

Plums: Their potential in cultivation, breeding, and use

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Abstract: Plums are one of the most important and most overlooked fruits. Their nutritional value, composition, antioxidant potential, and vitamin content place them at the forefront of the food industry. Their potential is so great that plums are one of the fruits being considered for space travel. Prunes are not just a hot topic for astronauts. The possibility of growing plums in a cultivation box at reduced or zero gravity has also been studied. The sharka virus (*Plum pox virus*) is responsible for the major economic losses worldwide. Efforts are being made to develop the most effective way to control the spread of the virus between trees, as there is still no reliable treatment against this disease. The main vectors of transmission in the orchards are aphids and grafting of infected material. Consistent control and testing of the health of propagating material can reduce the percentage of infection by plant material. Therefore, major efforts have been made to develop effective aphid control strategies to in both conventional and organic production systems. Hand in hand with the development of chemical treatments goes the breeding of new plum varieties that combine natural resistance or tolerance to sharka and the required high value of the fruit for the consumer. The trees themselves have not been able to develop a natural immunity to the disease, but a variety with the sharka coat protein encoded has been developed through genetic modification. This variety has shown a high level of resistance. At present, the use, development, and cultivation of GMO plants is under very strict control, and large-scale production is not possible, but in the future, these mutants are likely to be very interesting breeding material.

Keywords: genetic resources; *Prunus domestica* L.; *Plum pox virus*; SSR markers

HISTORY OF *PRUNUS*

Historically, the genus *Prunus* was widespread in temperate regions of the Northern Hemisphere and in subtropical areas of Asia, Africa, North America, and Australia. During the Eocene period, 35–60 million years ago, plants were distributed in different regions of the original continents, with different adaptations to the respective climatic conditions (Chin et al. 2014). There was also a natural migration of flora and mixing of plants. As a result, different species and varieties exist. With the emergence of more organised groups

of our ancestors, plants were used as an important source of food. According to Chin et al. (2014), discoveries suggest that plums originally appeared in the territory of ancient China (Figure 1), and from there have spread to Europe (*Prunus domestica*), to northern Asia, and then to the Americas (*Prunus americana*). Discovered stones of plum fruit have shown that the *Prunus* tree was widespread in the Neolithic period around 5 000 B.C. in Central and Eastern Europe. They have been planted and domesticated since the Neolithic period. Plums became an important part of human life (Zhebentyayeva et al. 2019). Written evidence

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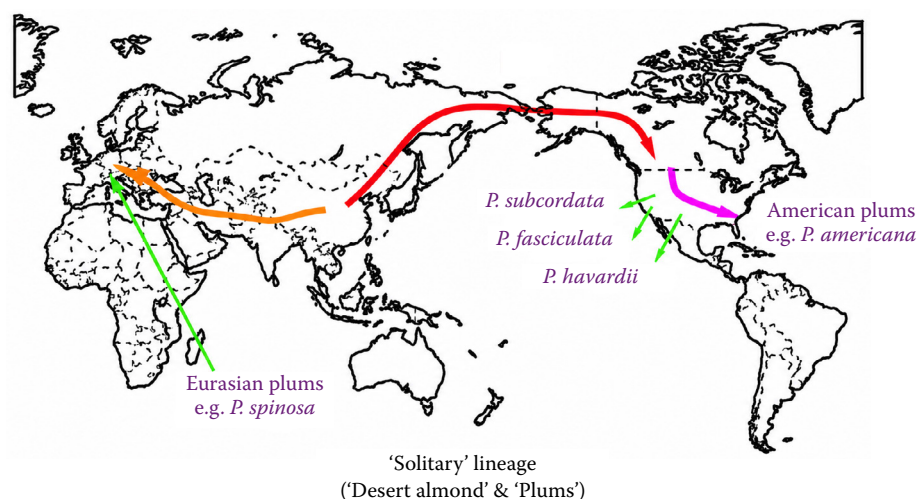


Figure 1. Historical biogeographic tracks of *Prunus*; predicted route of spread of plum trees together with almond trees to Europe and America (Chin et al. 2014)

from ancient Rome and Greece has shown that plums were very popular. Ancient authors Herodotus (484–430 B.C.) and Xenophon (431–355 B.C.) mentioned that there were many cherry plum trees in the mountains planted by different nations like the Scythians and the Armenians. It indicates that plums were very popular around the world. The first mention of the European type of plums was in Archilochus's Pollux (7th century B.C.). For centuries in modern history, plums were very important, particularly in all parts of Europe. More about the history of plum historical development can be found in Faust et al. (1998). The tradition of growing plums and breeding new varieties still continues. Human knowledge has reached a point where we are no longer dependent on natural, uncontrolled pollination but can intervene in it and select parental genotypes according to our requirements. The importance of breeding is visible in each fruit species, including plums (Noleppa 2016). The object of this review is to uncover the progress and objectives in European plum breeding.

BREEDING OF PLUMS

The European plum is generally better adapted to European weather conditions than the Japanese variety. The overall composition of the plum depends on the variety. When creating a new variety, it is necessary to find suitable parents to combine the best characteristics of the varieties. The main

objectives of breeding programs are various sensoric parameters of fruits or tree abiotic resistance. The most common requirements for fresh market or processing are large, dark blue fruits that are sweet and rich in flavour. Another breeding goal is to extend the harvest period to a larger part of the year. Plums cannot be stored for a long time, so it is necessary to have very early and very late ripening fruit. It is also very important for farmers to have regular production. In larger orchards, there is no time for repeated harvests. If trees are not able to produce mature fruit at the same time of the year, the chosen genotype is not suitable for larger production. Regular fruit production is important to growers. European-type cultivars are mostly self-pollinating, and due to the frequent presence of large numbers of bee colonies, pollination and cross-pollination between trees is common in Europe. In many countries, breeders focus on different plum traits. Table 1 gives an overview of plum breeding institutions and their objectives in Europe (Butac 2020). Another important role of the breeding stations is the evaluation of new plum varieties. Each variety responds differently to the local conditions, and the characteristics of the fruit depend on the region where it is grown. It is therefore necessary to collect data, compare it with traditional varieties and share it with the surrounding fruit growers. These comparative studies have been conducted, for example, in Lithuania, Iran, the Czech Republic, and other European Union countries (Ganji Moghaddam et al. 2011;

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Table 1. List of breeding institutes in Europe (Butac 2020)

Country	Institute	Objectives
Romania	Research Institute for Fruit Growing, Pitesti Fruit Growing Research Station, Valcea Research Station for Fruit Growing, Bistrita	– improvement of old cvs. Tuleu gras, Grase romanesti, Vinete romanesti – fruit quality – PPV resistance – ripening season extension – self-fertility
Serbia	Fruit Research Institute, Cacak Faculty of Agronomy, Cacak	– improvement of old cv. Pozegača – fruit size and quality – ripening time – resistance to PPV – productivity
Germany	Hochschule Geisenheim University University of Hohenheim, Stuttgart	– fruit quality (Toptaste, Tophit etc.) – PPV resistance by hypersensitivity
France	INRA, Bordeaux R. Bernhard, R. Renaud	– fruit quality – PPV resistance by transgenic plants
Italy	University of Bologna University of Firenze University of Forli Private program	Japanese and European plum breeding program: – fruit quality – fresh consumption – resistance to PPV
United Kingdom	East Malling Research Station, Kent	– late blooming – frost resistance – PPV resistance
Bulgaria	Fruit Growing Institute, Dryanovo Fruit Growing Institute, Troyan Fruit Growing Institute, Kyustendil Fruit Growing Institute, Plovdiv	– late blooming – extended ripening period – fruit quality – resistance to PPV
Latvia	Latvia State Institute of Fruit Growing, Dobeles	– winter hardiness – low vigour – precocity – fruit quality – self-fertility – early ripening
Republic of Moldova	Research Institute for Horticulture and Alimentary Technologies, Chisinau	– frost resistance – fruit quality
Belarus	Institute for Fruit Growing, Minsk	– fruit quality – frost resistance
Czech Republic	Research and Breeding Institute of Pomology, Holovousy	– fruit quality – sharka tolerance
Poland	Research Institute of Horticulture, Skierniewice	– fruit quality – productivity – PPV resistance
Russia	North-Caucasus Zonal Horticulture and Viticulture Research Institute, Krasnodar Krymsk Experiment Breeding Station Krymsk Far East Experiment Station, Pavlovsk St. Petersburg Maicop Experiment Station, Krasnodar Region Volgograd Experiment Station, Krasnoslobodsk	– winter hardiness – fruit quality – productivity
Sweden	University of Agricultural Sciences, Balsgard	– short period of vegetation – fruit quality
Norway	Ullensvang Research Centre Division Njos, Lofthus	– fruit quality – good storage
Hungary	Hungarian University of Agriculture and Life Sciences, Institute of Horticultural Sciences, Fruit Growing Research Institute, Research Station of Cegléd	– fruit quality – processing

Blažek, Pištěková 2012; Grävite, Kaufmane 2017; Wolf et al. 2020).

COMPOSITION OF PLUMS

Evolution and adaptation to changing conditions over the years have developed a unique nutritional fruit composition. Plum is one of the indispensable fruits of our life, and it is widely grown for the fresh market. The majority of the plum fruit species are important components of the human diet. The World Health Organisation recommended eating more than about 400 g of fruits or vegetables per day (WHO 2023). Stone fruits such as plums are one of the most common types of fruits that people can find in their stores. The health-promoting properties of the stone fruits are mainly due to vitamins A, C, and E, fibre, and a large number of secondary metabolites, such as flavonoids, anthocyanins, and hydroxycinnamates. These are naturally occurring in plums and are key components not only in health, but also in sensory attributes such as taste, aroma, and colour (Popovic et al. 2009). A wide range of beneficial health effects, such as protection against cardiovascular disease, digestive disorders, and diabetes, have been demonstrated (Kayano et al. 2003, 2004; Igwe, Charlton 2016; Liu et al. 2021). The levels of selected dietary components, fibre, and ions have been tested in different plum varieties. The studies showed a number of phenolic compounds, total antioxidant activity, pectin and total protein content, and the content of biogenic elements (phosphorus, potassium, calcium, magnesium, and sodium) contained in each variety. The phenolic compounds ranged from 2.27 to 4.95 mg/g FM gallic acid equivalents (GAE). Similar results were also obtained for the total antioxidant activity. The resulting activities ranged from 2.58 to 6.04 mg abscisic acid equivalents per gram of FM. The highest content of phenolic compounds and antioxidant activity was found in the cultivar 'Domaci velkoploda', and the lowest in the cultivar 'Vlaska'. The highest pectin content was determined in variety 'Svestka domaci', 35.4 ± 1.7 g/kg FM, and the lowest in the variety 'Durancie', 21.7 ± 1.4 g/kg FM. The highest total protein content (7.9 ± 0.6 g/kg FM) was observed in the variety 'Kirkeho'. The lowest was then found in the variety 'Wangenheimova' (6.3 ± 0.6 g/kg FM). The highest content of phosphorus ($369.5 \pm$

12.7 mg/kg FM), potassium ($3\,976.3 \pm 60.2$ mg per kg FM), and sodium (21.4 ± 1.1 mg/kg FM) has variety 'Kulovacka'. For more information, see Rop et al. (2009). The benefits and nutritional values of plums have also been demonstrated by other authors (Gill et al. 2019; Hussain et al. 2021; Cetin, Saraçoglu 2023). Another study investigated the nutrient, fibre, and biogenic element content of plums (Mehta et al. 2014). These were prunes purchased from a local store in India, so the variety is unknown. The total content of phenolics, dietary fibre, protein, and biogenic elements were measured. Compared to a previous study focusing on plum fruit composition, an increase in phenolic content of approximately 5.2 mg/g GAE was found. Due to the drying process, an increase in protein concentration to fourfold values can be observed, while the fibre and biogenic element contents are at a similar level. Differences are also in the content of these substances across varieties and types of plums. Japanese plums have a different composition than the Czech plums. Similar results were published by Igwe and Charlton (2016). Plums are also an important source of natural antioxidants (Kayano et al. 2004; Kimura et al. 2008). Flavonoids are one of the major groups of secondary metabolites. The initial increase in gene transcript levels of the early biosynthetic genes of flavonoids occurs in the early stages of fruit development. In contrast, another group of enzymes has an increased transcription rate during fruit ripening. Enzymes from different families, such as 2-oxosulutarate-dependent dioxygenase, cytochromes P450, glucosyltransferases, and lyases, are involved in their formation. Flavonoids participate in antioxidant processes in cells or in the colouration of flowers and their increased attractiveness to pollinators. A large group of flavonoids are the anthocyanins, which are derived from L-phenylalanine. In addition, a number of different rutinoside-derived anthocyanins, such as cyanidin-3-rutinoside, peonidin-3-rutinoside, and cyanidin-3-glucoside, are contained in plums. Anthocyanins are often responsible for the blue colouration of the fruit, suggesting that yellow-coloured plum varieties have a marked decrease in anthocyanin content (Ruiz et al. 2011). This reduction was also found by Kim et al. (2003). The original colour of the skin is green. Chlorophyll degradation occurs, and anthocyanins accumulate as the fruit ripens, which is accompanied by a colour change

GENETIC ANALYSIS AND MANIPULATION

genus contains about 400–430 species, initially divided into 5 subgenera: *Amygdalus* (peaches and almonds), *Cerasus* (sweet and tart cherries), *Prunus* (plums), *Laurocerasus* (evergreen laurel cherries), and *Padus* (bird cherries). The first reported plums were plum *P. domestica* and other Eurasian plum species such as *P. cerasifera* or *P. spinosa*. The European plum is a polymorphic allopolyploid (hexaploid) species ($2n = 6x = 48$) while the Japanese plum is only a diploid ($2n = 2x = 16$). As a result, alleles coding for important traits are stored in plums in multiple copies. The possibility of genome analysis is a very useful tool for verifying many characteristics of evolving hybrids. Modern methods allow a deep insight into the breeding process. Therefore, it is not possible to simply ‘switch off’ a gene using genetic engineering methods, because the silenced gene can be replaced. The most common method of transformation is *Agrobacterium*-mediated transformation. This uses the bacterium *Agrobacterium tumefaciens*, which is capable of transforming various plant species. The original transformation and regeneration protocol was developed in 1991 (Mante et al. 1991). Meanwhile, the success rate of transformation by modifications has increased up to 42%, and it is possible to obtain a self-rooted transgenic plant in the greenhouse in about 6 months (Gonzalez Padilla et al. 2003; Petri et al. 2008). Nevertheless, there are several varieties that have been created as a result of genetic mutation. One of the best-known variety, created by *Agrobacterium*-mediated transformation is ‘Honeysweet’, which contains an inserted gene encoding the sharka virus coat protein (PPV-CP) (Scorza et al. 2013; Callahan et al. 2021). This resulted in a clone that is highly resistant to PPV transmitted by aphids or grafting of infected material. It was found that although a larger amount of RNA encoding the PPV envelope protein was detected in the nuclei, very small amounts were detected in the cytoplasm. A post-transcriptional silencing system of PPV-CP RNA transcription was developed in the cells. This is a sophisticated siRNA (short interfering RNA)-based cellular protection system that provides repression of unwanted transcripts. The sequence for rapid identification was incorporated into the coat protein sequence cassette. Expression of the *uidA* gene (GUS) is used to reveal the resistance gene in ‘Honeysweet’ progeny (Scorza et al. 2016). It is

also used to check for potential unwanted spread of genetic material outside of isolated areas. The resistance of ‘Honeysweet’ was studied by Ravelonandro et al. (1997), who found in greenhouse experiments that this cultivar had extremely high resistance. The research moved to Europe because in the USA, where the original experiment was conducted, it was not allowed to work with PPV under field conditions. The experiments were conducted for almost 20 years in Europe, where the trees were exposed to high natural aphid-induced infection pressure. Then 99 trees of the ‘Honeysweet’ variety were tested, and none of them showed infection, while the susceptible control varieties were all infected. At the same time, the targeted infection of ‘Honeysweet’ was carried out by grafting infected material. Subsequent infection was detected only in tissues localised around the graft, but there was no systemic infection of the entire tree (Polák et al. 2012). Many studies have compared the fruit of ‘Honeysweet’ plum trees with commonly available varieties (Krška et al. 2017; Polák et al. 2017; Zagrai et al. 2017; Bobiš et al. 2019; Callahan et al. 2019). For example, Callahan et al. (2019) compared the fruit of this cultivar with ‘Jojo’, ‘Stanley’, ‘Toptaste’, ‘Haganta’, ‘Čačanska najbolja’, and others. The trees from which the samples were collected grew in various countries, including the Czech Republic, Spain, Poland, USA, Canada, Serbia, Bulgaria, Romania, Italy, Germany, France, and Poland. The following components were measured: starch, carbohydrates, calories, dietary fibre, moisture, ash, antioxidant activity, carotenes, acidity, acids, sugars, sugar alcohols, vitamins, total phenolics, Fe, Ca, Mg, Na, and K. The result of this comparison was that the fruit of the ‘Honeysweet’ cultivar was not as good as the commercially available plum varieties. The main factor in this study was the high level of acidity, which is not acceptable in the market. However, a different conclusion was reached by Polák et al. (2017), who compared the fruit of the ‘Honeysweet’ cultivar with the ‘Stanley’ and ‘Domáci velkoplodá’ varieties over a long period of time. The trees were grown in an orchard that was under high and permanent PPV pressure, and pomological data were collected over a period of 12 years. The result of this study was that the fruit of the cultivar ‘Honeysweet’ was of comparable quality to the other cultivars. Thus, this cultivar seems

to be a very interesting breeding material for the future, in the moment when the laws on the handling of GMO material are adjusted.

Genetic analysis focusing on the single sequence repeats (SSR) marker can be used to characterise an unknown hybrid resulting from open pollination or can serve as a verification mechanism to determine whether the hybrid is indeed the offspring of the selected parental combination (Gaši et al. 2020; Meland et al. 2020; Antanynienė et al. 2023). SSR markers are short, periodically repeated regions in the genome. The SSR marker motif is usually 1–6 bp in length. Genotyping is based on specific DNA primers that are designed to amplify SSR repeat regions (Zhao et al. 2023). In plants, an SSR is found approximately once every 50 kbp of genomic sequence. SSRs can be located in genes as well as in intergenic regions or non-coding regions and occur in multiple repeats across the genome. It is the number of these stretches in the genome that is unique to each plant. Modern techniques are based on the visualisation of DNA products by gel chromatography. The discovery of SSRs dates back to 1984. Since then, the search for SSR-based molecular markers has expanded to a very wide range of crop species such as wheat (Song et al. 2005), rice (McCouch et al. 2002), soybean (Hwang et al. 2009), cucumber (Danin-Poleg et al. 2001), sunflower (Tang et al. 2002), and fruit trees such as apples (Liebhard et al. 2002), peanuts (Peng et al. 2016), and plum (Spann et al. 2010). Nybom et al. (2020) established 9 SSR markers for plum (Table 2). These markers have been approved by the European Cooperative Program on Plant Genetic Resources (ECPGR; www.ecpgr.cgiar.org) and are recommended as a standard set for genotyping European plum accessions. ECPGR aims to ensure the long-term conservation of important genotypes in Europe and to maintain them for various needs, e.g. in plant breeding. One of the objectives is the careful selection of unique and well-documented genotypes with valuable traits of European origin or importance for Europe. The second task is to assess the variability between genotypes and to investigate possible subgroups caused, e.g., due to geographical differentiation. For fruit tree species such as pear (*Pyrus communis*) and bird cherry (*Prunus avium*), sets of recommended SSR loci have been identified and published by the ECPGR (Clarke, Tobutt 2009; Evans et al. 2009; Nybom et al. 2020).

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PLUM POX VIRUS AND TREES

The main breeding objectives are to produce nutritious plums with regular and abundant fruitfulness and no loss of yield due to disease. The most important pathogen of plum trees is the *Plum pox virus* (PPV), which causes sharka disease. It is a filamentous virus that reaches 700–800 nm in length and 13–15 nm in width. It belongs to the genus *Potyvirus* and the family *Potyviridae*. Viruses of this family infect a wide range of herbs and trees (James et al. 2013). It is the whole organism virus that attacks and causes significant yield losses. In an orchard, infection of one or more trees is most commonly caused by grafting of the infectious material (Blazek, Karesova 2004; Zagrai et al. 2010). These trees become the epicentres of infection for surrounding trees and subsequently for the entire orchard. Virus particles are most often transmitted from the infected tree via the insect vector aphid (Hazir et al. 2021). At least 20 species have been recorded as transmitters of PPV, including the most common aphid species such as *Brachycaudus cardui*, *Brachycaudus helichrysi*, *Myzus persicae* and *Phorodon humuli* (Garcia, Cambra 2007; Levy et al. 2000). Aphids can also spread the infection from neighbouring orchards. Therefore, orchard control is extremely important.

When an infestation is detected, early suppression and elimination of the affected trees is the only effective method of controlling the disease for the time being. Another possible prevention is to target the vectors. It must be remembered that the orchard is designed to produce fruit for profit. Therefore, it is not possible to use pesticides immediately at the first detection, as this is financially expensive, risky, and the indiscriminate use of pesticides can lead to the destruction of the soil and eventually the death of the trees. A compromise has to be found (Simon et al. 2011; Herz et al. 2019). However, insecticides alone cannot be relied upon to control vectors. They help to respond to vector infestations, not to control the infection. If the orchard is not adequately protected against the spread of viral disease, significant losses occur because there is no effective defence against this disease (Espinoza et al. 2021). Thus, a mixture of different orchard management strategies has been applied (Rimbaud et al. 2015). On the other hand, several species of plum trees and sharka can coexist. Trees that do not recognise the infection, allowing the virus to multiply and attack all available tissues, die. These susceptible trees have no defence against the virus disease, produce poor quality fruit and are destroyed (Rodamilans et al. 2014). However, Polák (2006) described several ways how the plum

Table 2. Simple sequence repeat (SSR) loci, DNA sequences, references and annealing temperature of the nine primer pairs selected by the European Cooperative Program on Plant Genetic Resources *Prunus* working group for the assessment of plum accessions (Nybom et al. 2020)

Locus	DNA sequence	Reference	Temp. (°C)
CPSCT026	3'-TCTCACACGCTTTTCGTCAAC-5' 3'-AAAAAGCCAAAAGGGGTGT-5'	Mnejja et al. (2004)	46
BPPCT034	3'-CTACCTGAAATAAGCAGAGCCAT-5' 3'-CAATGGAGAATGGGGTGC-5'	Dirlewanger et al. (2002)	56
UDP96-005	3'-GTAACGCTCGCTACCACAAA-5' 3'-CCTGCATATCACCACCCAG-5'	Cipriani et al. (1999)	56
BPPCT014	3'-TTGTCTGCCTCTCATCTTAACC-5' 3'-CATCGCAGAGAACTGAGAGC-5'	Dirlewanger et al. (2002)	58
BPPCT039	3'-ATTACGTACCCTAAAGCTTCTGC-5' 3'-GATGTCATGAAGATTGGAGAGG-5'	Dirlewanger et al. (2002)	58
BPPCT040	3'-ATGAGGACGTGTCTGAATGG-5' 3'-AGCCAAACCCCTCTTATACG-5'	Dirlewanger et al. (2002)	58
UDP98-407	3'-AGCGGCAGGCTAAATATCAA-5' 3'-AATCGCCGATCAAAGCAAC-5'	Cipriani et al. (1999)	58
PacA33	3'-TCAGTCTCATCCTGCATACG-5' 3'-CATGTGGCTCAAGGATCAAA-5'	Decroocq et al. (2003)	58
BPPCT007	3'-TCATTGCTCGTCATCAGC-5' 3'-CAGATTTCTGAAGTTAGCGGTA-5'	Dirlewanger et al. (2002)	60

trees can avoid the effects of the disease and their degrees can be divided into 4 further categories:

- Tolerance: Plum trees are affected by a virus, but this disease does not have a significant effect on the yield and viability of the tree. The problem is that such tolerant trees are epicentres for the transmission of virus particles throughout the orchard.
- Resistance: A mostly quantitative cellular defence response to infection based on the production of resistance genes. Virus spread is very limited and slow.
- Immunity: The plant own response to the presence of a virus particle and the production of antiviral substances. In trees infected with the sharka virus, the virus particles do not multiply and do not spread in the plant.
- Hypersensitivity: The presence of a virus particle triggers defence mechanisms that lead to controlled cell death around the site where the virus is detected. The virus is then contained within the dead cells, eliminating the possibility of spreading throughout the plant and infecting a greater number of cells.

Plants have a limited energy pool, and super-resistant varieties generally produce small fruits that do not reach the required eating quality, because the energy used for defence is not available when the fruit ripens (Usenik et al. 2009). This energy limitation has been demonstrated with *A. thaliana*. An overexpressing mutant of salicylic acid had a reduced leaf rosette (Janda et al. 2014; Pluhařová et al. 2019). On the other hand, tasty, large fruits of high consumption quality grow on trees generally susceptible to the sharka virus. Modern breeding tries to find a compromise between these two aspects. At present, tolerant varieties are currently the best option ('Gabrovská', 'Durancie', 'Čačanska leptotica', etc.) because, despite the attack of the sharka virus on the orchard, there is no large yield loss, but the virus disease spreads even on intolerant varieties. These are all very widespread cultivars, and so there seems to be that there is no reason to consider other options (Clemente-Moreno et al. 2014). But the problem is that they do not cover all sectors of the plum industry and other widely used cultivars, due to their unique characteristics ('President', 'Pozegaca' or 'Elena'), then suffer from the disease onslaught spread only by the tolerant cultivars (Malinowski et al. 2013). Another direction in which crossing is headed is the use of the

hypersensitive defence response to eliminate virus particles. When the virus is detected in the tissue, an extensive signalling cascade is activated, leading to the death of surrounding healthy tissue and enclosing the infection in an impenetrable cell. The most common way to recognise this type of defence is by the characteristic perforated leaves. This is a very effective defence with no risk of transmission to other storms. However, the sharka virus exists in several serotypes that differ in their ability to induce immune responses in the host. The most common serotypes are PPV-D and PPV-M. In the case of PPV-M, a rapid immune response is induced, leading to hypersensitivity reactions, but unfortunately, this is not the case with the PPV-D serotype (Kegler et al. 2001). Since this type is not as aggressive in its virulence as serotype M, there is no strong tissue response. Hypersensitivity means absolute susceptibility of the plant, not absolute resistance of the plant to the disease. PPV-D is therefore able to bypass this type of resistance and subsequently destroy the crop, because varieties based on hypersensitivity are otherwise very susceptible to sharka. The best-known variety with the ability to encapsulate virus particles in the tissue is the variety 'Jojo'. This is a very good variety for breeding (Zurawicz et al. 2013). For example, the very popular varieties 'Jofela' ('Jojo' × 'Felsina') and 'Joganta' ('Jojo' × 'Haganta') were developed by crossing of 'Jojo' (Hartmann 2019). Rodamilans et al. (2014) also investigated the alteration of selected markers of defence and metabolic pathways in cultivars showing a hypersensitive response to PPV. The selected hybrids were derived from the cultivar 'Jojo'. The results show that a very strong response occurs in the plant tissues, while it does not occur in susceptible cultivars. The analysis of induced genes in the hypersensitive response of the 'Jojo' cultivar to PPV was also performed by Markiewicz et al. (2019). Using RNA sequencing, they identified 3 020 genes that are induced upon infection, of which 154 correspond to some component of the defence mechanism. Further research on these genes and methods using infection simulations may serve as an effective tool for the selection of newly developed hybrids in the future.

USE NOT ONLY ON EARTH

Studies on the nutritional composition of plums agree that they are an important part of the human

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diet. So important, in fact, that plums (mostly prunes) have been identified as one of the food ingredients for astronauts during spaceflight (Spencer et al. 2017). NASA has tested growing trees in the zero-gravity conditions of space. They have developed a genetically engineered plum tree that has a reduced juvenile phase to less than one year by transforming the FT1 plant gene with the 35S promoter (35S::PtFT1). In addition, the dormancy requirement has been eliminated, and the plum trees exhibit a dwarf/bush growth habit (Mercado, Spencer 2017). More research is needed on trees in this regard. Light conditions, humidity, and temperature can be simulated in the cultivation boxes, and as previous studies have shown, the properly selected genotype can reliably produce fruit. However, zero gravity can be a potential challenge for growing plants in space. Roots are most often oriented in the direction of gravity, i.e. positive gravitropism, while the aerial part is oriented in the opposite direction. The question of how gravity affects the growth of a plant has already been studied by Andrew Thomas Knight (Shull, Stanfield 1939), who grew plants in a rotating wheel and observed the orientation of the growth (Figure 2). Understanding the mechanism of gravitropism is crucial for plant growth in long-duration space missions (Vandenbrink, Kiss 2019). Transcriptomic analyses were performed on *A. thaliana* dale plants and investigated which genes are affected by microgravity. Correll et al. (2013) found that a total of about 130 genes are affected in plants growing in space compared to the control growing on the ground. Most of the genes

were associated with the regulation of plant polarity related to auxins, calcium, and lipid metabolism, cell wall development, oxygen status and cell defence mechanisms. Similar results were found by Johnson et al. (2017). In this study, they additionally used a mutant that regulates the cytoskeleton and actin and investigated how zero gravity also affects genes associated with the cytoskeleton and actin. This knowledge is very important for the creation of new mutants and the development of crops for interplanetary travel.

CONCLUSION

The breeding of plum trees has a long tradition. Plums are becoming an important part of the human diet due to their unique content of nutritionally beneficial compounds. They are rich in vitamins, antioxidants, pectin, and fibre. It is therefore important to produce sufficient quantities of high-quality fruit to supply both the fresh fruit market and the processing industry. As with other fruits, there is a constant need for breeding stations to develop new genotypes that reflect market trends while adapting to the changing climates. Breeding stations need to be networked and willing to collaborate and share data with each other. Fruit quality and tree growth depend on location, so varieties need to be tested in different climates. Most genotypes are currently produced by controlled pollination of blossoms with selected pollen or spontaneously through pollinators. This process of creating new varieties is time-consuming. With the introduction of modern molecular technologies, new genotypes can be “programmed” on demand. An example is the ‘Honeysweet’ variety, which has shown over the long term that it is possible to create a genetically modified plum capable of controlling the sharka virus while maintaining the required fruit quality. Breeding work hand in hand with modern technology will allow us to find many promising genotypes in a much shorter time and thus respond more effectively to a changing climate or for space travel.

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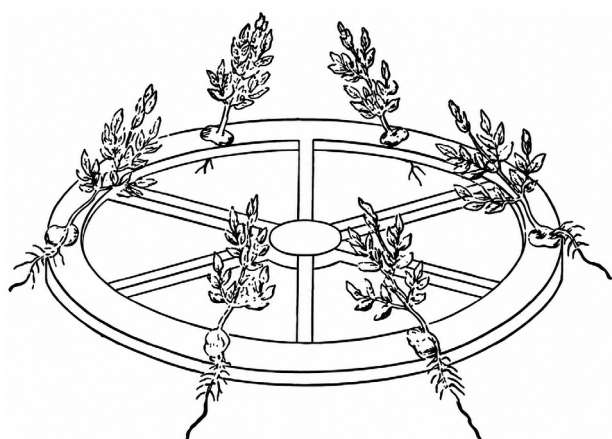


Figure 2. Scheme of Knight's gravitropism wheel test (Shull, Stanfield 1939)

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