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GENE ENGINEERING FOR PRODUCTION COLD-TOLERANT SWEET POTATO (*IPOMOEA BATATAS)*

Abstract: Sweet potato is produced in more than 100 countries as food security product and. More than 105 million tons are produced annually. Despite the fact that sweet potato are tropical plant, cultivation prospects in temperate zones is optimistic. The main limiting factor in the distribution of sweet potato in Kazakhstan is the cold factor.

Traditional breeding methods have limitations for success production of cold tolerant agricultural plants. Genetic engineering is the most effective approach for increasing plant tolerance to biotic and abiotic factors, method allows gene transfer and directionally regulate the gene expression. The article discusses the use of various genes and transcription factors for producing cold tolerant sweet potato cultivars.

Key words: Sweet potato, agrobacterium-mediated transformation, cold factor, cold tolerance.

Sweet potato is an important crop that is grown in more than 100 countries, annually produced over 105 million tons, while developing countries account for 95% of total production (FAO). Sweet potato is considered as a food security cultivar and the staple food in the rural economy of many countries [1, 2, 3, 4]. The total area under cultivation is more than 8,600,000 hectares, of which more than 74% is produced in Asia and 21% in Africa. China is the largest sweet potato producer in the world, 67% of world production and consumes 40% of the total production [5]. The importance of sweet potato as a food crop is rapidly growing in some parts of the world: Southeast Asia, sub-Saharan Africa, South America.

In the Message of the President of the Republic of Kazakhstan - Leader of the Nation Nursultan Nazarbayev to the People of Kazakhstan "Strategy" Kazakhstan-2050 "- a new political course of the established state," the threat of global food security has identified among the ten global challenges of the XXI century for the Republic of Kazakhstan and sweet potato can be the answer to challeneges [6].

Tubers of sweet potato are juicy, with delicate pulp and thin skin. Sprouts develop from hidden buds. Tubers of different varieties can vary greatly in shape - round, oval, elliptical; the color of the pulp is white, yellow, orange, cream, purple; to taste - from fresh to very sweet; in texture - from soft and juicy to dry and hard; the color of the peel - almost all the colors of the rainbow. Most cultivated varieties are more or less sweet, due to the sucrose, glucose and fructose content. Milky sap protrudes on a tuber cut (or on a stem cut) [7].

The composition of tubers may vary depending on the specific cultivar and growing conditions. Orange pulp sweet potato are an important source of β-carotene, provitamin A, 125g of fresh sweet potato tubers, from most varieties with orange pulp, contain enough β-carotene to provide the preschooler with daily requirement. Sweet potato is also a valuable source of B_6, B_2, C, E vitamins and contains sufficient amounts of copper, manganese, iron and zinc. Nutritionists in the United States are exploring the potential prevention of cancer with the properties of violet flesh sweet potato [8]. Anthocyanins that form purple pigmentation in tubers (also in berries and vegetables for example blueberries and red cabbage) are powerful antioxidants and have good bioavailability, which means that they are easily absorbed from the gastrointestinal tract into the bloodstream [9]. In addition, sweet potato has the status of a dietary product, is used as a vitamin and fortifying agent [10]. Despite the name "sweet", sweet potato can be used in diabetic nutrition, helps stabilize blood sugar levels and reduce insulin resistance. The level of

carbohydrates, potassium and sodium in sweet potato is noticeably higher than spinach [11], and its calorie level is 1.2-1.5 times higher than potato.

Sweet potato is successfully applied in agriculture as a cheap source of cattle feed. Green mass can be used in the compost, which, unlike potato, is not affected by fungal diseases. Recent studies show that animals that eat high-protein sweet potato vines produce less methane in comparison with other feeds, potentially helping to reduce harmful emissions.

Despite the fact that sweet potato is tropical plant, the prospect of cultivation in temperate zones is quite high. It is known that tropical plants such as potato, tomato, corn, soybeans, barley, rice, etc. successfully cultivated in countries with a temperate climate [12]. In the future, due to the achievements of breeding and biotechnology, it will be possible to eliminate the main limiting factors heat-loving plants propagation in the northern regions as well as, increasing the sustainability and productivity of already cultivated tropical plant species, and opportunities will only increase.

Kazakhstan is in dire need of dietary foods. One of the sources of which may be sweet potato, industrial production of sweet potato depends on the development of new forms and varieties adapted to the growing conditions in Kazakhstan. At the Institute of Plant Biology and Biotechnology, establish work on the cultivation of sweet potato (*Ipomoea batatas* L.) in the conditions of southeast Kazakhstan.

As a result, 20 genotypes characterized received from the Korean Institute of Biology and Biotechnology was analyzed. Further, was formed collection, as the starting material for cultivation suitability studies and harvest sweet potato in the conditions of southeast Kazakhstan. Promising lines were identified for further large-scale planting in the Almaty region [13].

In 2018, a large-scale planting of sweet potato was conducted on the IPBB test field in the Almaty region (43°10'41.1"N 76°19'53.5"E). Ten promising lines of sweet potato surved as a planting material. Primary data were collected indicating the possibility of large-scale cultivation of sweet potato in Kazakhstan. From one sweet potato bush was collected maximum 1.45 kg, average 0.4 kg.

Three lines of sweet potato showed good results, comparable to traditional producers of sweet potato. The growing period of sweet potato is 90-120 days.

It was determined that the main problem during the cultivation of sweet potato in the field was the abiotic cold stress factor. In the year of cultivation in the South-East of Kazakhstan in June, the temperature occasionally dropped to 7°C at night, which affected on plants (Fig. 1). In some genotypes, the leaves died off, while at the same time most of the genotypes were able to preserve the living state of the meristem zones, which allowed the plants to survive.

Using appropriate technology, it is possible to adjust the limiting abiotic factors such as drought, soil salinity, pH, etc. without big expenses. However, to increase resistance to cold, it is more efficient to create resistant varieties and forms of plants.

a) b) c)

Figure 1 - a) Leaf necrosis after cold shock. b) Sweet potato recovery. c) Field view

Among abiotic stresses, it is known that cold stress is one of the main environmental factor that limit agricultural production, causing damage before and after harvesting, which leads to huge financial losses in agriculture every year [14]. Cold stress also has a huge impact on the survival and geographical distribution of plants [15].

Standard breeding methods demonstrate limited success in developing cold-resistant agricultural plants, since for most cold-sensitive plants there is a need for interspecific or even intergeneric hybridization. Genetic engineering is the most effective approach to increase plant tolerance to biotic and abiotic factors, which will not only transfer target genes from one organism to another, but also directionally regulate the expression of plant own genes, combining various transcriptional promoters and translational enhancers [16, 17, 18].

Currently, the problem of improving the cold tolerance of plants is solved by various genetic engineering methods, the most effective should be recognized the production of transgenic plants, constitutively expressing a number of proteins related to cold adaptation of plants.

Among these proteins, should be mentioned a number of transcription factors (CBF1/DREB1A, ThpI, MYBS3, ZAT12, HOS10, abi3, etc.) [19]. The introduction of foreign genes into plants through genetic transformation is a very promising addition to traditional breeding. The use of agrobacterial transformation remains the most successful among various gene transfer strategies, since it does not require sophisticated equipment; and this method has a greater potential for obtaining the expected result than the alternative bioballistic transformation method and new CRISPR/Cas9 technology [20, 21, 22].

For agrobacterial transformation, commonly used competent cells of the strain Agrobacterium tumefaciens. Constructs with the desired genes are introduced into a tube with competent agrobacterial cells. Heat shock is conducted and incubated in a nutrient medium. This is followed by selection with specific antibiotics. Next, perform PCR for the initial check for the presence of a gene, promoter and plasmid. To increase the percentage of transformation using embryonic calli. After generation plantlets from transformed calli, the presence of the insert and the further targeted use of the transgenic plant are evaluated.

There are numerous data on the successful application of agrobacterial transformation and the production of transgenic plants tolerant to cold, for example potato, [23], rice [24, 25], sweet potato [26]. As well as a lot of data with arabidopsis [27, 28, 29, 30].

To generate cold tolerant plant, it is important to understand the mechanisms of acclimatization and the plant stress response.

The first thing that happens after cold stress in plant cells is an increase in cytosolic Ca^{2+} as an important secondary messenger. It is assumed that cytosolic Ca^{2+} is an important component of signal transmission and the development of cold acclimatization [31, 32, 33, 34, 35]. As well, other non-biotic and abiotic stresses increase cytosolic calcium to transmit the message. Adequate plant response to stresses by changes in gene expression is very important [36].

When plants are stressed by cold, some dysfunctions appear at the cellular level, such as membrane degradation, ROS formation, protein denaturation and toxic product accumulation, etc. [37, 38]. Plants furthermore try to respond to this stress by altering gene expression, modifying the membrane composition, synthesis of cold shock proteins and antioxidant enzymes, which are thought to play a role in protecting cells from freezing damage. In particular, when plants are gradually exposed to cold stress, these changes at the cellular level can cause resistance to cold stress, a process known as “cold acclimatization” [39, 40, 41].

A modification of the membrane composition occurs when plants are exposed to cold stress, plant trying to change the plasma membrane lipid composition and chloroplast envelopes. It is assumed that these changes play a role in acquiring frost resistance during cold acclimatization: they can prevent membrane damage caused by freezing by stabilizing the two-layer lamellar configuration [41, 42, 43].

Synthesis of compatible solutions or osmoprotectors. Carbohydrates, amino acids (proline, glycine, alanine and serine) and polyamines are considered compatible solutions. Compatible solutions of low molecular weight molecules that are produced in large quantities under various stress factors such as salinity, drought, cold, etc. So that the plant can withstand stressful conditions. In the case of cold stress, during the freezing period, with the initial formation of ice in the apoplastic space, the water potential decreases, which leads to the release of water from the cell into the extracellular compartment, causing intracellular dehydration [41]. To prevent cell dehydration, compatible solutes, such as carbohydrates, accumulate in the cell to reduce the difference in water potential between the apoplastic space and within the cell. Dehydrins may play a role in resistance to cold, possibly by preventing membrane destabilization that occurs during osmotic contraction associated with cold [41].

Cold shock proteins (CSP). While a significant amount of research has been done to characterize cold shock proteins in bacteria and animals, little is known about their functions in plants.

The main goal of heat shock proteins is to help the cell overcome changes in stress during cold. When the temperature decreases, the fluidity in the cell membrane decreases, which affects the active transport and secretion of the protein. In addition, the efficiency of transcription and translation is reduced due to the stabilization of the secondary structures of DNA and RNA, protein folding is inefficient, and the ribosomes must be adapted to cold before they can function properly [44].

The first functionally characterized plant CSD (cold shock domain) protein was wheat CSP (WCSP1). WCSP1 contains an area rich in glycine interspersed with three C-terminal zinc fingers CCHC. WCSP1 mRNA is activated in response to cold, the corresponding protein accumulates in the coronal tissue during prolonged acclimatization to cold. WCSP1 transcript levels are not modulated by other environmental stresses, such as salinity, drought, and high temperatures or abscisic acid treatment, suggesting that WCSP1 is specific to cold stress. WCSP1 binds to DNA and RNA and melts double-stranded nucleic acids *in vitro* and *in vivo* [445, 46, 47].

Rice has two CSD proteins [OsCSP1 (Os02g0121100) and OsCSP2 (Os08g0129200)]. The expression of OsCSPs slightly increased in the tissues of the shoots and roots during short-term low-temperature processing. However, OsCSP protein levels were not increased in the apical for 10 days of low-temperature treatment [48]. This data is very different from the observed expression characteristics for WCSP1.

Four CSD proteins (AtCSP1-AtCSP4) have been identified in *Arabidopsis thaliana*. The AtCSP3 knockout mutant (At2g17870) (atcsp3-2) was more susceptible to freezing than the wild type, both under non-acclimatization and acclimatization under cold conditions. Overexpression of *AtCSP3* provides enhanced resistance to freezing in *Arabidopsis thaliana* without obvious developmental defects. *AtCSP3* does not affect the expression of CBF and COR genes, but it regulates the expression of genes associated with stress, whose roles in resistance to freezing are unknown [49].

Dehydrins. One of the reactions of plants to cold stress is the accumulation of hydrophilic proteins, which, by hypothesis, form an amphipathic α-helix. Many of the genes encoding these proteins were first characterized as sensitive to cold, drought, and abscisic acid (ABA). Therefore, many of them were called cold-regulated COR (cold-responsive), LTI (low temperature-induced), RAB (responsive to abscisic acid), KIN (cold-induced), or ERD (early responsive to dehydration). These include dehydrins, which define group II proteins with excess late embryogenesis (LEA). Dehydrins may play a role in resistance to freezing, possibly by preventing membrane destabilization that occurs during osmotic contraction associated with freezing [50].

Dehydrins belonging to the LEA proteins of group II are considered as stress proteins involved in the formation of plant defense reactions to dehydration. They can also be considered hydrophilins [51].

Although the role of dehydrins has not been fully defined, various studies have demonstrated their role in tolerance to cold stress. Hara et al. [52] In particular, co-segregation of the dehydrin gene with cooling resistance in cowpea was found [53], and transgenic tobacco with dehydrin overexpression showed greater resistance to frost than wild-type plants without cold acclimatization [54]. Thus, the production of dehydrin, as expected, is one of the important strategies for plants to obtain resistance to cold stress.

ROS. There are many reports that demonstrate the production of ROS in conditions of cold stress. To remove reactive oxygen species under normal and stress conditions, plants use a variety of antioxidants, such as ascorbic acid, glutathione, and enzymes absorbing ROS, such as superoxide dismutase (SOD), ascorbate peroxidase (APX), catalase (CAT), glutathione peroxidase (GPX) and peroxiredoxin (PrxR), thereby protecting potential cell damage and tissue dysfunction [55, 56].

Superoxide dismutase can catalyze the conversion of superoxide radicals to H_2O_2 and O_2. CAT, PrxR and APX can eliminate hydrogen peroxide, which has a damaging effect on many enzymes [57, 58].

Transcription factors. Among several cold signaling pathways, CBF / DREB1-dependent cold signaling pathway is best characterized and is a key regulatory pathway [59]. In Arabidopsis, three CBF / DREB1 are involved in regulating the expression of the COR gene and resistance to cold [60, 61]. The path of CBF / DREB1 (mainly CBF3 / DREB1A) is controlled by a MYC ICE1 type transcription factor (CBF1 expression inducer) [62].

ICE1 can bind to the MYC cis-recognition elements (CANNTG) in the CBF3/DREB1A promoter and induce the expression of CBF3/DREB1A and its regulon during cold acclimatization (Figure 1) [62]. Approximately 40% of the COR genes and 46% of the cold-regulated transcription factor genes are regulated by ICE1, suggesting that ICE1 functions as the main regulator controlling CBF3/DREB1A and many other COR genes (Figure 2) [63].

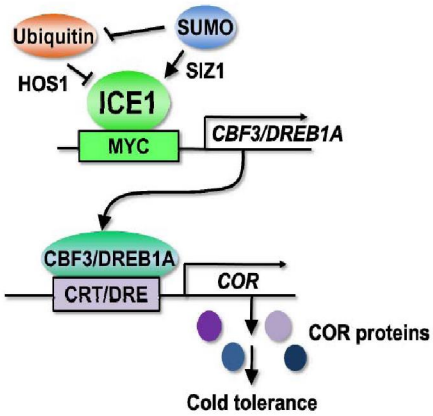

Figure 2 - Cold Signal Path, which includes ICE1 and CBF3 / DREB1A. ICE1 is a type-MYC transcription factor and binds to cis-elements in the CBF3/DREB1A promoter to induce its expression. CBF3/DREB1A is a transcription factor of type AP2 for regulating the expression of COR (genes regulated by cold) and resistance to cold. Ubiquitilation ICE1 is mediated by HOS1, ubiquitin-E3-ligase for proteasome-dependent degradation. SIZ1, the SUMO E3 ligase, mediates the sumoylation (SUMO conjugation) of ICE1, probably leading to the blocking of ubiquitination and stabilization of ICE1 (by Maruyama K. et.al. 2004)

CBF/DREB1 can bind to the cis-elements of CRT/DRE, A/GCCGAC, in the promoter of the COR genes to regulate the expression of the gene of the COR [64] and belong to the (APF) group of ERF / AP2 transcription factors. [65]. A genomic analysis showed that the CBF/DREB1 genes are organized in tandem (CBF1/DREB1B-CBF3/DREB1A-CBF2/DREB1C) on chromosome IV of Arabidopsis, CBF1/DREB1B and CBF3/DREB1A are induced simultaneously and earlier than CBF2/DREB1C after cold working [66].

Transcriptome analysis in transgenic plants with overexpression of CBF/DREB1 shows that approximately 12% of the COR genes in *Arabidopsis thaliana* are controlled by CBF/DREB1, but no significant target specificity is observed among the three CBF factors [67, 68]. Some transcription factors, such as ERF/AP2, RAP2.1 and RAP2.6 and C2H2-type zinc finger, STZ/ZAT10, are attributed to CBF regulon [69, 70].

CBF1/DREB1B and CBF3/DREB1A have different functions than CBF2/DREB1C. Although CBF1/DREB1B and CBF3/DREB1A control the same group of genes, they are consistently necessary for the induction of all CBF/DREB1 regulon and the completion of cold acclimatization [59,71].

Transcription factors involved in cold stress. When plants are exposed to low temperatures, they react to cold stress by changing gene expression. These genes encode proteins that are involved in cold resistance. What genes can be used in transformation in order to produce cold-resistant sweet potatoes? Using the database, gene expression after low temperature stress can be divided into 3 promising genes.

1) CBF3. As noted above, the CBF transcription factor and its genes are among the most important elements involved in responding to cold. CBF genes have a key role in the Pinot et al. experiment. Overexpression of *AtCBF1* and *AtCBF3* increased freezing tolerance whereas AtCBF2 overexpression failed to increase freezing tolerance [72].

Further evidence of successful suppression of the expression of CBF1 and CBF3, which led to a 60% decrease in tolerance to freezing during cooling [73]. Conversely, constitutive overexpression of CBF1 or CBF3 in Arabidopsis plants causes increased tolerance to freezing. The fact that overexpression of CBF leads to constitutive resistance to freezing has been noted in *Thlaspi arvense*, *Oryza sativa*, *Lolium perenne, Brassica napus* and *Ipomoea batatas* [74, 75].

Cook D. et al. demonstrate that the metabolome of *Arabidopsis* is extensively reconfigured in response to low temperature, and that the CBF cold response pathway has a prominent role in this process. Of these 325 metabolites, 256 (79%) increased in nonacclimated Ws-2 plants in response to overexpression of CBF3. [76].

2) BZR1. Hui et al. investigated the function of brassinasteride signaling components under low temperature stress [77]. Brassinasteroid-signaling kinases BZR1 (brassinazole-resistant 1) plays a positive role in regulating the response of plants to low-temperature stress. BZR1 upregulates the expression of CBF genes by directly binding to their promoters *in vitro* and *in vivo*. Moreover, some genes and pathways independent of the CBF pathway are regulated by BZR1. These data indicate that BZR1 positively regulates plant resistance to freezing through CBF-dependent and CBF-independent pathways (Figure 3).

Insensitive brassinosteroid 2 (BIN2) is a GSK3-like kinase in BR signaling [78]. In the absence of BR, active BIN2 constitutively phosphorylates two homologous transcription factors, brassinazole-resistant 1 (BZR1) and BRI1-EMS suppressor 1 (BES1), to promote their degradation. In the presence of BRs, BIN2 is dephosphorylated by BSU1 and cleaved by 26S proteasome, which subsequently releases inhibition of BZR1 and BES1 by BIN2 [79, 80, 81]. Dephosphorylated BZR1 and BES1 accumulate in the nucleus and bind to their target genes, triggering a BR response [80, 81, 82, 83]. BZR1 and BES1 are two well-characterized major helix-loop-helix transcription factors in the BR signal pathway, which have 88% sequence identity at the amino acid level. Both BZR1 and BES1 bind BRRE (CGTGT/CG) and E-box (CANNTG) through a conservative N-terminal DNA-binding domain and target a number of common genes for regulating BR-related responses [84, 85].

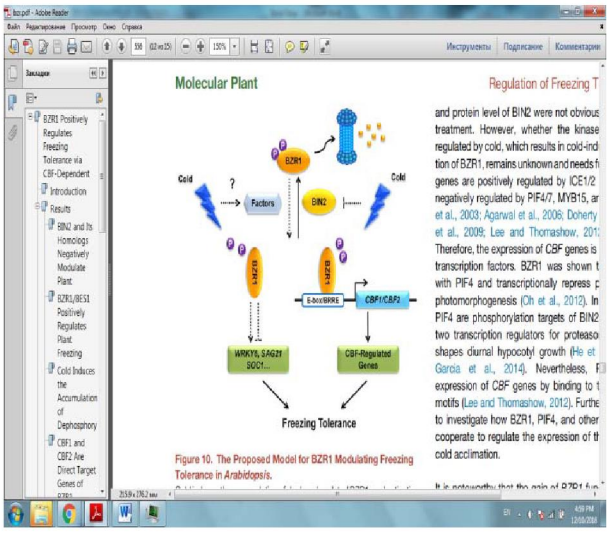

Figure 3 - The proposed model for modulating BZR1 cold resistance.
(by Hui et al. 2017)

The cold induces the accumulation of dephosphorylated BZR1, and the activation of BZR1 induces the expression of CBF1 / 2 and CBF-independent genes by binding their promoters to E-box / BRRE conservative motifs, while BIN2 negatively regulates the response of plants to cold stress by inhibiting cold-induced dephosphorylated protein BZR1. BZR1 also directly regulates some COR-genes, including WRKY6, SAG21 and SOC1, which are not dependent on CBF, to modulate plant resistance to freezing.

3) WRKY31. WRKY transcription factors are one of the largest families of transcriptional regulators in plants and form an integral part of the signaling pathways that regulate many plant processes. New data show that WRKY proteins often act as repressors, as well as activators, of important plant processes. In addition, it becomes clear that a single transcription factor WRKY may be involved in the regulation of several seemingly disparate processes.

The signaling and regulation mechanisms of transcription are distributed by determining the functions of the WRKY protein through interaction with a diverse set of protein partners, including MAP kinases,

MAP kinase kinases, 14-3-3 proteins, calmodulin, histone deacetylases, resistant proteins and other transcription WRKY factors [86] .

Some early studies of WRKY showed that the isolated WRKY gene from the xerophytic evergreen shrub C3, creosote bush, is an activator of abscisic acid signaling (ABA) [87]. ABA serves as a link in the reactions of plants to abiotic stresses, including low-temperature, therefore, it is called the "stress hormone". In the study of aleuron cells, it was shown that *OsWRKY24* and *OsWRKY45* act as repressors of the ABA inducible promoter, and *OsWRKY72* and *OsWRKY77* are activators of the same promoter [88]. ABA is also involved in responding to low temperature stress, the level of ABA increases in many plants in response to low temperature [89], including *Arabidopsis* [90], and many reacting to cold genes respond to ABA [91].

For example, in rice induced by heat shock protein HSP101 with overexpression of *OsWRKY11*, resistance to high temperatures and drought was increased [92]. Similarly, overexpression of *OsWRKY45* led to increased salt and drought tolerance, in addition to increased resistance to various diseases [93]. In *Arabidopsis thaliana*, overexpression of *AtWRKY25* or *AtWRKY33* increases salt tolerance [94].

These examples illustrate that WRKY transcription factors are part of the signaling processes associated with plant response to various abiotic and biotic stress conditions.

The selected genes WRKY31 and BZR1 also showed significant changes in expression, before and after 12 hours of low-temperature stress. In particular, cold 12h / NT 0h Log2 (fold change) WRKY31 - 4.49 and BZR1 - 1.45, which indicate their role at low temperatures.

The collected data indicate the promising use of agrobacterial transformation to develope sweet potato resistant to the abiotic cold factor. Cultivation of sweet potato on an industrial scale is possible in Kazakhstan. What is necessary is to develop an agricultural technology that allows obtain a high yield and high quality of the agricultural product in order to improve the food and agricultural security of the country. Ultimately, Sweet Potatoes, as a valuable dietary product, can replenish the main list of products available to the population of the country. With the genes given in the article, work is underway, in particular, the design with stress by the inducible promoter SWPA2 of sweet potato was developed and regenerates were obtained from embryonic calluses of sweet potato. This design and genes can be applied in other plants.

Studying and understanding the processes of plant response to the cold factor has a fundamental and applied character; by affecting certain processes in a plant, tolerance and productivity of a plant can be increased.

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СУЫҚҚА ТӨЗІМДІ ТӘТТІ КАРТОПТЫ (*IPOMOEA BATATAS*) ӨНДІРУДЕГІ ГЕНЕТИКАЛЫҚ ИНЖЕНЕРИЯ

Аннотация. Тәтті картоп 100-ден астам елде өндіріледі, сонымен қатар азық-түлік қауіпсіздігін қамтамасыз етеді. Жыл сайын 105 млн. тоннадан астам тәтті картоп өндіріледі. Тәтті картоп тропикалық өсімдіктер болғанына қарамастан, қоңыржай аймақтарында өсіп жетілдірудің болашағы бар. Қазақстанда тәтті картопты тежейтін негізгі фактор, ол суық факторы болып табылады.

Суыққа төзімді ауылшаруашылық өсімдіктерін шығаруда сұрыптаудың негізгі әдістері шектеулі табыс көрсетеді. Гендік инженерия - биотикалық және абиотикалық факторларға өсімдіктердің төзімділігін арттыруда ең тиімді тәсіл, бұл әдіс гендік трансфер, сондай-ақ өсімдіктің меншікті гендерінің өрнегін реттеуге бағытталған. Мақалада тәтті картоптың суыққа төзімді сорттарын алу үшін әртүрлі гендерді және транскрипция факторларын пайдалану туралы баяндалады.

Түйін сөздер: Тәтті картоп, агробактериальді трансформация, суық фактоы, суыққа төзімділік.

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ГЕННАЯ ИНЖЕНЕРИЯ ДЛЯ ПОЛУЧЕНИЯ ХОЛОДОУСТОЙЧИВОГО СЛАДКОГО КАРТОФЕЛЯ (*IPOMOEA BATATAS)*

Аннотация: Сладкий картофель производится более чем в 100 странах и является продуктом продовольственной безопасности. Ежегодно производится более 105 млн. тонн сладкого картофеля. Несмотря на то, что сладкий картофель является тропическим растением, перспектива его выращивания в умеренных зонах оптимистичны. Основным лимитирующим фактором распространения сладкого картофеля в Казахстане это фактор холода.

Стандартные методы селекции демонстрируют ограниченную успешность при получении холодоустойчивых сельскохозяйственных растений. Генная инженерия представляет собой наиболее эффективный подход для увеличения толерантности растений к биотическим и абиотическим факторам, которые позволяют переносить гены, а также направленно регулировать экспрессию собственных генов растений. В статье обсуждаются использования различных генов и транскрипционных факторов для получения холодоустойчивых сортов сладкого картофеля.

Ключевые слова: Сладкий картофель, агробактериальная трансформация, фактор холода, холодоустойчивость.

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