses together with somatic embryos. Studies have reported that some factors (explant source, culture medium, cultivar/genotype, culture medium, and others) affect the efficiency of grapevine initial inducing embryogenic callus and adventitious buds for plant regeneration. Photos of the embryogenesis development of different grapevine (*V. vinifera* L.) organs are given in **Figure 1**. Until today, several grapevine cultivars have been transformed with genes associated with various functions by biolistic bombardment, Agrobacterium-mediated transformation, and transgenic grapevine lines have been obtained using established regeneration systems. However, a healthy plant regeneration is affected by many factors. Especially explant source, variety/genotype, and environment are the most important ones. Furthermore, the selection and use of acceptor materials, cell density, bacterial strain, selectable markers, and selection methods also affect conversion efficiency. In many of the studies, it has been reported that the regeneration capacity of rootstock varieties in organogenesis and somatic embryogenesis is higher than hybrids and varieties belonging to the *V. vinifera* species. [30].

Badouin et al. [31] generated a high-quality de novo reference genome for *V. sylvestris*, onto which they map whole-genome re-sequencing data of a cross to locate the sex locus. They described the genomic and evolutionary characterization of the sex locus of wild and cultivated grapevines, providing a coherent model of sex determination in the latter and for the transition from dioecy (separate sexes) to hermaphroditism during domestication.

With the help of RNA sequencing, one of the next-generation sequencing systems developed in recent years, short readings of cDNA sequences that can be quantified absolutely can be made by aligning them with reference sequences [32]. With the development of this technology, it has become possible for many researchers working on grape breeding to conduct important studies on the grapevine genome. In particular, the RNA sequencing technique has been widely used to identify single nucleotide

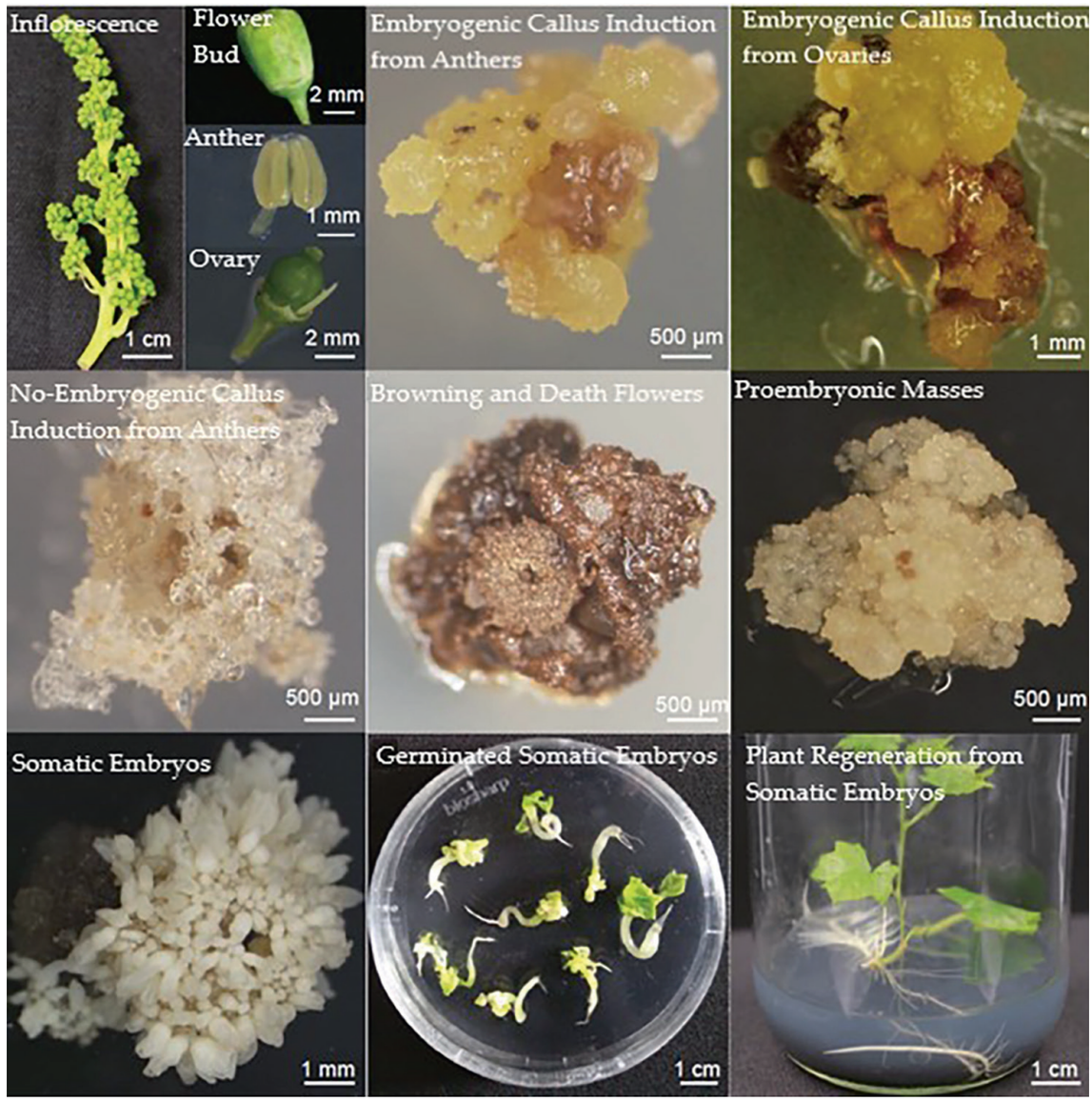


Figure 1.
Photographs of various regeneration systems during somatic embryogenesis of Vitis vinifera cv. "Thompson seedless" grape [30].

polymorphisms and new cultivar-specific transcripts, also splicing variants [33–35]. As a result of the latest advances in plant biotechnology, full-length cDNA sequencing readings can now be made with much higher accuracy. In addition to all these, it is seen that this developed system is also used to accurately detect alternative transcripts that play a role in different biological processes and stress responses [34, 36–39]. While the reference genome was needed before the full-length cDNA sequencing technique, it is no longer needed thanks to this technique. Thus, it has become possible to obtain healthy information about many traits related to plant breeding, in a much shorter time.

Integration of data banks with the results obtained in genomic studies is of great importance in terms of using the obtained results in breeding studies. In particular, studies on the grapevine genome in different countries and the collection of existing data in different databases continue. Standing out as the most comprehensive of these studies, VitisGDB provides the most comprehensive information of *Vitis* genomic data. The *Vitis* genome and genetic database (VitisGDB) is an integrated

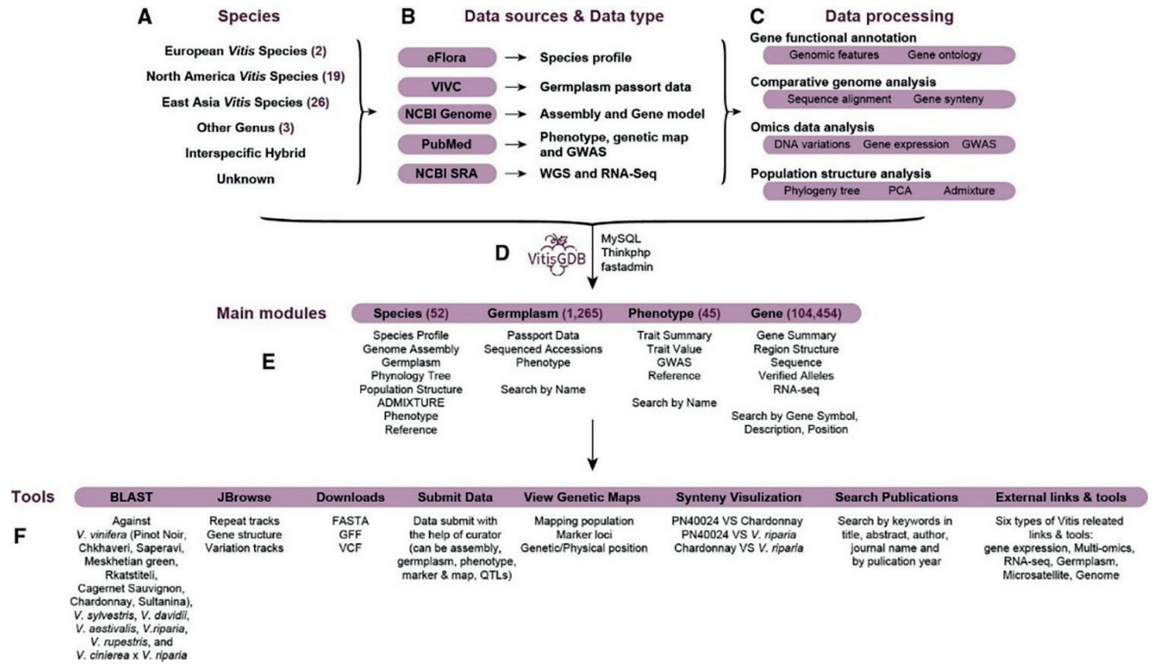


Figure 2.
Schematic VitisGDB platform. (A) Species information for species, (B) data type and source, (C) data processing explanation (D) framework of VitisGDB, (E) main modules, (F) VitisGDB overview [4].

genomic resource and a global web of *Vitis* resources. This platform contains up-to-date genomic data and very important information for Vitis agronomy, breeding, and genomic development studies. VitisGDB is a platform created to make vine research results widely available. As genomic data from sequencing studies become clear and available, they are constantly updated on VitisGBD and presented to relevant researchers VitisGDB provides long-term support to grapevine researchers on a variety of grapevine genomics issues [4]. Schematic information about the working system of this platform is given in **Figure 2**.

Transferable DNA markers are of great importance for the success of breeding and genetic studies. Although grapevine breeders have been using the disease resistance-related alleles of closely related species for many years, it has been reported that the interspecies transmission rates of the current Vitis markers are quite low. Zhu et al. [40] in their study with the Vitis core genome of 40 accessions, they were able to identify PCR primary binding sites of conserved nuclei with high information content surrounding polymorphic haplotypes. Researchers developed markers (2000 rhAmpSeq) as PCR multiplexes from target sites and confirmed this in four biparental populations, also increased the transferability to a very high rate.

2.2 Polyploidy and embryo recovery researches

Polyploidy refers to the condition in which a diploid organism has an excess of chromosomes as a result of the addition of one or more sets of chromosomes. A general classification of polyploids is made as allopolyploids, auto-polyploids, and segmental allopolyploids [41]. In order to obtain polyploid structures, triploid or tetraploid new genotypes were tried to be obtained with different applications and mutations by increasing the chromosome numbers in grapevine and other plant species. However, a high success rate could not be mentioned in these techniques, and sequence-specific mutations were mostly dependent on chance [42].

Somatic embryogenesis is one of the methods preferred by many researchers for the micro propagation of different plant species. It is also used for the removal of many phytopathogens that have infected different plant organs under in vitro conditions [43]. However, abnormalities may be encountered during somatic embryogenesis due to some somaclonal variations. These mutations are desirable in some cases as they sometimes allow the formation of polyploid forms. In particular, induced polyploidy and natural polyploidy are frequently used to obtain new genotypes for polyploidy breeding studies. Because it is reported that new polyploid genotypes have more resistant structures against many biotic and abiotic stress conditions. It is known that plants with polyploid form have some advantages compared to plants with diploid form. Especially polyploid plants are among the most important advantages with their ability to tolerate harmful mutations, larger structures, high heterozygous, and heterozygous structures [44–46]. Polyploid seedless cultivars are obtained in polyploid structure due to some errors during meiosis, and this is common in grapevines. It also allows the reproduction of hybrid genotypes in a sterile structure by doubling the genome [47, 48].

One of the most used methods to provide polyploidy in plants is the application of colchicine to the apical meristem, and it is reported that it is not very effective in applications made on grapevines [49]. Many studies have been carried out to obtain polyploid genotypes by using different species and cultivars belonging to the *Vitis* species. It has been tried to obtain tetraploid genotypes, especially in American grape rootstocks (*Vitis rupestris* and *Vitis riparia*) and *Muscadinia* species [50]. In some studies, on the somatic embryoids and polyploidization of shoot tips of seedless grape cultivars, it has been reported that non-chimeric autotetraploid plants can be obtained [40]. Different studies on the effect of colchicine on proembryogenic cells have reported that it can lead to the regeneration of true utopolyploids [51, 52]. In addition, researchers have identified and published the most effective protocols for the induction of polyploidy [53]. Recently, a significant relationship has been found between the frequency of polyploidy detected in the meristem tissues of plants grown under in vitro conditions and the number of chloroplasts in the stomata of grape somaclones. However, it has been reported that there is a reverse relationship or correlation between the frequency of polyploidy and the stomata number in the leaf area [54]. Cross-breeding between cultivars/genotypes with different ploidy is one of the effective methods to create new germplasms. Most of the triploid fruit plants are sterile and their fruit is seedless.

Triploid breeding researchers have presented a new method for seedless grape breeding as it allows high sterilization and obtaining of parthenocarpic fruits, and ultimately facilitated the achievement of desired results [55]. Seedless is generally desired by breeders, and it has become a more important issue, especially for table grape breeding researchers in recent years. Because the demand for seedless grape cultivars is much higher than the seedless cultivars [56, 57]. However, there exists some mating obstacles in crosses between diploid and tetraploid grape cultivars. Embryo rescue or embryo recovery technique has been used with increasing success rate in recent years to overcome these obstacles. The embryo rescue technique may prevent the early-stage abortion of triploid young embryo, so triploid plants can be produced [58]. The majority of the studies on grape embryo rescue involved studies using seedless or early ripening grape cultivars as the female parent and cross-breeding studies, also the research of a cross between subgenus. There are few studies on embryo rescue from an interspecific cross between diploid and tetraploid grape species. There was a very limited number of studies on cross-breeding and embryo recovery between

diploid and tetraploid grape cultivars, including interspecies, but these studies have begun to increase with the techniques and technologies developed in recent years [55, 59–61]. Different studies have been carried out to obtain triploid and tetraploid new genotypes that have larger berry and seedless from different *Vitis* species. It has been stated that the tetraploid grapes obtained as a result of colchicine application have weak vegetative growth, low resistance to cold, and also not at the desired level in terms of yield. Although artificial tetraploids have these disadvantages, they have been successfully used in breeding studies where different *Vitis* species (especially *Vitis rotundifolia*, *Vitis vinifera,* and *Vitis labrusca*) are crossed with each other. In these studies, especially the tetraploid "Kyoho" cultivar (4x = 76), which is an interspecies hybrid, was widely used. Apart from "Kyoho" cultivar, Osuzu (3X) and King Dela (3X) cultivars were also obtained as triploid cultivars as a result of breeding studies. Intensive breeding studies are still continuing on polyploidy breeding, especially in the Far East [62].

Triploid genotypes usually have strong plant formation with seedless berry [63]. Researchers reported that some superior hybrid genotypes were obtained in triploid breeding studies carried out on grapevines. It has been reported that especially larger berry formation is frequently seen in triploid individuals. For this reason, it is seen that both natural and artificial polyploidy studies have increased in recent years [64, 65]. Despite all these studies, the commercial use of polyploid genotypes is still far from the desired levels. Polyploidization can change some phenotypes in plants, but without affecting the appearance of many of the fundamental characteristics of the cultivars. Due to these advantages, polyploidy breeding studies allow the development of some important characteristics (such as quality, yield, and resistance to stress conditions). Researchers still cannot fully explain the genetic and physiological mechanisms affected in the plant as a result of polyploidy. It can also increase the adaptation of artificial tetraploid (4x) grapevine rootstocks to the conditions of biotic and abiotic stresses in *Vitis* spp. Studies on synthetic polyploidy in plant species are still very limited. Due to the high adaptability of polyploid cultivars to different stress conditions, it has become an important study subject in breeding programs. In addition, the importance of polyploid cultivars and rootstocks for sustainable agriculture and their use in production has begun to increase [66].

Sequence-specific nucleases that generate double-stranded DNA breaks in targeted genes are the most important parts of site-specific genome editing in some plants. Induction of knockout mutations to inactivate undesirable features in genome editing has become the preferred method in many plant species in recent years. Different applications of sequence-specific nucleases have come to be used as robust tools for introducing functional mutations in many polyploid species, including grapes. The main approach here to utilize knowledge of biological mechanisms for targeted induction of double-stranded DNA breaks and their error-prone repair. Moreover, these regions may allow very specific changes at designated genome loci [41].

2.3 Biotic stress researches

The main phytopathogenic organisms that cause biotic stress in vines are organisms such as bacteria, nematodes, fungi, oomycetes, and viruses, which cause different infections in the vine and adversely affect many of their functions. All these pathogens get what they need for growth and reproduction from the host plant. Plant pathogens are divided into three different classes based on their infection strategy. In

this classification, the differences of the pathogens according to their feeding patterns and the necrosis they form in the plants are based [67].

Fungal diseases are among the most important biotic stress factors in grapes. Among the fungal diseases, downy mildew (*P. viticola*), powdery mildew (*E. necator*) and botrytis (*B. cinerea*) are the most common and most damaging diseases. Most of the grape cultivars consumed in different ways (such as table grapes, wine grapes, and raisins) belong to *V. vinifera* species whose gene source is Eurasia. This species is mostly preferred because of its unique taste, aroma, and better fruit quality. However, this species has a very high sensitivity to fungal pathogens despite these superior properties, and therefore, grape growers apply very intense fungicides for quality cultivation [68, 69].

Since this intensive fungicide application poses a great risk for both human and environmental health, grape breeding studies have focused on breeding more resistant varieties to diseases that will not need such intensive spraying in recent years. In grape breeding programs, many breeding studies are carried out by researchers in different countries to determine gene regions that are resistant to these diseases and to develop new wine and table varieties that carry these gene regions [13].

Although many of the North American origin wild *Vitis* species show varying levels of resistance to powdery mildew, unfortunately, the fruit quality is not at the desired level. These species are used as a very important genetic resource as a natural resistance source in grapevine breeding programs. To date, many resistant species have been described within these species. These species include *Vitis V. aestivalis, V. cinerea, V. riparia, V. berlandieri, V. labrusca* and *Muscadinia rotundifolia*. [70, 71]. However, some cultivars such as "Dzhandzhal kara" and "Kishmish vatkana" belong to the *V. vinifera* species, which are known to be susceptible to diseases, were found to be resistant [72, 73].

As a result of revealing the characteristics and related gene regions related to resistance in grape breeding studies, much more successful results have been obtained in breeding programs. To date, some resistance loci related to fungal diseases have been identified and their mapping has been done. In recent years, not only fungal diseases but also numerous genetic loci associated with a particular phenotype have been identified in the grapevine. Regions associated with these diseases are very important in grapevine breeding studies as they are determined with the help of marker-assisted selection (MAS) and provide a great advantage in achieving results. Gene regions associated with many traits in grapevines have been reported by the Vitis International Variety Catalog [74].

Overall, the table reports potential gene regions found to be related to 20 different traits. In particular, the table includes loci and alleles associated with downy and powdery mildew diseases. Eight sites associated with non-mildew diseases, five with metabolites, five refer to morphology traits, and four with phenology. This table is updated regularly to provide accurate access to loci and markers associated with many of the commercial traits and stress factors required by grapevine research. It also helps the researchers in correct naming and following the same systematic (**Figures 3**–5).

The resistance of hybrid genotypes obtained from different grape breeding studies against downy and powdery mildew diseases has been compared in several studies [6, 73, 75–79]. According to the studies conducted by the researchers so far, 31 genomic regions have been associated with downy mildew resistance (Rpv loci) and 13 with powdery mildew disease resistance (Run/Ren loci) (**Figure 3**). In order to determine the presence of these loci in hybrid genotypes, marker-assisted selection (MAS) studies have been successfully performed [75–77, 80–83].

Trait	Symbol	Chr	Position on chr [Mb]	Associated marker	Parent 1	Parent 2	Population size	Genotype of origin	Original species of trait
Resistance									
Agrobacterium spec.	*Rrg1*	15	7.1	UDV015	Kunbarát	Sárfehér	272	Kunbarát	*V. amurensis*
			9.3	9M3-3					
Colletotrichum gloeosporioides (Glomerella cingulata)	*CgR1*	14	4.1	np19345	Cabernet Sauvignon	Shuang Hong	91	Shuang Hong	*V. amurensis*
Daktulosphaira vitifoliae	*Rdv1*	13		GF13_1	GF.V3125	Börner	188	Börner	*V. cinerea*
			21.9	GF13_9					
				GF13-1	GF.V3125	Börner	188	Börner	*V. cinerea*
			21.5	GF13-7					
Daktulosphaira vitifoliae	*Rdv2*	14	4.9	S14_4921219	V. cinerea C2-50	Riesling	90	V. cinerea C2-50	*V. cinerea*
Daktulosphaira vitifoliae	*Rdv3*	14	5.0	S14_5049399	MN1264	MN1246	125	MN1264	
Daktulosphaira vitifoliae	*Rdv4*	10			MN1264	MN1246	125	MN1246	
Daktulosphaira vitifoliae	*Rdv5*	5			MN1264	MN1246	125		
Daktulosphaira vitifoliae	*Rdv6*	7			VRH8771	Cabernet Sauvignon	135	VRH8771	*M. rotundifolia*
Daktulosphaira vitifoliae	*Rdv7*	3	5.5	3_5494608	VRH8771	Cabernet Sauvignon	135	VRH8771	*M. rotundifolia*
Daktulosphaira vitifoliae	*Rdv8*	10			VRH8771	Cabernet Sauvignon	135	VRH8771	*M. rotundifolia*
Diaporthe ampelina (Phomopsis viticola)	*Rda1*	15	19.6	S15_19560016	Chardonnay	V. cinerea B9	148	*V. cinerea* B9	*V. cinerea*
				S15_19591538	Horizon	V. cinerea B9	162	*V. cinerea* B9	*V. cinerea*
			19.3	S15_19300044	Horizon	Illinois 547-1	366	Illinois 547-1	*V. cinerea*
Diaporthe ampelina (Phomopsis viticola)	*Rda2*	7	1.2	VVMD7	Horizon	*V. cinerea* B9	162	Horizon	
			1.8	VrZAG62					
			3.1	VVIb22					
			3.1	S7_3127568					
			1.9	S7_1912889	Horizon	Illinois 547-1	366	Horizon	
Erysiphe necator	*Ren1*	13		UDV020	Nimrang	Krishnish varikana	310	Krishnish varikana	*V. vinifera*
			18.4	VMC9h4-2					
			18.4	VMCNg4e10.1					
Erysiphe necator	*Ren2*	14	26.9	CS25	Horizon	Illinois 547-1	58	Illinois 547-1	
Erysiphe necator	*Ren3*	15	7.1	UDV013b	Regent	Lemberger	153	Regent	
			10.9	VVIv67					
				ScORA7-760	Regent	Lemberger	152	Regent	
			4.9	VChr15CenGen02	Regent	RedGlobe	206	Regent	
			10.9	GF15-28 / VVIv67	GF.GA-47-42	Villard blanc	151		
			9.3	GF15-42	Regent	Lemberger	132	Regent	
Erysiphe necator	*Ren4*	18	26.9	VMC7f2	C166-043	F8909-08	42	C166-043	*V. romanetii*
			26.9	SNPs	C87-41	B70-57	57	C87-41	*V. romanetii*
Erysiphe necator	*Ren5*	14	4.8	VMC9c1	Regale	Regale	191	Regale	*M. rotundifolia*
Erysiphe necator	*Ren6*	9	8.6	PN9-057	F2-35	V. piasezkii (DVIT.2027)	277	V. piasezkii (DVIT.2027)	*V. piasezkii*
			9.1	PN9-068					
Erysiphe necator	*Ren7*	19	0.2	VVIp17.1	F2-35	V. piasezkii (DVIT.2027)	277	V. piasezkii (DVIT.2027)	*V. piasezkii*
			0.9	VMC9a2.1					
Erysiphe necator	*Ren8*	18	13.2	UDV117	GF.GA-47-42	Villard blanc	151		
				SP8_P_SNP632GF					
Erysiphe necator	*Ren9*	15	1.4	CenGen6	Regent	Lemberger	153	Regent	
Erysiphe necator	*Ren10*	2	17.9	S2_17854965	MN1264	MN1214	147	Seyval blanc	
		2		Haploblock validation	MN1264	MN1246	125		
Erysiphe necator	*Ren11*								

(a)

Trait	Symbol	Chr	Position on chr [Mb]	Associated marker	Parent 1	Parent 2	Population size	Genotype of origin	Original species of trait
Erysiphe (Uncinula) necator	*Run1*	12	13.1	VMC4f3.1	VRH3082-1-42	Cabernet Sauvignon	161	VRH3082-1-42	*M. rotundifolia*
			20.4	VMC8g9					
			16.4	49SRP1 P3	VRH3082-1-42	Cabernet Sauvignon	2575		
			16.8	CB33.54	VRH3176-21-11	Cabernet Sauvignon	722		
					VRH3161-6-4	Cabernet Sauvignon	110		
					BC1.M. rotundifolia	Syrah	139		
Erysiphe (Uncinula) necator	*Run2.1*	18	26.9	VMC7f2	JB81-107-11	Chenin Blanc	97	Magnolia	M. rotundifolia
			20.9	VMCNg1e3					
			23.4	VVIn16	JB81-107-11	Tokay	47		
			26.9	VMC7f2					
			26.9	VMC7f2	A90-71	Flame Seedless	80		
Erysiphe (Uncinula) necator	*Run2.2*	18	26.9	VMC7f2	e2-9	Malaga Rosada	255	Trayshed	*M. rotundifolia*
Erysiphe necator	*Sen1*	9	13.6 - 18.0	S8_19258484	*V. rupestris* B38	Chardonnay	85	Chardonnay	*V. vinifera*
Guignardia bidwellii	*Rgb1*	14	26.7	GF14-42	GF.V3125	Börner	202	Börner	
Guignardia bidwellii	*Rgb2*	16	15.3	VChr16c	GF.V312	Börner	202	Börner	
Meloidogyne javanica (root knot nematode)	*MjR1*	18	31.2	S18_31160355	C2-50	Riesling	90	C2-50	*V. cinerea*
			34.0	S18_33954011					
Pierce's disease (*Xylella fastidiosa*)	*Pdr1*	14	25.3	VMCNg3h8	*V. rupestris*	*V. arizonica*	181		*V. arizonica*
			26.6	VVIp64					
			26.1	UDV095					
Plasmopara viticola	*Rpv1*	12	10.3	VVIb32	Syrah	28-8-78		28-8-78	*M. rotundifolia*
Plasmopara viticola	*Rpv2*	18			Cabernet Sauvignon	86.24	129	86.24	*M. rotundifolia*
Plasmopara viticola	*Rpv3*	18		UDV112	Regent	Lemberger	153	Regent	
			24.9	UDV305	Chardonnay	Bianca	116	Bianca	
			26.9	VMC7f2					
			26.9	VMC7f2	Regent	RedGlobe	206	Regent	
	Rpv3.1 (=Rpv3 [589-271])		24.9	UDV305				Seibel 4614	*V. rupestris*
			26.1	UDV737					
			25.9	GF18-06 GF18-08	GF.GA-47-42	Villard blanc	151	Villard blanc	*V. rupestris*
	Rpv3.2 (=Rpv3 [no6-291])		24.9	UDV305				Munson (Jaeger 70)	*V. rupestris* or *V. lincecumii*
			26.1	UDV737					
			25.9	GF18-06 GF18-08	GF.GA-47-42	Villard blanc	151	GF.GA-47-42	*V. rupestris* or *V. lincecumii*
	Rpv3.3 (=Rpv3 [no6-277])		24.9	UDV305				Noah	*V. labrusca* or *V. riparia*
			26.1	UDV737					
			23.4	VVIN16	Merzling	Teroldego	136	Merzling	
			26.1	UDV737					
	Rpv3 321-312		24.9	UDV305				Noah	*V. labrusca* or *V. riparia*
			26.1	UDV737					
	Rpv3 [01-299]		24.9	UDV305				*V. rupestris* Ganzin	*V. rupestris*
			26.1	UDV737					
	Rpv3 [09-314]		24.9	UDV305				*V. rupestris* Ganzin	*V. rupestris*
			26.1	UDV737					
	Rpv3 no8-287		24.9	UDV305				Bayard (Couderc 28-112)	*V. rupestris* or *V. labrusca*
			26.1	UDV737					
Plasmopara viticola	*Rpv4*	4	4.7	VMC7h3	Regent	Lemberger	153	Regent	
			5.3	VMCNg2e1					
Plasmopara viticola	*Rpv5*	9	4.0	VVIa52b	Cabernet Sauvignon	Gloire de Montpellier	138	Gloire de Montpellier	*V. riparia*
Plasmopara viticola	*Rpv6*	12	20.4	VMC8g9	Cabernet Sauvignon	Gloire de Montpellier	138	Gloire de Montpellier	*V. riparia*
Plasmopara viticola	*Rpv7*	7	11.4	UDV097	Chardonnay	Bianca	116	Bianca	
Plasmopara viticola	*Rpv8*	14	6.6	Chr14V015	*V. amurensis* Ruprecht	*V. amurensis* Ruprecht	232	*V. amurensis* Ruprecht	*V.amurensis*
Plasmopara viticola	*Rpv9*	7	16.6	CCoAOMT	Moscato Bianco	*V. riparia* W63	174	*V. riparia* W63	*V.riparia*

(b)

Trait	Symbol	Chr	Position on chr [Mb]	Associated marker	Parent 1	Parent 2	Population size	Genotype of origin	Original species of trait
Plasmopara viticola	*Rpv10*	9	3.7	GF09-46	GF.GA-52-42	Solaris	256	Solaris	*V. amurensis*
Plasmopara viticola	*Rpv11*	5	4.5	VVMD27	Regent	Lemberger	153	Regent	
				CS1E104J11F	Chardonnay	Bianca	116	Chardonnay	
			4.1	VCHR05C	GF.GA-52-42	Solaris	256	Solaris	
Plasmopara viticola	*Rpv12*	14	8.0	UDV014	99-1-48	Pinot noir	180	99-1-48	*V. amurensis*
			9.3	UDV304	Cabernet Sauvignan	20/3		20/3	*V. amurensis*
				rgvvin180					
			10.1	UDV370					
Plasmopara viticola	*Rpv13*	12	10.0	VMC1g3.2	Moscato Bianco	*V. riparia* W63	174	*V. riparia* W63	*V.riparia*
Plasmopara viticola	*Rpv14*	5	20.2	GF05-13	GF.V3125	Börner	202	Börner	*V. cinerea*
Plasmopara viticola	*Rpv15*	18			*V. piasezkii* (DVIT.2027)	F2-35	94	*V. piasezkii* (DVIT.2027)	*V. piasezkii*
Plasmopara viticola	*Rpv16*								
Plasmopara viticola	*Rpv17*	8	11.7		*V. rupestris* B38	Horizon	163	Horizon	
Plasmopara viticola	*Rpv18*	11	15.4		*V. rupestris* B38	Horizon	163	Horizon	
Plasmopara viticola	*Rpv19*	14	29.5		*V. rupestris* B38	Horizon	163	*V. rupestris* B38	*V. rupestris*
Plasmopara viticola	*Rpv20*	6	0.9		Horizon	*V. cinerea* B9	152	Horizon	
Plasmopara viticola	*Rpv21*	7	2.1		Horizon	*V. cinerea* B9	152	Horizon	
Plasmopara viticola	*Rpv22*	2	2.1		Cabernet Sauvignan	Shuanghong	91	Shuanghong	*V. amurensis*
			3.5						
Plasmopara viticola	*Rpv23*	15	9.9		Cabernet Sauvignan	Shuanghong	91	Shuanghong	*V. amurensis*
			13.9						
Plasmopara viticola	*Rpv24*	18			Cabernet Sauvignan	Shuanghong	91	Shuanghong	*V. amurensis*
Plasmopara viticola	*Rpv25*	15	3.0	Marker561375	Red Globe	Shuangyou	149	Shuangyou	*V. amurensis*
			3.9	Marker549779					
Plasmopara viticola	*Rpv26*	15	14.7	Marker525926	Red Globe	Shuangyou	149	Shuangyou	*V. amurensis*
			15.0	Marker526446					
Plasmopara viticola	*Rpv27*	18	24.6	VVCS1H07H16R1-1	Norton	Cabernet Sauvignon	182	Norton	*V. aestivalis*
			26.9	UDV737					
Plasmopara viticola	*Rpv28*	10	1.2	VVIB01	*V. rupestris* B38	*V. riparia* HP-1	294	*V. rupestris* B38	*V. rupestris*
			1.3	UDV-073					
Plasmopara viticola	*Rpv29*	14	21.6	chr14_21613512_C_T	Mgaloblishvili	Mgaloblishvili	132	Mgaloblishvili	*V. vinifera*
Plasmopara viticola	*Rpv30*	3	16.2	cn_C_T_chr3_16729046	Mgaloblishvili	Mgaloblishvili	132	Mgaloblishvili	*V. vinifera*
Plasmopara viticola	*Rpv31*	16	21.3	ti_T_C_chr16_21398409	Mgaloblishvili	Mgaloblishvili	132	Mgaloblishvili	*V. vinifera*
Xiphinema index	*XiR1*	19	20.9	VMC5a10	*V. rupestris*	*V. arizonica*	185		*V. arizonica*
			20.9	1N3R3b					
				M4F3R					
Xiphinema index	*XiR2*	9		VVBX-A-06	VRH8771	Cabernet Sauvignon	135	VRH8771	
Xiphinema index	*XiR3*	10		SC8-03	VRH8771	Cabernet Sauvignon	135	VRH8771	
Xiphinema index	*XiR4*	18	29.1	UDV108	VRH8771	Cabernet Sauvignon	135	VRH8771	

(c)

Figure 3.
Table of loci for diseases and pests traits in grapevine relevant for breeding and genetics (details in www.vivc.de/data) [96].

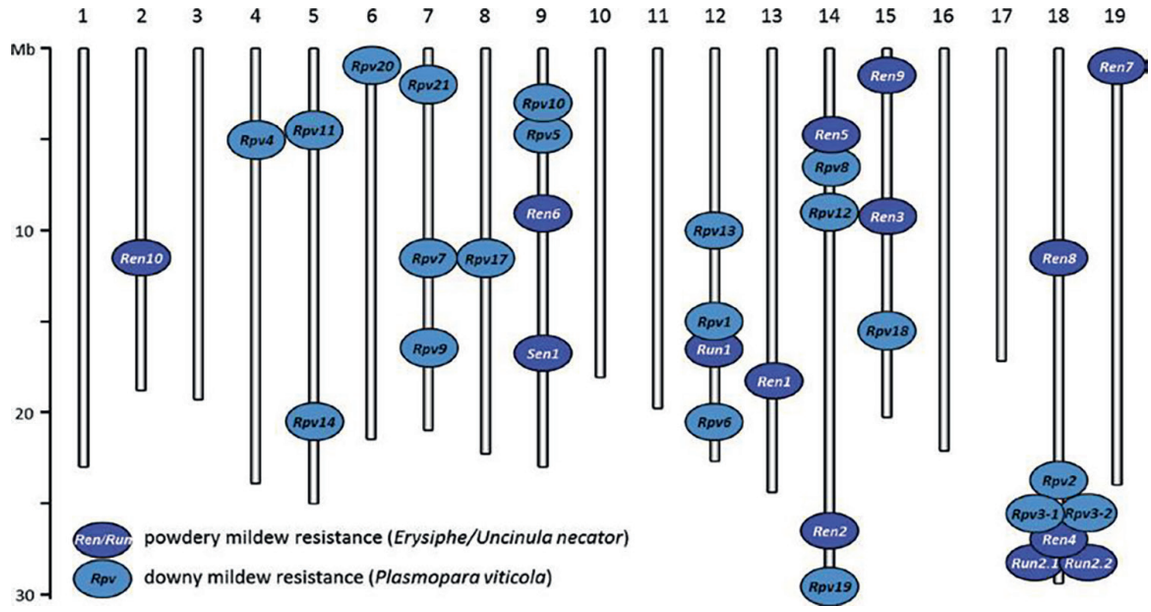


Figure 4.
Downy mildew (P. viticola) and grapevine powdery (E. necator) resistance loci position in the genome. Scale is in megabases (Mb) [74].

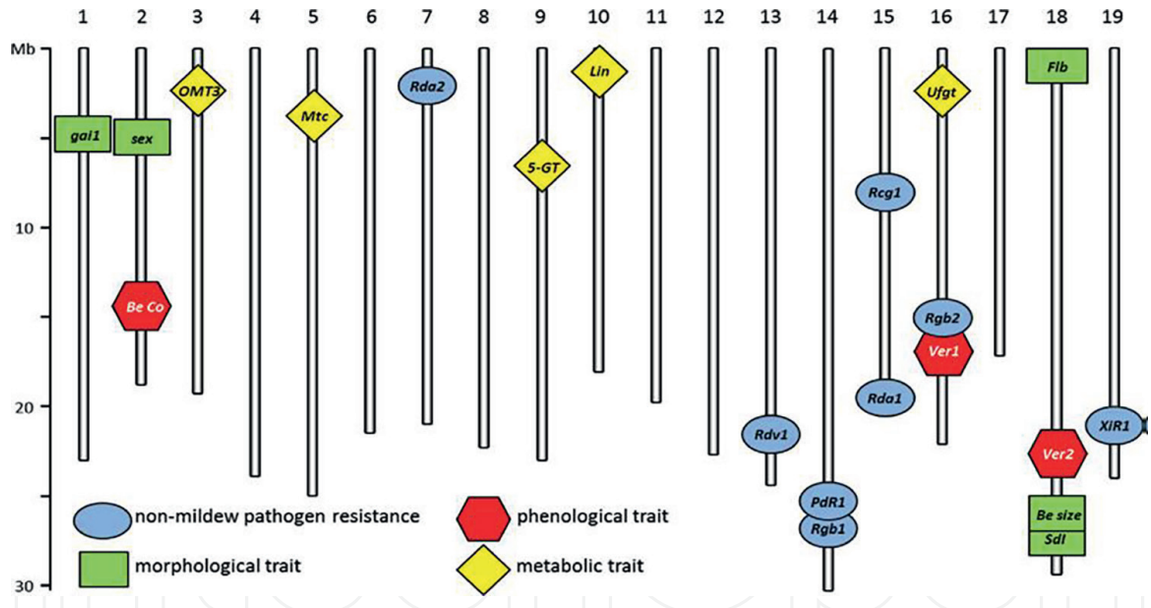


Figure 5.
Genomic positions of morphological, phenological, metabolic trait loci, non-mildew disease, and pest resistances. Scale is in megabases (Mb) [74].

However, the presence of these gene regions alone often does not prove that the variety is resistant to diseases. In addition, the resistance of the genotypes should be tested in the field and under controlled greenhouse/laboratory conditions [84–89]. New downy and powdery mildew resistant cultivar "Regent" was obtained in Germany, its pedigree includes American species carrying Ren3, Ren9, Rpv3, Rpv4, and Rpv11 [90–92]. In recent years, new resistant loci have been identified in different species, especially in relation to resistance to fungal diseases from biotic stress factors. In one of these studies, [93]. discovered the REN11 locus from *Vitis aestivalis* for stable resistance to grape powdery mildew.

After determining the gene regions associated with resistance and thus the resistant genotypes, another problem may be encountered in resistance breeding studies. New pathogen races may break this resistance. In order to solve this problem that may arise, one of the methods that breeders usually resort to is to try to collect more than one gene region associated with resistance into new genotypes. Thus, the resistance of the new genotypes is further increased. For example, even if the vine plant is infected with a new virus, it limits the development of the pathogen and shows more resistance against it. Marker-assisted gene pyramid applications have been a highly preferred application by researchers in grape breeding studies in recent years. With the use of molecular markers in grape breeding programs, genotypes that may exhibit the same phenotype in appearance but carry more than one resistance gene in their genomes can be determined [94–96]. In recent years, breeders and pathologists have worked together to achieve significant success in grape breeding, especially in studies related to resistance. In one of them, with the VitisGen project carried out in partnership with different organizations in the USA, they collected different isolates against powdery mildew disease and identified complementary resistance loci sets to evaluate the phenotypic and genetic resistance gene stacks against them [97].

It has been reported as a result of studies that different chemicals have important effects on defense mechanisms in plants also grapevines. Among them, ethylene, jasmonic acid, and salicylic acid are the most important ones. These chemicals can act synergistically or vice versa, depending on the pathogen. While jasmonic acid and ethylene help plants to defend themselves against necrotrophic pathogens, defense against biotrophic pathogens is mediated by salicylic acid, unlike them. Cultivars of *V. vinifera* species have very low resistance to many pathogens of fungal origin. This is probably related to their insufficient defense systems against these pathogens. However, although studies have been carried out with the details of this defense system in recent years, more information is needed regarding the interaction of cultivars with grapevine diseases. In recent years, researchers have been working intensively on these interactions to obtain useful information for breeders, especially in parallel with the advances made in molecular methods. In one of the studies conducted for this purpose, it was reported that the modulation of chloroplast-associated lipids in the first hours of interaction with downy mildew is important for the protection of photosynthetic machinery and for the biosynthesis of jasmonic acid [67].

Cavaco et al. [98] identified subtilisin-like proteases as strong resistance-associated candidates. The relationship between fungal diseases and phenolic components has become increasingly important in recent years. Researchers evaluated changes in total phenolics, total antioxidant activity, and phenolic compounds in different *Vitis* species and genotypes. After fungal diseases, it has been reported that there is an increase in the amount of total phenolics, total antioxidant activity, and some phenolic compounds [99–101]. Resistance mechanism of *V. vinifera* cv. "Mgaloblishvili", which was grown in Georgia and resistant to downy mildew, was investigated by Ricciardi et al. [102] Researchers explained the disease resistance of the cultivar with low disease density, low sporulation, damaged mycelium, production of antimicrobial compounds such as volatile organic compounds (VOCs) whose activity on the pathogen was evaluated by leaf experiments. These results contain data that can assist and accelerate future resistance breeding programs.

Chibutaru et al. [103] first examined the reaction of mono-locus resistant genotypes against downy mildew after the first and second infection, and also evaluated the pyramid resistance genotypes. Researchers especially investigated different

metabolites (not stilbenes and stilbenoids), which accumulate significantly in resistant and susceptible genotypes as a result of disease infection and can be used as potential resistance-related markers. Also, they investigated whether these metabolites could be markers of infection. In their study, it was aimed to provide a better understanding of the different resistance mechanisms of hybrid-pathogen interaction that can affect different *Vitis* species and to find previously undetected resistance biomarkers. As a result of their studies, they determined the components that increased after downy mildew and could be used as biomarkers.

The development of highly reproducible genetic engineering methods for grapevine rootstocks, cultivars, and genotypes now allows the identification, screening, and/or introduction of grapevine-derived genes related to desirable traits, such as disease or pest resistance. It has been reported that genetically modified grapevines constitutively expressing rice chitinase genes have been screened for the responses of pathogenesis-related proteins to fungal pathogen infection, and show increased resistance to powdery mildew disease. As a result of studies, it has been revealed that other grape-derived genes such as polygalacturonase inhibitor protein and other lytic peptides increase resistance to fungal diseases [104, 105].

Grapevine breeding programs have been started in order to develop new resistant hybrid genotypes against powdery mildew and downy mildew diseases in different countries [106]. In one of these, Ruiz-García et al. [107] evaluated the degree of phenotypic resistance or susceptibility for downy and powdery mildew of 28 new genotypes obtained from crosses between "Monastrell" and "Regent". In particular, three genotypes from the hybrid population showed strong combined resistance, and they could be used as a very important source of resistance parents in future breeding studies in terms of both powdery mildew and downy mildew. As a result of their study, they reported that multi-resistant lines provide very valuable material for obtaining resistant genotypes and help to characterize the molecular basis of downy and powdery mildew resistance.

Wild grapevine species are widely recognized as an important source of resistance or tolerance genes for diseases and environmental stresses. Recent studies revealed partial resistance to powdery mildew (*Erysiphe necator*) in *V. sylvestris* from Central Asia. Lukšić et al. [108] investigated the resistance of in situ *V. sylvestris* seedlings collected from different regions of Croatia against powdery mildew. Ninety-one in situ individuals and 67 *V. sylvestris* seedlings were evaluated for Powdery mildew resistance according to OIV 455 descriptor. Three SSR markers (SC47-18, SC8-071-0014, and UDV-124) linked to Powdery mildew resistance locus *Ren1* were used to decipher allelic structure. As a result, they determined that there were varying numbers of resistant genotypes in individuals in different *V. sylvestris* populations. Thus, in their study, powdery mildew resistance was proved for the first time in the germplasm of *V. sylvestris* in the eastern Adriatic region.

In order to increase the resistance to different biotic and abiotic stress conditions in grapevine, research programs have increased primarily on the determination of the responsible gene regions and then the introgression of these regions into susceptible cultivars or the mutation of the genes that cause the susceptibility in recent years. Sometimes the resistance obtained as a result of mutation of the genes can provide a longer-term protection. Especially in breeding studies, genotypes with genes containing resistance are selected as parents and it is aimed to transfer these characteristics to new genotypes. According to Pirello et al. [109] used Arabidopsis as a model in their study, worked with resistant mutants, and investigated the effectiveness of DMR6 and DLOs genes that could confer downy mildew resistance in grapevines.

By examining the relationships between genes and the links between the VviDLO1, VviDMR6-1, and VviDMR6-2 gene groups, they reported that they are associated with genes sensitive to pathogenesis. In particular, the researchers concluded that the VviDMR6-1 region may be a candidate that can be used to produce resistant cultivars by gene editing.

2.4 Abiotic stress researches in grapevine breeding

As a result of climate change affecting the whole world, the development of new grape genotypes with high adaptability to abiotic stress conditions has become a more important priority in recent years. Successful programs are carried out for sustainable viticulture, with the aim of grapevine breeding studies and the transfer of many resistance-related genes in wild grapevine species to new genotypes through interspecies cross-breeding. Different studies are being conducted to identify these alleles in the grapevine genome and understand how they can be used to manipulate phenotypes. The diversity of abiotic constraints (heat stress, drought, salinity, mineral deficiency, etc.) and their timing, duration, and intensity must be taken into account. It is seen that topics such as the type of factors causing abiotic stress (extreme temperatures, salt stress, excessive water, heavy metals, and others), duration, and intensities are taken into account in these studies. It is necessary to clearly identify these by thoroughly examining the characteristics and sensitive development stages underlying the adaptation of the vine plant to different stress factors. Targeted traits are often quite complex and under the control of various genetic mechanisms. Especially in the last decade, various researches on grapevine genome (sequencing, genetics, phenotype development, modeling) and functional characterization of related genes) and significant results have been obtained by carrying out successful projects. In the light of recent developments in grape physiology and genome, molecular mechanisms related to adaptation processes to changing climatic conditions and the gene regions controlling them are explained. The physiology of the vine is actually quite complex, and this complex mechanism is polygenically controlled. However, in recent years, very important information has been obtained about new grapevine genotypes that are more tolerant/resistant to different abiotic stress conditions. Responses to extreme temperatures, heavy metals, droughts, and some other stress conditions have been extensively studied by different researchers in order to obtain new more compatible hybrid genotypes [110].

Grapevine (*Vitis* spp.) can adapt well to environments under different stress conditions. It has even been reported that moderate abiotic stress has a positive effect on the quality of grape products such as wine. In addition, as a result of the high variation in *Vitis vinifera* cultivars and their combination with different rootstocks, it becomes possible for grapevine cultivation in different ecology and soil types [111]. Grapevine plants are considered drought resistant when compared with other horticultural plant species. However, most of the time, as a result of insufficient irrigation, significant decreases in yield and quality can be observed [112, 113]. By utilizing the wide variation in drought tolerance within the Vitis species in breeding studies, new varieties more tolerant to the desired drought can be developed [114–117]. There is very limited information about the mechanisms related to drought tolerance, but promising studies have been carried out in recent years. In order to develop longer-term sustainable irrigation programs for drought, which has become a growing problem in many parts of the world, new drought-resistant/tolerant varieties must be developed.

In a study investigating the response of grapevine plants to temperature, Luchare et al. [118] studied the effects of increases in temperature on carbon balance using microvine mutants. The grapevine plants under controlled conditions studied in detail the photosynthesis, respiration, and carbon allocation in different parts of the plants at different temperature ranges. As a result of the study, they reported that especially net photosynthesis decreased after peaking at 25–30°C, and that respiration at night increased steadily with the increase in temperature. In addition, a less favorable carbon balance was formed at higher temperatures compared to lower temperatures. In another similar study, it was reported that although organogenesis and leaf area was stimulated by high temperature, there was a decrease in carbon balance [119].

In case of exposure to high temperatures, there can be significant changes in the amount of compounds in the content of grapes, especially aroma compounds [120]. For example, in a study with "Gewürztraminer" × "Riesling" hybrids, it was observed that high temperature had different effects on geraniol content linalool and linalool content in grape berries. While geraniol content increased with the high temperature in all genotypes used in the study, linalool content decreased. This was interpreted as the regulatory pathways for the deposition of the components were different for both components. This also showed that high temperatures increased the complexity of the quality control parameters [121].

Roots are vine organs that play an important role in biotic stress factors. Despite the fact that they are less studied due to their underground location, there has been a significant increase in the studies on roots in recent years due to the understanding that roots have an important role in resistance against many stress conditions. Since most of the vines are grafted, rootstocks can be used especially for mineral deficiency/toxicity or drought tolerance, and there is a chance to choose the best scion × rootstock combinations for different soil/climate types [122].

One of the most important problems in mineral nutrition and roots is that genetic variation cannot be fully characterized and the lack of extensive investigation of the genetic architecture of mineral nutrition-related traits. Important studies have been published on limestone tolerance [123] and recently salt tolerance [124] Since rootstocks are often derived from interspecific crosses, it should reveal the extent to which different species possess the relevant alleles that define and differentiate their feeding activities. These alleles can be used successfully in breeding studies to grow highly efficient rootstocks. As a result of the evaluation of the variability between rootstocks from different genetic backgrounds, important data can be provided to achieve the desired goals. In one of these studies, it was reported that rootstocks with *V. riparia* among the parents had a lower phosphorus concentration than the others when their petioles were evaluated [110, 125].

With a full understanding of the conditions that cause abiotic stress, successful results can be obtained by applying the effects of this stress on plants and fruits to breeding studies with integrated approaches of ecophysiological and genetic modeling [126, 127]. With plant modeling, many complex traits can be divided into simpler traits, and as a result, complex traits adapt to the environment and growing environments much more stably with simple genetic control. For the grapevine, researchers are working on the details of the different models. In recent years, important studies have been carried out to describe the physiological and genetic mechanisms of grapevine responses to important abiotic stress conditions. These studies, the number of which has increased in recent years. The increasing development of modern phenotyping and genotyping tools with approaches in molecular physiology, modeling,

ecophysiology, and genetics, and their integration with each other, show how knowledge on this subject can be further increased. With the help of these extensive studies, new components related to regulatory pathways have been found and the genetic structure of important traits has been analyzed. As a result, these data provided very important information for the breeding of advanced cultivars and rootstocks in the fight against different diseases and their agents. Despite all these developments and advances in technology, much remains to be done in order to describe the responses of plants to abiotic stress factors and to fully understand how to adapt to these extreme climates. There is still a large gap between the phenotypes and genotypes of newly developed cultivars. We are far from the desirable level of fully understanding and responding to the interactions of plants, both with the environment and with their own structures [110, 128].

2.5 Seedlessness researches in grapevine breeding

Seedless grape cultivars constitute a very important part of table grape production. Especially in recent years, consumers have been demanding more seedless cultivars. This situation has led to the start of studies in many countries for the breeding of high quality, larger berry, long storage life, high yielding, and relatively more disease tolerant seedless cultivars. These breeding programs are carried out by state institutions, private sector, and grower [129].

It is known that the seedless grape cultivars have two different types (parthenocarpic and stenospermocarpic seedless). In stenospermocarpic seedless genotypes, the embryo fails to develop shortly after fertilization during seed development, and such cultivars are used as parents in breeding to obtain seedless genotypes with larger berry size [130]. Berries of parthenocarpic grapes have rather a small berry size that develops without fertilization. For this reason, the embryo rescue/recovery technique is widely used together with conventional breeding methods to obtain new seedless grape varieties.

In traditional hybridization studies on the breeding of seedless grape varieties, seedless parents are used as the father (pollinator) and the seed parent is used as the mother. However, the seedlessness rate in the genotypes obtained from these crosses varies between 0% and 49% depending on the parent combination [131]. As a result of the abortive embryos of stenospermocarpic vine cultivars to continue their development in tissue culture, seedless x seedless hybridizations have been possible in traditional hybridization studies. This application (embryo rescue technique) increased the seedless rate observed in seedless x seedless hybrids in F1 plants between 16.7% and 92% depending on the parent combination. Has changed. For this reason, the embryo rescue technique is widely used together with traditional breeding methods to obtain new seedless grape cultivars [132–136]. Success rate in embryo recovery studies depends on the genotype of the parents [132], sampling time, and composition of the culture medium [137]. Embryo forming capacity and germination of embryos of hybrid genotypes may differ according to both their male and female parents [133]. Seed trace of stenospermocarpic grape cultivars can be in 3 different sizes (small, medium, and large). Generally, those with a larger seed trace have a higher rate of transformation into a living plant with the embryo rescue method [138].

Also, in another study, Li et al. [56] conducted studies to obtain seedless, disease-resistant and high-quality grape cultivars by using the embryo recovery method and reported that the sampling time has a very significant effect on the development and recovery of the embryo. The genetic structure of seedlessness in grapes has been

studied by different researchers. Finally, a model of three recessive genes (independent and complementary) by a seed development inhibitor at the 18th linkage group on the dominant locus was proposed [139, 140]. In addition, it has been reported that two SSR markers (VMC7f2 and p3_VvAGL11) are very close to the seed development inhibitor region and can be used in marker-based selection breeding studies [141, 142].

It has been reported that VvAGL11, one of these two markers, is located in a region between the promoter region and can be used successfully to identify seedless genotypes. Two markers selected in association with the Seed Development Inhibitor locus region were selected as candidate markers because of their low number of false positives [143, 144]. The VviAGL11 marker belongs to the D-lineage of the MADS-box genes controlling the identity of the grape ovules and stands out as the major functional candidate gene for seedless grape morphogenesis [145–147]. In addition, two SCAR markers (SCC8 and SCF27), which are related to seedlessness and could be used to identify seedless genotypes, have also been developed [140, 148]. Of these, the SCC8 marker was used to distinguish seedless from hybrid genotypes belonging to seeded × seedless combinations [129, 149]. Mejía and Hinrichsen [148], on the other hand, used both markers to determine seedless genotypes in Ruby seedless' X "Sultanina" combination and reported that SCF27 marker can be used with a much higher percentage to identify seedless ones in F1 hybrid genotypes. Studies on seedlessness trait at the molecular level have shown that there is a very important relationship between the efficacy of the markers used and the genetic background when evaluating the seedlessness property of different hybrid genotypes. In the absence of lignified seeds in seedless grapes, the p3_VvAGL11 marker can accurately identify seedlessness in approximately 85% of hybrid genotypes [150]. When some seedless hybrid populations with different genetic backgrounds were evaluated with some markers (VvIn16, p3—VvAGL11, SCF27 andVMC7f2), it was reported that the VMC7f2 and p3—VvAGL11 markers showed the most accurate allelic variability. In addition, researchers reported that each combination of parents should be evaluated specifically by markers related to seedlessness [144]. In **Table 1**, primers and their sequences used by different researchers to identify seedless hybrid genotypes are given.

2.6 Rootstock breeding

Grape rootstocks are used around the world, especially against phylloxera, but despite many difficulties in choosing a better rootstock, research is being carried out. The studies on rootstock breeding started after Phylloxera damage, especially in the vineyard areas in Europe towards the end of the nineteenth century [10]. The use of a very limited number of rootstocks in the viticulture industry is expected to change in the coming years. The large-scale application of microsatellite markers has become the preferred and most reliable tool for *Vitis* spp. identification, although data on rootstock genotyping are very limited. There are rootstock collections in different centers around the world and these are of great importance for rootstock and variety breeding studies. One of the richest of these rootstock collections is at the University of Milan in Italy. It was established to collect most of the genetic diversity of *Vitis* species useful for rootstock genetic breeding programs. The idea was to select the most suitable parents for new breeding programs to develop sustainable viticulture models [157]. In another grapevine rootstock breeding study carried out in the same institution, a study was conducted on drought, which is an important problem for many vineyard regions. Although the grapevine is not very sensitive to drought, irrigation is very important in terms of fruit quality, especially in areas where table grapes are

Primer	Forward primer Sequence 5′–3′	Reverse primer Sequence 5′–3′	Tm (°C)	Band size (bp)	References
SCC8	GGTGTCAAGTTGGAAGATGG	TATGCCAAAAACATCCCC	60	1018	Lahogue et al. [140]
SCF27	CAGGTGGGAGTAGTGGAATG	CAGGTGGGAGTAAGATTTGT	62	2000	Mejía and Hinrichsen [148]
P3_VvAGL11	CTCCCTTTCCCTCTCCCTCT	AAACGCGTATCCCAATGAAG	Touch down	198/188	Bergamini et al. [143]
VMC7F2	AAGAAAGTTTGCAGTTTATGGTG	AAGATGACAATAGCGAGAGAA	61	198	Adam-Blondon et al. [151]
GSLP1	CCAGTTCGCCCGTAAATG	—	32	569	Wang and Lamikanra [152]
ScORA7-760	GAAACGGGTGTGAGGCAAAGGTGG	GGCCATTAGGAAATCAACATTAC	56	760	Akkurt et al. [153]
OPB 15_{1274}	CGGCAGACCTTACTGAAAGGATGAGT	CAACCACCATCCAATGATGGCGGGCTTC	37	1274	Kim et al. [154]
S382-615	TGGGCGTCAA	—	36	615	Zhang et al. [155, 156]

Table 1.
Primers, sequences, and references are used by different researchers to identify seedless hybrid genotypes [56].

grown. For this reason, a study was carried out to develop more suitable rootstocks for areas with drought problems. Researchers assessed the drought tolerance of M-rootstocks physiological (gas exchange and stem water potential) and transcriptomic performances (genes involved in ABA synthesis and ABA-mediated responses to drought) were evaluated under well-watered and water-stressed conditions. In the study, drought-resistant genotypes were determined by using novel genotypes (M-rootstocks) developed by the University of Milan [158].

Due to the demand for new grapevine genotypes that are especially resistant to biotic and abiotic stress conditions, grape and rootstock breeding studies have increased in recent years and many studies have been carried out on gene regions that may be associated with these stress conditions, especially with the help of molecular methods. Due to their different advantages as rootstock, the most preferred species are *V. berlandieri, V. riparia* and *V. rupestris*. The rootstocks not only protect the grapevines from phylloxera pests but also provide the water and nutrients needed by the cultivar/genotype in different soil types. It has been reported that different rootstock species show differences in supply the nutritional needs of the grafted cultivars/genotypes. Gautier et al. [159] investigated the extent to which rootstocks with different genetic backgrounds modify the mineral composition of the petioles of the scion. In a study conducted by grafting vines of the Cabernet-Sauvignon cultivar on 13 different rootstock genotypes, it was reported that the mineral content of the petioles of the genotypes containing *Vitis riparia* in their genetic history can vary greatly. This is important proof that rootstocks can greatly affect mineral intake. An example of the effective use of rootstocks against different biotic stress factors is the study of Dalbó and Souza [160]. Researchers used rootstocks for grapevine decline and dieback, which is a big problem especially in Southern Brazil. This disease is characterized a set of symptoms that lead to the weakening and death of affected plants. In soils with insufficient aeration, root rot fungi can seriously damage the roots of vines and even cause death. The development of root rot resistant grape rootstocks is the one of the main goal in grapevine and rootstock breeding programs. In these breeding programs, first of all, resistant cultivars/genotypes should be determined. In one of the studies, some of the *Vitis caribaea* hybrids were resistant to root rot, while at the same time some undesirable characteristics such as overgrowth and absence of winter dormancy were detected. *Vitis palmata* and *Vitis shuttleworthii* species were also reported to have high resistance. But, the performance of the genotypes and their hybrids was very poor in dry soil conditions and further cross-breeding programs would be required to eliminate undesirable characteristics. Selected lines are evaluated for productivity and fruit quality in rootstock trials with different scion cultivars.

Resistance to phylloxera has been investigated for a long time at UC Davis, which has been working on grape rootstocks and breeding for many years. Recent studies here are investigating the evolution of possible phylloxera strains capable of aggressive nodosite feeding against some resistant rootstocks and foliar feeding strains once rare in the region. In these studies, the reproduction of phylloxera strains was investigated and molecular markers were developed for physical maps associated with resistance genes. As a result of the studies, rootstocks resistant to aggressive root knot nematodes have been developed. [161].

Different studies are carried out on rootstock breeding, especially in the USA, Brazil, Europe, Australia, Iran, and China. In these studies, crosses are made in order to develop new rootstocks that are tolerant or resistant to different biotic and abiotic stress conditions, and then their compatibility with the varieties grafted on these rootstocks and their effects on fruit quality are examined. Since rootstock breeding

studies are much more laborious and time-consuming than other cultivar breeding programs, they are preferred by a limited number of researchers. However, as the mechanisms that cause stress factors become more understandable at the physiological and genetic level, much more successful breeding programs with promising results will become more preferable all over the world. In addition, with interspecies breeding, there is an increasing number of studies in the world that these new interspecies hybrid genotypes can be used directly in growing instead of using rootstock. Because it is reported that new interspecies hybrids will be much more tolerant in terms of different stress conditions and therefore the need for rootstock usage may decrease.

3. Conclusion

Since grapes are among the most traded fruit types in the world, they have a significant impact on the agricultural economies of the countries. In particular, grapes are preferred by many people due to their different consumption patterns and important effects on human health. However, the demands of consumers can vary rapidly. In order to respond to these rapidly changing consumer demands, quality new grape cultivars should be developed through breeding programs. In these breeding programs, while mainly trying to develop new table and wine grape cultivars, rootstock breeding studies have started to increase in recent years. As a result of research studies carried out by many researchers on the grapevine genome, many characters related to gene regions have been determined and it has become possible to reach the targeted results in grapevine breeding studies in a much shorter time. In recent years, the number of new grape cultivars that are more resistant to biotic and abiotic stress conditions has been increasing rapidly in parallel with climate change and consumer preferences. It is predicted that in the coming years, hybrid cultivars between species will have a greater share in the market with their more resistance to different stress conditions and more friendly characteristics in terms of human and environmental health. As a result of the intensive studies carried out by many scientists with the grapevine genome, it is expected that transgenic grapevine plants, which are more accepted by many parts of the society, will take their place in the markets in a short time. With the integration of biotechnology into breeding programs in a way that will address the ethical concerns of consumers, breeding studies will gain momentum and it will be possible to feed the growing world population and make more sustainable viticulture.

Funding

This research did not receive any external funding.

Conflicts of interest

The author declares that there is no conflict of interest in this article.

Data availability statement

Not applicable here.

IntechOpen

IntechOpen

Author details

Arif Atak
Agriculture Faculty, Department of Horticulture, Uludag University, Bursa, Turkey

*Address all correspondence to: atakarif@gmail.com; arifatak@uludag.edu.tr

IntechOpen

© 2022 The Author(s). Licensee IntechOpen. This chapter is distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/3.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. (cc) BY

References

[1] FAOSTAT. Available from: https://www.fao.org/faostat/en/#data/QCL [Accessed: February 10, 2022]

[2] OEC. Available from: https://oec.world/en/profile/hs/grapes [Accessed: May 01, 2022]

[3] Alston JM, Sambucci O. Grapes in the world economy. In: Cantu D, Walker A, editors. The Grape Genome. Basel: Springer Nature; 2019. pp. 1-24. DOI: 10.1007/978-3-030-18601-2_1

[4] Dong X, Chen W, Liang Z, Li X, Nick P, Chen S, et al. VitisGDB: The multifunctional database for grapevine breeding and genetics. Molecular Plant. 2020;**13**(8):1098-1100. DOI: 10.1016/j.molp.2020.05.002

[5] Reisch BI, Owens CL, Cousins PS. In: Badenes ML, Byrne DH, editors. "Grape," in Fruit Breeding. New York, NY: Springer; 2012. pp. 225-262. DOI: 10.1007/978-1-4419-0763-9_7

[6] Atak A, Şen A. A grape breeding programme using different *Vitis* species. Plant Breeding. 2021;**140**:1136-1149. DOI: 10.1111/pbr.12970

[7] Paul HW. Science, Vine, and Wine in Modern France. Cambridge: Cambridge University Press; 1996

[8] Campbell C. The botanist and the vintner: How wine was saved for the world. Chapel Hill: Algonquin Books of Chapel Hill; 2005

[9] Cahoon GA. French hybrid grapes in North America. In: Ferree DC, editor. A History of Fruit Cultivars. Yakima, Washington: Good Fruit Grower Magazine; 1998. pp. 152-168

[10] Kambiranda D, Obuya J, Snowden J. Grapevine improvement through biotechnology. In: Genetic Transformation in Crops. London, UK: IntechOpen; 2020. DOI: 10.5772/intechopen.91851

[11] Ferreira R, Monteiro S, Picarra-Pereira M, Teixeira AR. Engineering grapevine for increased resistance to fungal pathogens without compromising wine stability. Trends in Biotechnology. 2004;**22**(4):168-173. DOI: 10.1016/j.tibtech.2004.02.001

[12] Naidu RA, Maree HJ, Burger JT. Grapevine leafroll disease and associated viruses: A unique pathosystem. Annual Review of Phytopathology. 2015;**53**:613-634. DOI: 10.1146/annurev-phyto-102313-045946

[13] Armijo G, Espinoza C, Loyola R, Restovic F, Santibáñez C, Schlechter R, et al. Grapevine biotechnology: Molecular approaches underlying abiotic and biotic stress responses. In: Morata A, Loira I, editors. Grape and Wine Biotechnology [Internet]. London: IntechOpen; pp. 1-40. Available from: https://www.intechopen.com/chapters/52240 DOI: 10.5772/64872

[14] Lund K. Grapevine breeding programs for the wine industry. Traditional and molecular techniques. Woodhead Publishing Series in Food Science, Technology and Nutrition. Oxford, UK: Woodhead Publishing; 2015. pp. 359-378. DOI: 10.1016/B978-1-78242-075-0.00015-6

[15] Montaigne E, Coelho A, Zadmehran SA. Comprehensive economic examination and prospects on innovation in new grapevine varieties dealing with global warming and fungal diseases.

Sustainability. 2021;**13**(23):13254. DOI: 10.3390/su132313254

[16] Kicherer A, Herzog K, Bendel N, Klück H-C, Backhaus A, Wieland M, et al. Phenoliner: A new field phenotyping platform for grapevine research. Sensors. 2017;**17**:1625. DOI: 10.3390/s17071625

[17] Rist F, Herzog K, Mack J, Richter R, Steinhage V, Töpfer R. High-precision phenotyping of grape bunch architecture using fast 3D sensor and automation. Sensors. 2018;**18**:763. DOI: 10.3390/s18030763

[18] Zhu NY, Liu X, Liu ZQ, Hu K, Wang YK, Tan JL, et al. Deep learning for smart agriculture: Concepts, tools, applications, and opportunities. International Journal of Agricultural and Biological Engineering. 2018;**11**:32-44. DOI: 10.25165/ijabe.v11i4.4475

[19] Grimm J, Herzog K, Rist F, Kicherer A, Töpfer R, Steinhage V. An adaptable approach to automated visual detection of plant organs with applications in grapevine breeding. Biosystems Engineering. 2019;**183**:170-183. DOI: 10.1016/j.biosystemseng.2019.04.018

[20] Martinson TE, Reisch B. Grapevine Breeding and Genetics, Grapes 101, Appellation Cornell. USA: Cornell University; 2020. DOI: hdl.handle.net/1813/103808

[21] Wang Q, Li P, Hanania U, Sahar N, Mawassi M, Gafny R, et al. Improvement of Agrobacterium mediated transformation efficiency and transgenic plant regeneration of *Vitis vinifera* L. by optimizing selection regimes and utilizing cryopreserved cell suspensions. Plant Science. 2005;**168**:565-571. DOI: 10.1016/j.plantsci.2004.09.033

[22] Kikkert JK, Ali GS, Wallace PG, Reisch B, Reustle GM. Expression of fungal chitinase in *Vitis vinifera* L. 'Merlot' and 'Chardonnay' plants produced by biolistic information. Acta Horticulturae. 2000;**528**:299-306. DOI: 10.17660/ActaHortic.2000.528.41

[23] Franks T, He DG, Thomas MR. Regeneration of transgenic *Vitis vinifera* L. Sultana plants: Genotypic and phenotypic analysis. Molecular Breeding. 1998;**4**:321-333. DOI: 10.1023/A:1009673619456

[24] Iocco P, Franks T, Thomas MR. Genetic transformation of major vine grape cultivars of *Vitis vinifera* L. Transgenic Research. 2001;**10**:105-112. DOI: 10.1023/a:1008989610340

[25] Colby SM, Juncosa AM, Meredith CP. Cellular differences in Agrobacterium susceptibility and regenerate capacity restrict the development of transgenic grapevines. Journal of the American Society for Horticultural Science. 1991;**166**:356-361. DOI: 10.21273/JASHS.116.2.356

[26] Berres R, Otten L, Tinland B, Malgarini-Clog E, Walter B. Transformation of *Vitis* tissue by different strains of Agrobacterium tumefaciens containing T-6b gene. Plant Cell Reports. 1992;**11**:192-195. DOI: 10.1007/bf00232531

[27] Sabbadini S, Capriotti L, Limera C, Navacchi O, Tempesta G, Mezzetti B. A plant regeneration platform to apply new breeding techniques for improving disease resistance in grapevine rootstocks and cultivars. BIO Web of Conferences. 2019a;**12**:01019. DOI: 10.1051/bioconf/20191201019

[28] Sabbadini S, Capriotti L, Molesini B, Pandolfini T, Navacchi O, Limera C, et al.

Comparison of regeneration capacity and Agrobacterium-mediated cell transformation efficiency of different cultivars and rootstocks of *Vitis* spp. via organogenesis. Scientific Reports. 2019;**9**:582. DOI: 10.1038/s41598-018-37335-7

[29] Maillot P, Deglène-Benbrahim L, Walter B. Efficient somatic embryogenesis from meristematic explants in grapevine (*Vitis vinifera* L.) cv. Chardonnay: An improved protocol, Trees. 2016;**30**:1377-1387. DOI: 10.1007/s00468-016-1374-9

[30] Zhang XM, Wu YF, Li Z, Song CB, Wang XP. Advancements in plant regeneration and genetic transformation of grapevine (*Vitis* spp.). Journal of Integrative Agriculture. 2021;**20**(6):1407-1434. DOI: 10.1016/S2095-3119(20)63586-9

[31] Badouin H, Velt A, Gindraud F, et al. The wild grape genome sequence provides insights into the transition from dioecy to hermaphroditism during grape domestication. Genome Biology. 2020;**21**:223. DOI: 10.1186/s13059-020-02131-y

[32] Mortazavi A, Williams BA, McCue K, Schaeffer L, Wold B. Mapping and quantifying mammalian transcriptomes by RNA-seq. Nature Methods. 2008;**5**(7):621-628. DOI: 10.1038/nmeth.1226

[33] Gambino G, Dal Molin A, Boccacci P, Minio A, Chitarra W, Avanzato CG, et al. Whole-genome sequencing and SNV genotyping of 'Nebbiolo' (*Vitis vinifera* L.) clones. Scientific Reports. 2017;**7**(1):17294. DOI: 10.1038/s41598-017-17405-y

[34] Minio A, Massonnet M, Figueroa-Balderas R, Vondras AM, Blanco-Ulate B, Cantu D. Iso-Seq allows genome-independent transcriptome profiling of grape berry development. G3 (Bethesda, MD). 1 March 2019;**9**(3):755-767. DOI: 10.1534/ g3.118.201008

[35] Cantu D, Walker A. In: Cantu D, Walker MA, editors. The Grape Genome. Cham: Springer International Publishing (Compendium of Plant Genomes); 2019:367. DOI: 10.1007/978-3-030-18601-2

[36] Cheng B, Furtado A, Henry RJ. Long-read sequencing of the coffee bean transcriptome reveals the diversity of full-length transcripts. Gigascience. 2017;**6**(11):1-13. DOI: 10.1093/gigascience/gix086

[37] Kim MA, Rhee JS, Kim TH, Lee JS, Choi AY, Choi BS, et al. Alternative splicing profile and sex-preferential gene expression in the female and male Pacific *Abalone Haliotis discus hannai*. Genes. 2017;**8**(3):99. DOI: 10.3390/genes8030099

[38] Li J, Harata-Lee Y, Denton MD, Feng Q, Rathjen JR, Qu Z, et al. Long read reference genome-free reconstruction of a full-length transcriptome from *Astragalus membranaceus* reveals transcript variants involved in bioactive compound biosynthesis. Cell Discovery. 2017a;**3**:17031. DOI: 10.1038/celldisc.2017.31

[39] Zhu FY, Chen MX, Ye NH, Shi L, Ma KL, et al. Proteogenomic analysis reveals alternative splicing and translation as part of the abscisic acid response in *Arabidopsis* seedlings. The Plant Journal. 2017;**91**(3):518-533. DOI: 10.1111/tpj.13571

[40] Zou C, Karn A, Reisch B, et al. Haplotyping the *Vitis c*ollinear core genome with rhAmpSeq improves

marker transferability in a diverse genus. Nature Communications. 2020;**11**:413. DOI: 10.1038/s41467-019-14280-1

[41] Zaman QU, Li C, Cheng H, Hu Q. Genome editing opens a new era of genetic improvement in polyploid crops. Crop Journal. 2019;**7**(2):141-150. DOI: 10.1016/j.cj.2018.07.004

[42] Li G, Jain R, Chern M, Pham NT, Martin JA, et al. The sequences of 1504 mutants in the model rice cultivar Kitaake facilitate rapid functional genomic studies. Plant Cell. 2017b;**29**(6):1218-1231. DOI: 10.1105/tpc.17.00154

[43] Bhat AI, Rao GP. Characterization of plant viruses. New York, NY: Humana; 2020. pp. 479-489. DOI: 10.1007/978-1-0716-0334-5_48

[44] Golino DA, Fuchs M, Sim S, Farrar K, Martelli G. Improvement of grapevine planting stock through sanitary selection and pathogen elimination. In: Meng B, Martelli G, Golino D, Fuchs M, editors. Grapevine Viruses: Molecular Biology, Diagnostics and Management. Cham: Springer; 2017. DOI: 10.1007/978-3-319-57706-7_27

[45] Julião SA, Ribeiro CDV, Lopes JML, Matos EMD, Reis AC, et al. Induction of synthetic polyploids and assessment of genomic stability in *Lippia alba*. Frontiers in Plant Science. 2020;**11**:292. DOI: 10.3389/fpls.2020.00292

[46] Longa YL, Qiaoc F, Jianga XF, Congc HQ, Suna ML, Xu ZJ. Screening and analysis on the differentially expression genes between diploid and autotetraploid watermelon by using of digital gene expression profile. Brazilian Journal of Biology. 2019;**79**(2):180-190. DOI: 10.1590/1519-6984.174475

[47] Sattler MC, Carvalho CR, Clarindo WR. The polyploidy and its key role in plant breeding. Planta. 2016;**243**:281-296. DOI: 10.1007/s00425-015-2450-x

[48] Touchell DH, Palmer IE, Ranney TG. In vitro ploidy manipulation for crop improvement. Frontiers in Plant Science. 2020;**11**:722. DOI: 10.3389/fpls.2020.00722

[49] Kuliyev VM. The study of polyploid mutant forms of grapes. Cytology & Histology International Journal. 2020;**4**(1):1-6

[50] Xie X, Agüero CB, Wang Y, Walker MA. In vitro induction of tetraploids in *Vitis*X *Muscadinia* hybrids. Plant Cell, Tissue and Organ Culture. 2015;**122**:675-683. DOI: 10.1007/s11240-015-0801-8

[51] Sinski I, Dal Bosco D, Pierozzi NI, Maia JDG, Ritschel PS, Quecini V. Improving in vitro induction of autopolyploidy in grapevine seedless cultivars. Euphytica. 2014;**196**:299-311. DOI: 10.1007/s10681-013-1034-8

[52] Acanda Y, Martínez Ó, González MV, Prado MJ, Rey M. Highly efficient in vitro tetraploid plant production via colchicine treatment using embryogenic suspension cultures in grapevine (*Vitis vinifera* cv. Mencía). Plant Cell, Tissue and Organ Culture. 2015;**123**:547-555. DOI: 10.1007/s11240-015-0859-3

[53] Zlenko VA, Likhovskoy VV, Volynkin VA, Khvatkov PA, Vasylyk IA, Dolgov SV. Induction of in vitro somatic embryogenesis in grapes (*Vitis vinifera* L.) of domestic and foreign breeding. Biotechnology. 2017;**33**(5):35-44. DOI: 10.21519/02342758-2017-33-5-35-44

[54] Klimenko V, Lushchay E, Zlenko V. BIO Web Conferences. 2021;**34**:03002. DOI: 10.1051/bioconf/20213403002

[55] Guo Y, Zhao Y, Li K, Liu Z, Lin H, Guo X, et al. Embryo rescue of crosses between diploid and tetraploid grape cultivars and production of triploid plants. African Journal of Biotechnology. 2011;**10**(82):19005-19010. DOI: 10.5897/AJB11.977

[56] Li S, Li Z, Zhao Y, Zhao J, Luo Q, Wang Y. New disease-resistant, seedless grapes are developed using embryo rescue and molecular markers. 3 Biotech. 2020;**10**:4. DOI: 10.1007/s13205-019-1993-0

[57] Giancaspro A, Mazzeo A, Carlomagno A, Gadaleta A, Somma S, Ferrara G. Optimization of an in vitro embryo rescue protocol for breeding seedless table grapes (*Vitis vinifera* L.) in Italy. Horticulturae. 2021;**8**:121. DOI: 10.3390/horticulturae8020121

[58] Sun L, Zhang G, Yan A, Xu H. The study of triploid progenies crossed between different ploidy grapes. African Journal of. Biotechnology. 2011;**10**(32):5967-5971. DOI: 10.5897/AJB10.1850

[59] Wakana A, Hiramatsu M, Park SM, Hanada N, Fukudome I, Yasukochi K. Seed abortion in crosses between diploid and tetraploid grapes and recovery of triploid plants through embryo culture. Journal of the Faculty of Agriculture, Kyushu University. 2003;**48**(1):39-50. DOI: 10.5109/4524

[60] Motosugi H, Naruo T. Production of triploid grape rootstocks by embryo culture and their growth characteristics. Journal of the Japanese Society for Horticultural Science. 2003;**72**(2):107-115

[61] Yang DL, Li W, Li S, Yang XL, Wu JL, Cao ZY. In vitro embryo rescue culture of F1 progenies from crosses between diploid and tetraploid grape cultivars. Plant Growth Regulation. 2007;**51**(1):63-71. DOI: 10.1007/s10725-006-9148-9

[62] Park SM, Wakana A, Kim JH, Jeong CS. Male and female fertility in triploid grapes (*Vitis* complex) with special reference to the production of aneuploid plants. Vitis. 2002;**41**(1):11-20

[63] Wang X, Cheng Z, Zhi S, Xu F. Breeding triploid plants: A review. Czech Journal of Genetics and Plant Breeding. 2016;**52**:41-54. DOI: 10.17221/151/2015-CJGPB

[64] Shengjian Z, Zijuan G, Shuyun Z, Xinzhong Z, Licun Z. The breeding of the new triploid grape cultivar 'Hongbiao seedless' with large berries and high quality. Chinese Agricultural Science Bulletin. 2005;**21**:230-232

[65] Wu JH, Ferguson AR, Murray BG, Jia Y, Datson PM, Zhang J. Induced polyploidy dramatically increases the size and alters the shape of fruit in *Actinidia chinensis*. Annals of Botany. 2012;**109**:169-179. DOI: 10.1093/aob/mcr256

[66] Ruiz M, Oustric J, Santini J, Morillon R. Synthetic polyploidy in grafted crops. Frontiers in Plant Science. 2020;**11**:540894. DOI: 10.3389/fpls.2020.540894

[67] Pieterse CM, Leon-Reyes A, Van der Ent S, Van Wees SC. Networking by small molecule hormones in plant immunity. Nature Chemical Biology. 2009;**5**(5):308-316. DOI: 10.1038/nchembio.164

[68] Qiu W, Feechan A, Dry I. Current understanding of grapevine defense mechanisms against the biotrophic fungus (*Erysiphe necator*), the causal

agent of powdery mildew disease. Horticulture Research. 2015;**2**:15020. DOI: 10.1038/hortres.2015.20

[69] Atak A. Determination of downy mildew and powdery mildew resistance of some grape cultivars. South African Journal of Enology and Viticulture. 2017;**38**(1):11-17. DOI: 10.21548/38-1-671

[70] Gadoury DM, Cadle-Davidson L, Wilcox WF, Dry IB, Seem RC, Milgroom MG. Grapevine powdery mildew (*Erysiphe necator*): A fascinating system for the study of the biology, ecology and epidemiology of an obligate biotroph. Molecular Plant Pathology. 2012;**13**(1):1-16. DOI: 10.1111/j.1364-3703.2011.00728.x

[71] Pauquet J, Bouquet A, This P, Adam-Blondon AF. Establishment of a local map of AFLP markers around the powdery mildew resistance gene Run1 in grapevine and assessment of their usefulness for marker assisted selection. Theoretical and Applied Genetics. 2001;**103**(8):1201-1210. DOI: 10.1007/s001220100664

[72] Coleman C, Copetti D, Cipriani G, Hoffmann S, Kozma P, Kovacs L, et al. The powdery mildew resistance gene REN1 cosegregates with an NBS-LRR gene cluster in two Central Asian grapevines. BMC Genetics. 2009;**10**:89. DOI: 10.1186/1471-2156-10-89

[73] Hoffmann S, Di Gaspero G, Kovacs L, Howard S, Kiss E, Galbacs Z, et al. Resistance to *Erysiphe necator* in the grapevine 'Kishmish vatkana' is controlled by a single locus through restriction of hyphal growth. Theoretical and Applied Genetics. 2008;**116**(3):427-438. DOI: 10.1007/s00122-007-0680-4

[74] Hausmann L, Maul E, Ganesch A, Töpfer R. Overview of genetic loci for traits in grapevine and their integration into the VIVC database. Acta Horticulturae. 2019;**1248**:221-226. DOI: 10.17660/ActaHortic.2019.1248.32

[75] Kozma P, Kiss E, Hoffmann S, Galbacs Z, Dula T. Using the powdery mildew resistant *Muscadinia rotundifolia* and *Vitis vinifera* 'Kishmish vatkana' for breeding new cultivars. Acta Horticulturae. 2009;**827**:559-564. DOI: 10.17660/ActaHortic.2009.827.97

[76] Vezzulli S, Vecchione A, Stefanini M, Zulini L. Downy mildew resistance evaluation in 28 grapevine hybrids promising for breeding programs in Trentino region (Italy). European Journal of Plant Pathology. 2017;**150**:485-495. DOI: 10.1007/s10658-017-1298-2

[77] Vezzulli S, Malacarne G, Masuero D, Vecchione A, Dolzani C, Goremykin V, et al. The Rpv3-3 haplotype and stilbenoid induction mediate downy mildew resistance in a grapevine interspecific population. Frontiers in Plant Science. 2019;**10**:234. DOI: 10.3389/fpls.2019.00234

[78] Bove F, Savary S, Willocquet L, Rossi V. Designing a modelling structure for the grapevine downy mildew pathosystem. European Journal of Plant Pathology. 2020;**157**:251-268. DOI: 10.1007/s10658-020-01974-2

[79] Possamai T, Migliaro D, Gardiman M, Velasco R, De Nardi B. Rpv mediated defense responses in grapevine offspring resistant to *Plasmopara viticola*. Plants. 2020;**9**:781. DOI: 10.3390/plants9060781

[80] Eibach R, Zyprian E, Welter L, Töpfer R. The use of molecular markers for pyramiding resistance genes in grapevine breeding. Vitis. 2007;**46**:120-124

[81] Zini E, Dolzani C, Stefanini M, Gratl V, Bettinelli P, Nicolini D, et al.

R-loci arrangement versus downy and powdery mildew resistance level: A *Vitis* hybrid survey. International Journal of Molecular Sciences. 2019;**20**:3526. DOI: 10.3390/ijms2014

[82] Yıldırım Z, Atak A, Akkurt M. Determination of downy and powdery mildew resistance of some *Vitis* spp. Ciência e Técnica Vitivinícola. 2019;**34**(1):15-24. DOI: 10.1051/ctv/20193401015

[83] Shidfar M, Akkurt M, Atak A, Ergül A, Söylemezoğlu G. Evaluation of grapevine resistance to downy and powdery mildew in 'Regent' × 'Boğazkere' hybrid population segregating for resistance genes. Acta Scientiarum Polonorum Hortorum Cultus. 2019;**18**(1):181-188. DOI: 10.24326/asphc.2019.1.18

[84] Brown MV, Moore JN, Fenn P, McNew RW. Comparison of leaf disk, greenhouse, and field screening procedures for evaluation of grape seedlings for downy mildew resistance. HortScience. 1999;**34**:331-333. DOI: 10.21273/HORTSCI.34.2.331

[85] Boso S, Martinez MC, Unger S, Kassemeyer HH. Evaluation of foliar resistance to downy mildew in different cv. Albariño clones. Vitis. 2006;**4**:23-27

[86] Boso S, Alonso-Villaverde V, Santiago JL, Gago P, Dürrenberg M, Duggelin M, et al. Macro- and microscopic leaf characteristics of six grapevine genotypes (*Vitis* spp.) with different susceptibilities to grapevine downy mildew. Vitis. 2010;**49**:43-50

[87] Boso S, Alonso-Villaverde V, Gago P, Santiago JL, Martínez MC. Susceptibility to downy mildew (*Plasmopara viticola*) of different *Vitis* varieties. Crop Protection. 2014;**63**:26-35. DOI: 10.1016/j.cropro.2014.04.018

[88] Prajongjai T, Poolsawat O, Pornbungkerd P, Wongkaew S, Tantasawat PA. Evaluation of grapevines for resistance to downy mildew (*Plasmopara viticola*) under laboratory and field conditions. South African Journal of Enology and Viticulture. 2014;**35**:43-50. DOI: 10.21548/35-1-983

[89] Atak A, Akkurt M, Polat Z, Çelik H, Kahraman KA, Akgül DS, et al. Susceptibility to downy mildew (*Plasmopara viticola*) and Powdery mildew (*Erysiphe necator*) of different Vitis cultivars and genotypes. Ciência e Técnica Vitivinícola. 2017;**32**(1):23-32. DOI: 10.1051/ctv/20173201023

[90] Fischer BM, Salakhutdinov I, Akkurt M, Eibach R, Edwards KJ, Töpfer R, et al. Quantitative trait locus analysis of fungal disease resistance factors on a molecular map of grapevine. Theoretical and Applied Genetics. 2004;**108**:501-515. DOI: 10.1007/s00122-003-1445-3

[91] Welter LJ, Göktürk-Baydar N, Akkurt M, Maul E, Eibach R, Töpfer R, et al. Genetic mapping and localization of quantitative trait loci affecting fungal disease resistance and leaf morphology in grapevine (*Vitis vinifera* L). Molecular Breeding. 2007;**20**:359-374. DOI: 10.1007/s11032-007-9097-7

[92] Zendler D, Topfer R, Zyprian E. Confirmation and fine mapping of the resistance locus Ren9 from the grapevine cultivar 'Regent'. Plants. 2021;**10**(1):24. DOI: 10.3390/plants10010024

[93] Karn A, Zou C, Brooks S, Fresnedo-Ramírez J, Gabler F, Sun Q, et al. Discovery of the REN11 locus from *Vitis aestivalis* for stable resistance to grapevine powdery mildew in a family segregating for several unstable and tissue-specific quantitative

resistance loci. Frontiers in Plant Science. 2021;**12**:733899. DOI: 10.3389/fpls.2021.733899

[94] Dry I, Feechan A, Anderson C, Jermakow A, Bouquet A, Adam-Blondon A, et al. Molecular strategies to enhance the genetic resistance of grapevines to powdery mildew. Australian Journal of Grape and Wine Research. 2010;**16**:94-105. DOI: 10.1111/j.1755-0238.2009.00076.x

[95] Katula-Debreceni D, Lencsés AK, Szőke A, Veres A, Hoffmann S, Kozma PK, et al. Marker-assisted selection for two dominant powdery mildew resistance genes introgressed into a hybrid grape population. Scientia Horticulturae. 2010;**126**(4):448-453. DOI: 10.1016/j.scienta.2010.08.012

[96] Table of loci for traits in grapevine relevant for breeding and genetics. Update: April 30, 2021. Available from: https://www.vivc.de

[97] Cadle-Davidson LE. A perspective on breeding and implementing durable powdery mildew resistance. Acta Horticulturae. 2019;**1248**:541-548. DOI: 10.17660/ActaHortic.2019.1248.72

[98] Cavaco AR, Figueiredo J, Laureano G, Sousa Silva M, Matos AR, Figueiredo A. Subtilisin-like proteins and lipid signalling events: The missing links in grapevine resistance to *Plasmopara viticola*. Acta Horticulturae. 2019;**1248**:567-574. DOI: 10.17660/ActaHortic.2019.1248.76

[99] Romero-Perez AI, Lamuela-Raventos MR, Andres-Lacueva C, de La Torre-Boronat MC. Method for the quantitative extraction of resveratrol and piceid isomers in grape berry skins. Effect of powdery mildew on the stilbene content. Journal of Agricultural and Food Chemistry. 2001;**49**:210-215

[100] Atak A, Göksel Z, Çelik H. Relations between downy/powdery mildew diseases and some phenolic compounds in *Vitis* spp. Turkish Journal of Agriculture and Forestry. 2017;**2017**(41):69-81. DOI: 10.3906/tar-1610-61

[101] Atak A, Göksel Z, Yılmaz Y. Changes in major phenolic compounds of seeds, skins, and pulps from various *Vitis* spp. and the effect of powdery and downy mildew diseases on their levels in grape leaves. Plants. 2021;**10**:2554. DOI: 10.3390/plants10122554

[102] Ricciardi V, Marcianò D, Sargolzaei M, Fassolo EM, et al. Dissecting the susceptibility/resistance mechanism of *Vitis vinifera* for the future control of downy mildew. BIO Web Conferences. 2022;**44**:4002. DOI: 10.1051/bioconf/20224404002

[103] Ciubotaru RM, Franceschi P, Zulini L, Stefanini M, Škrab D, et al. Mono-locus and pyramided resistant grapevine cultivars reveal early putative biomarkers upon artificial inoculation with *Plasmopara viticola*. Frontiers in Plant Science. 2021;**12**:693887. DOI: 10.3389/fpls.2021.693887

[104] Gray DJ, Li ZT, Dhekney SA. Precision breeding of grapevine (*Vitis vinifera* L.) for improved traits. Plant Science. 2014;**228**:3-10. DOI: 10.1016/j.plantsci.2014.03.023

[105] Nirala NK, Das DK, Srivastava PS, Sopory SK, Upadhyaya KC. Expression of a rice chitinase gene enhances antifungal potential in transgenic grapevine (*Vitis vinifera* L.). Vitis. 2010;**49**(4):181-187

[106] Villano C, Aversano R. Towards grapevine (*Vitis vinifera* L.) mildews resistance: Molecular defence mechanisms and new breeding

technologies. Italus Hortus. 2020;**27**:1-17. DOI: 10.26353/j.itahort/2020.3.0117

[107] Ruiz-García L, Gago P, Martínez-Mora C, Santiago JL, Fernádez-López DJ, Martínez MC, et al. Evaluation and pre-selection of new grapevine genotypes resistant to downy and powdery mildew, obtained by cross-breeding programs in Spain. Frontiers in Plant Science. 2021;**12**:674510. DOI: 10.3389/fpls.2021.674510

[108] Lukšić K, Zdunić G, Hančević K, Mihaljević MJ, Mucalo A, Maul E, et al. Identification of powdery mildew resistance in wild grapevine (*Vitis vinifera* subsp. *sylvestris* Gmel Hegi) from Croatia and Bosnia and Herzegovina. Scientific Reports. 2022;**12**:2128. DOI: 10.1038/s41598-022-06037-6

[109] Pirrello C, Malacarne G, Moretto M, Lenzi L, Perazzolli M, Zeilmaker T, et al. Grapevine DMR6-1 is a candidate gene for susceptibility to downy mildew. Biomolecules. 2022;**12**:182. DOI: 10.3390/biom12020182

[110] Ollat N, Cookson SJ, Destrac-Irvine A, Lauvergeat V, et al. Grapevine adaptation to abiotic stress: An overview. Acta Horticulturae. 2019;**1248**:497-512. DOI: 10.17660/ActaHortic.2019.1248.68

[111] Gambetta GA, Herrera JC, Dayer S, Feng Q, Hochberg U, Castellarin SD. The physiology of drought stress in grapevine: Towards an integrative definition of drought tolerance. Journal of Experimental Botany. 2020;**71**(16):4658-4676. DOI: 10.1093/jxb/eraa245

[112] Marguerit E, Boury C, Manicki A, Donnart M, Butterlin G, Némorin A, et al. Genetic dissection of sex determinism, inflorescence morphology and downy mildew resistance in grapevine. Theoretical and Applied Genetics. 2009;**118**(7):1261-1278. DOI: 10.1007/s00122-009-0979-4

[113] Simonneau T, Lebon E, Coupel-Ledru A, Marguerit E, Rossdeutsch L, Ollat N. Adapting plant material to face water stress in vineyards: Which physiological targets for an optimal control of plant water status? OENO One. 2017;**51**(2):167-179. DOI: 10.20870/oeno-one.2017.51.2.1870

[114] Padgett-Johnson M, Williams LE, Walker MA. Vine water relations, gas exchange, and vegetative growth of seventeen *Vitis* species grown under irrigated and nonirrigated conditions in California. Journal of the American Society for Horticultural Science. 2003;**128**(2):269-276. DOI: 10.21273/JASHS.128.2.0269

[115] Chaves MM, Zarrouk O, Francisco R, Costa JM, Santos T, Regalado AP, et al. Grapevine under deficit irrigation: Hints from physiological and molecular data. Annals of Botany. 2010;**105**(5):661-676. DOI: 10.1093/aob/mcq030

[116] Serra I, Strever A, Myburgh PA, Deloire A. Review: The interaction between rootstocks and cultivars (*Vitis vinifera* L.) to enhance drought tolerance in grapevine. Australian Journal of Grape and Wine Research. 2014;**20**(1):1-14. DOI: 10.1111/ajgw.12054

[117] Tomás M, Medrano H, Escalona JM, Martorell S, Pou A, Ribas-Carbó M, et al. Variability of water use efficiency in grapevines. Environmental and Experimental Botany. 2014;**103**:148-157. DOI: 10.1016/j.envexpbot.2013.09.003

[118] Luchaire N, Rienth M, Romieu C, Nehe A, Chatbanyong R, Houel C, et al. Microvine: A new model to study grapevine growth and developmental

patterns and their responses to elevated temperature. American Journal of Enology and Viticulture. 2017;**68**(3): 283-292. DOI: 10.5344/ajev.2017.16066

[119] Torregrosa L, Bigard A, Doligez A, Lecourieux D, Rienth M, Luchaire N, et al. Developmental, molecular and genetic studies on the grapevine response to temperature open breeding strategies for adaptation to warming. OENO One. 2017;**51**(2):155-165. DOI: 10.20870/oeno-one.2017.51.2.1587

[120] Pons A, Allamy L, Schüttler A, Rauhut D, Thibon C, Darriet P. What is the expected impact of climate change on wine aroma compounds and their precursors in grape? OENO One. 2017;**51**(2):141-146. DOI: 10.20870/oeno-one.2017.51.2.1868

[121] Duchêne E, Butterlin G, Claudel P, Jaegli N. Consequences of elevated temperatures during ripening on the biosynthesis of monoterpenols in grape berries. In: Sustainable Grape and Wine Production in the Context of Climate Change – Climwine2016; Bordeaux, France, 10-13 April 2016

[122] Ollat N, Peccoux A, Papura D, Esmenjaud D, Marguerit E, et al. Rootstocks as a component of adaptation to environment. In: Geros H, Chaves MM, Medrano H, Delrot S, editors. Grapevine in a Changing Environment: A Molecular and Ecophysiological Perspective. 1st ed. Chichester, UK: John Wiley & Sons; 2016. pp. 68-108

[123] Bert PF, Bordenave L, Donnart M, Hévin C, Ollat N, Decroocq S. Mapping genetic loci for tolerance to lime-induced iron deficiency chlorosis in grapevine rootstocks (*Vitis* sp.). Theoretical and Applied Genetics. 2013;**126**(2):451-473. DOI: 10.1007/s00122-012-1993-5

[124] Henderson SW, Dunlevy JD, Wu Y, Blackmore DH, Walker RR, Edwards EJ, et al. Functional differences in transport properties of natural HKT1;1 variants influence shoot Na+ exclusion in grapevine rootstocks. The New Phytologist. 2018;**217**(3):1113-1127. DOI: 10.1111/nph.14888

[125] Gautier A, Cookson SJ, Lagalle L, Ollat N, Marguerit E. Influence of the three main genetic backgrounds of grapevine rootstocks on petiolar nutrient concentrations of the scion, with a focus on phosphorus. OENO One. 2020;**54**:1-13. DOI: 10.20870/oeno-one.2020.54.1.2458

[126] Chenu K, Van Oosterom EJ, McLean G, Deifel KS, Fletcher A, Geetika G, et al. Integrating modelling and phenotyping approaches to identify and screen complex traits: Transpiration efficiency in cereals. Journal of Experimental Botany. 2018;**69**(13):3181-3194. DOI: 10.1093/jxb/ery059

[127] Tardieu F, Simonneau T, Muller B. The physiological basis of drought tolerance in crop plants: A scenario-dependent probabilistic approach. Annual Review of Plant Biology. 2018;**69**(1):733-759. DOI: 10.1146/annurev-arplant-042817-040218

[128] Varshney RK, Thudi M, Pandey MK, Tardieu F, Ojiewo C, et al. Accelerating genetic gains in legumes for the development of prosperous smallholder agriculture: Integrating genomics, phenotyping, systems modelling and agronomy. Journal of Experimental Botany. 2018;**69**(13):3293-3312. DOI: 10.1093/jxb/ery088

[129] Akkurt M, Tahmaz H, Veziroglu S. Recent developments in seedless grapevine breeding. South African Journal of Enology

and Viticulture. 2019;**40**:2. DOI: 10.21548/42-2-3342

[130] Ledbetter CA, Ramming DW. Seedlessness in grapes. Horticultural Reviews. 1989;**11**:159-184

[131] Spiegel-Roy P, Sahar N, Baron J, Lavi U. In vitro culture and plant formation from grape cultivars with abortive ovules and seeds. Journal of the American Society for Horticultural Science. 1985;**110**:109-112

[132] Tian L, Wang Y. Seedless grape breeding for disease resistance by using embryo rescue. Vitis. 2008;**47**:15-19

[133] Tian L, Wang Y, Niu L, Tang D. Breeding of disease-resistant seedless grapes using Chinese wild *Vitis* spp. I. In vitro embryo rescue and plant development. Scientia Horticulturae. 2008;**117**:136-141. DOI: 10.1016/j.scienta.2008.03.024

[134] Ji W, Wang Y. Breeding for seedless grapes using Chinese wild *Vitis* spp. II. In vitro embryo rescue and plant development. Journal of the Science of Food and Agriculture. 2013;**93**:3870-3875. DOI: 10.1002/jsfa.6342

[135] Ji W, Li ZQ, Zhou Q, Yao WK, Wang YJ. Breeding new seedless grape by means of in vitro embryo rescue. Genetics and Molecular Research. 2013;**12**:859-869. DOI: 10.4238/2013.March.26.1

[136] Li T, Li Z, Yin X, Guo Y, Wang Y, Xu Y. Improved in vitro *Vitis vinifera* L. embryo development of F1 progeny of 'delight' × 'ruby seedless' using putrescine and marker-assisted selection. In Vitro Cellular & Developmental Biology-Plant. 2018;**54**:291-301. DOI: 10.1007/s1162 7-018-9895-0

[137] Emershad RL, Ramming DW, Serpe MD. In ovulo embryo development and plant formation from stenospermic genotypes of *Vitis vinifera*. American Journal of Botany. 1989;**76**:397-402

[138] Pommer CV, Ramming DW, Emershad RL. Influence of grape genotype, ripening season, seed trace size, and culture date on in ovule embryo development and plant formation. Bragantia. 1995;**54**:237-249

[139] Bouquet A, Danglot Y. Inheritance of seedlessness in grapevine (*Vitis vinifera* L.). Vitis. 1996;**35**:35-42

[140] Lahogue F, This P, Bouquet A. Identification of a codominant scar marker linked to the seedlessness character in grapevine. Theoretical and Applied Genetics. 1998;**97**:950-959. DOI: 10.1007/s001220050 976

[141] Pellerone FI, Edwards KJ, Thomas MR. Grapevine microsatellite repeats: Isolation, characterisation and use for genotyping of grape germplasm from Southern Italy. Vitis. 2001;**40**:179-186

[142] Mejía N, Soto B, Guerrero M, et al. Molecular, genetic and transcriptional evidence for a role of VvAGL11 in stenospermocarpic seedless in grapevine. BMC Plant Biology. 2011;**11**:57. DOI: 10.1186/1471-2229-11-57

[143] Bergamini C, Cardone MF, Anaclerio A, Perniola R, Pichierri, et al. Validation assay of p3_VvAGL11 marker in a wide range of genetic background for early selection of stenospermocarpy in *Vitis vinifera* L. Molecular Biotechnology. 2013;**54**(3):1021-1030. DOI: 10.1007/s12033-013-9654-8

[144] Bennici S, Guardo MD, Distefano G, Malfa SL, et al. Influence of the genetic background on the performance of molecular markers linked to seedlessness in table grapes. Scientia Horticulturae.

2019;**252**:316-323. DOI: 10.1016/j.scienta.2019.03.060

[145] Ocarez N, Mejía N. Suppression of the D-class MADS-box AGL11 gene triggers seedlessness in fleshy fruits. Plant Cell Reports. 2016;**35**:239-254. DOI: 10.1007/s00299-015-1882-x

[146] Malabarba J, Buffon V, Mariath JEA, Maraschin FS, Margis-Pinheiro M, Pasquali G, et al. Manipulation of VviAGL11 expression changes the seed content in grapevine (*Vitis vinifera* L.). Plant Science. 2018;**269**:126-135. DOI: 10.1016/j.plantsci.2018.01.013

[147] Royo C, Torres-Perez R, Mauri N, Diestro N, et al. The major origin of seedless grapes is associated with a missense mutation in the MADS-box gene VviAGL11. Plant Physiology. 2018;**177**:1234-1253. DOI: 10.1104/pp.18.00259

[148] Mejía N, Hinrichsen P. A new, highly assertive scar marker potentially useful to assist selection for seedlessness in table grape breeding. Acta Horticulturae. 2003;**603**:559-564

[149] Fatahi R, Zamani Z, Ebadi A, Mehlenbacher SA. The inheritance of seedless SCC8-SCAR and SSRs loci alleles in progeny of 'Muscat Hamburg' x 'Bidane Quermez' grapes. Leuven, Belgium: International Society for Horticultural Science (ISHS); 2004. pp. 329-335. DOI: 10.17660/actahortic.2004.652.42

[150] Conner PJ, Gunawan G, Clark JR. Characterization of the p3-VvAGL11 marker for stenospermocarpic seedlessness in *Euvitis* × *Muscadinia* grape hybrid progenies. Journal of the American Society for Horticultural Science. 2018;**143**:167-172. DOI: 10.21273/jashs 04366-18

[151] Adam-Blondon AF, Lahogue-Esnault F, Bouquet A, et al. Usefulness of two SCAR markers for marker-assisted selection of seedless grapevine cultivars. Vitis. 2001;**40**(3):147-156

[152] Wang YJ, Lamikanra O. Application and synthesis on the DNA probe for detecting seedless genes in grapevine. Journal of Northwest Sci-Tech University of Agriculture and Forestry. 2002;**30**:42-46

[153] Akkurt M, Welter L, Maul E, Töpfer R, Zyprian E. Development of SCAR markers linked to powdery mildew (Uncinula necator) resistance in grapevine (*Vitis vinifera* L. and *Vitis* sp.). Molecular Breeding. 2007;**19**:103-111. DOI: 10.1007/s1103 2-006-9047-9

[154] Kim G et al. Identification of AFLP and RAPD markers linked to anthracnose resistance in grapes and their conversion to SCAR markers. Plant Breeding. 2008;**127**:418-423. DOI: 10.1111/j.1439-0523.2008.01488.x

[155] Zhang Y, Zhang J, Wang Y. Screening the RAPD markers linked to the gene resistant to downy mildew in Chinese wild species of *Vitis*. Journal of Fruit Science. 2008;**25**:816-820

[156] Zhang J, Wang Y, Wang Y, Zhang Y. Marker-assisted selection for hybrids from cross between seedless and disease-resistant grape. Journal of Northeast Agricultural University. 2010;**41**:55-63

[157] Migliaro D, De Lorenzis G, Di Lorenzo GS, De Nardi B, Gardiman M, Failla O, et al. Extensive genotyping of a large collection of rootstocks, population structure analysis and core collection extrapolation for new breeding programs. Acta Horticulturae. 2019;**1248**:301-304. DOI: 10.17660/ActaHortic.2019.1248.43

[158] Bianchi D, Caramanico L, Grossi D, Brancadoro L, Lorenzis GD. How do novel M-rootstock (*Vitis* Spp.) genotypes cope with drought? Plants. 2020;**9**:1385. DOI: 10.3390/plants9101385

[159] Gautier A, Cookson SJ, Hevin C, Vivin P, Lauvergeat V, Mollier A. Phosphorus acquisition efficiency and phosphorus remobilization mediate genotype-specific differences in shoot phosphorus content in grapevine. Tree Physiology. 2018;**38**(11):1742-1751. DOI: 10.1093/treephys/tpy074

[160] Dalbó MA, Souza ALK. Rootstock breeding for resistance to grapevine decline and dieback in southern Brazil. Acta Horticulturae. 2019;**1248**:123-128. DOI: 10.17660/ActaHortic.2019.1248.18

[161] Walker MA, Lund K, Agüero C, Riaz S, Fort K, Heinitz C, et al. Breeding grape rootstocks for resistance to phylloxera and nematodes—It's not always easy. Acta Horticulturae. 2014;**1045**:89-97. DOI: 10.17660/ActaHortic.2014.1045.12

IntechOpen