Summary. Progress in cereals transformation which can be observed for last two decades has great importance in the development of plant science and agriculture. So far, non-vector techniques, particularly direct gene transfer using „gene gun”, have been often applied in cereals transformation. However, agrobiotechnology achievements enabled cereals transformation with the soil bacterium Agrobacterium tumefaciens. Initially, it was believed that this technique cannot be applied to cereals because monocotyledones are outside the host range of the crown gall disease. Nowadays, the top five cereals with the highest economic significance – rice (Oryza sativa L.), maize (Zea mays L.), wheat (Triticum aestivum L.), barley (Hordeum vulgare L.) and sorghum (Sorghum bicolor L.) are quite efficiently transformed by A. tumefaciens. By means of molecular genetic tools it is possible to obtain cereals with new, improved traits. The present paper is focused on agricultural development which can by observed by the application of GM cereals tolerant to biotic and abiotic stress factors. Moreover, we summarized the latest achievements in cereals transformation.

Key words: transformation, Agrobacterium tumefaciens, cereals, stress tolerance, GM crops

INTRODUCTION

The highest global importance in cereals production has quality and quantity of grain. The major limitations of these two factors are abiotic and biotic stresses that can lead to 30–60% yield loss [Dhlamini et al. 2005]. Drought, salinity, and temperature represent the major abiotic threats, whereas biotic stresses that include bacterial, viral and fungal pathogens, weeds, and pests have caused historically severe yield reductions. For this reason, designing of wide cereals genetic variation with higher grains production is big challenge to agricultural researchers and plant breeders. Thanks to conventional
breeding, the resistance/tolerance to both abiotic and biotic stresses has advanced greatly with a spectacular yield increase during the last century [Ji et al. 2013].

The cereals: wheat, barley, rice, maize and sorghum provide approximately 40% of the energy and protein component in human diet. Economic growth of developing countries will lead to higher demand for grain [Dunwell 2014]. However, current tendency to soil erosion, global warming and other environmental problems cause losing of farm lands on a global scale (Intergovernmental Panel on Climate Change¹). Environmental conditions caused plant response through numbers of physiological and biochemical processes. Identification of stress-protective and adaptation-related genes that are activated by stress factors is subject of many scientific researches. Overexpression of those genes is necessary in creating stress tolerant plant. It was proved that many active stress-responsive genes that are regulated by transcription factors, are useful in application in transgenic studies [Mrízowá et al. 2014].

Besides human consumption, some cereals are used as malt in brewing and distilling industry or as an additive for animal feeding. Moreover, last time cereals were successfully used in production of grains with modified quality. Transgenic cereals are able to produce modified proteins, carbohydrates, oils and other nutritional components [Morell 2012, Rawat et al. 2013]. Vaccine antigens, pharmaceuticals and other therapeutic proteins can be also produced in that expression systems [Dunwell 2014]. For that and many other reasons, application of biotechnology to crop improvement plays key role to sustain and elevate grain production. Developing of knowledge of the molecular mechanisms in plants, analysis of genes effects, transgenes regulation and commercialization of GM plants can bring numbers of beneficial economic effects.

Application of Agrobacterium tumefaciens is the most common technique for dicotyledonous species transformation. A. tumefaciens has ability to transfer the part of bacterial DNA segment from Ti plasmid (T-DNA) into plant cells. This T-DNA region contains genes encoding enzymes responsible for occurrence of plant tumors that are called crown gall. Developing biotechnology enabled the use of A. tumefaciens in generating transgenic plants without symptoms of disease. The first plant genetic modification with A. tumefaciens took place in 1983 and it was performed on tobacco plant [Hoekema et al. 1983]. At that time it was believed that this technique cannot be applied for monocotyledones, because these plants are outside the host range of the crown gall. For this reason, cereals were transformed mainly by gene gun method. The first successful transformation of cereal using Agrobacterium technique was applied for maize [Graves and Goldman 1986]. Now, after years of experiments and tests, Agrobacterium transformation is the most common and efficient transformation technique for major cereal crops: wheat (Triticum aestivum L.), barley (Hordeum vulgare L.), [summarized in: Dunwell 2008] maize (Zea mays L.), rice (Oryza sativa L.) [Hiei and Komari 2008] and sorghum (Sorghum bicolor L.) [Wu et al. 2014].

In the summaries below the most significant achievements of crops transformation are presented. We shortly reviewed the first trails and the progress of cereals transformation with Agrobacterium with focus on agriculture development by application of modified cereals tolerant on biotic and abiotic stress factors.
The first trials of monocotyledones transformation with Agrobacterium

The main problem of monocotyledonous plant transformation by Agrobacterium was the fact that these plants are mostly outside the host range of crown gall disease, in contrast to dicotyledonous species. The first breakthrough was performed by Douglas et al. [1985] who tested bamboo plants. They found that A. tumefaciens is able to attach specifically to the bamboo cells in the same way as to the dicotyledonous plant cells. However, low level of compounds that induce vir genes limited transfer of bacterial T-DNA region [Usami et al. 1987]. Nevertheless, induction of vir genes can be obtained by artificially added chemicals with acetosyringone [Stachel et al. 1985]. Although numbers of tests were performed, some issues were still unsolved and the statement that monocotyledones could be transform by Agrobacterium was still controversial.

The most significant changes in results of cereal transformation were reported in the mid-1990s. The biggest breakthrough was performed by Chan et al. [1993] that have successfully transferred and expressed a reporter gene driven by an alpha-amylase promoter in a japonica type of rice (Oryza sativa L. cv. Tainung 62) using the Agrobacterium-mediated gene transfer system. One year later, Hiei et al. [1994] tested transformation of various tissues: shoot apices, segments of roots from young seedlings, scutella, immature embryos, calli induced from young roots and scutelia or cells in suspension cultures induced from scutella. Obtained results indicated that transgenic rice from calli co-cultivated with A. tumefaciens gave the highest frequency (23%) of tissues pieces that produced hygromycin resistant cells. Additionally, Ishida et al. [1996] obtained transgenic maize from immature embryos. The frequency of transformation was remarkably high, between 10 and 30%.

In 1982 it was proved that induction of cell division in response to wounding is crucial for transformation (Kahl 1982). For this fact, another approach consisted difficulties in monocotyledones transformation showed that cereals do not show wound response [Potrykus 1990]. Thus, lack of wound response in monocotyledonous plant can be a reason why transformation via leaf is so difficult. Hiei [1994] and Ishida’s [1996] studies confirmed that hypothesis by using actively dividing cells not leaves. They showed that plant regeneration abilities were essential in cereal transformation.

Transgenic cereals with enhanced tolerance to biotic stress

For this moment, there are no commercial GM cereals that are tolerant to pathogens. However, many intense studies are performed mostly on wheat, that combine laboratory and field tests. In fact, wheat is attacked by the highest number of various fungal diseases. Among dangerous pathogens are Puccinia graminis (stem rust), Mycosphaerella graminicola (Septoria tritici blotch – STB) or the most common Fusarium (head blight or/and crown root). Fusarium infection leads to numbers of plant diseases and causes huge economical losses by decrease or total reduction of grain yield. Crops losses can reach even more than 40%. Fusarium growth and development is dependent on numbers of environmental factors, mostly on temperature (lower than for other fungal species) and
amount of rain. Agronomic factors such as soil cultivation, nitrogen fertilization, fungicides or the host genotype are very significant as well [Wisniewska et al. 2014].

Additional risk of Fusarium infection is contamination of the grain with mycotoxins that are recognized as very dangerous for human and animals' organisms. Diseases can occur by indirect (with infected meat, milk or eggs) or direct (with infected food of plant origin e.g. grains) reaction. That can cause a number of digestive or immune system disorders. Consuming of infected food can lead to diarrhoea, kidney damage, cancer and eventually to death. Mycotoxins are also a huge danger for plants and cause disorders in plant development by induction of chromosomal aberration, necrosis and reduction activity of many enzymes [Wisniewska et al. 2014]. Additionally, toxins cause inhibition of yeast growth during fermentation process, what disturbs bioethanol production.

Last studies showed that introduction of selected genes can significantly reduce the damages caused by Fusarium (about 53%) in GM cereals compared to control (non-GM). Among these genes are: bovine lactoferrin gene (all transgenic lines exhibited a significant level of resistance compared to untransformed) [Han et al. 2012], NPR1 gene (non-expressor of PR genes) from Arabidopsis thaliana [Gao et al. 2013], PvPGIP (polygalacturonase-inhibiting protein) gene from Phaseolus vulgaris [Ferrari et al. 2012] or the wheat lipid transfer protein gene TaLTP5 [Zhu et al. 2012].

Another approach consists the powdery mildew resistance. Many studies were performed on wheat and numbers of genes were tested. It was proved that mildew resistant wheat can be achieved by using of virus-induced gene silencing (VIGS) of Mlo genes [Varallyay et al. 2012] and alleles of the resistance locus Pm3 in wheat, conferring race-specific resistance [Brunner et al. 2012]. However, next studies suggest that GM wheat which is resistant to one pest (powdery mildew) can be more susceptible to another pest (aphids) [von Burg et al. 2012, Zeller et al. 2013].

Similar studies, concerning powdery mildew, were performed on barley and showed positive effect of modification of the HvNAC6 transcription factor expression on plant resistance. Barley HvNAC6 is a member of the plant-specific NAC transcription factor family and it was shown that it acts as a positive regulator of basal resistance in barley against the biotrophic pathogen Blumeria graminis f. sp. hordei (Bgh) [Chen et al. 2013]. NAC transcription factor was originally derived from the names of three proteins, no apical meristem (NAM), ATAF1-2 (Arabidopsis transcription activation factor), and CUC2 (cup-shaped cotyledon) [http://planttfdb.cbi.pku.edu.cn/family.php? fam=NAC].

Rice blast caused by Magnaporthe oryzae was also examined. Chitin which is a component of fungal cell walls, acts as an elicitor in many plants. The CEBiP (plasma membrane glycoprotein) is a receptor for the chitin elicitor (CE) in rice. It was demonstrated that the perception of CE by CEBiP contributes to disease resistance against the rice blast fungus, Magnaporthe oryzae. Additionally, it was proved that knockdown of CEBiP expression allowed increased spread of the infection hyphae. To enhance defense response, chimeric genetic construct, composed of CEBiP and Xa21 was constructed, which mediate resistance to rice bacterial leaf blight [Kishimoto et al. 2010]. Similar reaction was observed in lines with overexpression of the WRKY30 gene [Peng et al. 2012]. Rice showed improvement of resistance to rice blast caused by Magnaporthe grisea but also to rice sheath blast that is caused by Rhizoctonia solani. Additionally, it
was found that JA (jasmonic acid) plays a crucial role in the WRKY30-mediated defense responses to fungal pathogens.

Kumar et al. [2003] produced *Rhizoctonia solani* tolerant rice by inserting rice chitinase gene – *chi11*. Moreover, Ignacimuthu and Ceasar [2012] showed increase resistance to leaf blast caused by *Pyricularia grisea* in finger millet by expression of the same rice gene encoding chitinase (*chi11*). Next to chitinase, the glucanase gene has been given the highest priority in development of resistant plants. Introduction of β-1,3 and 1,4-glucanase gene (*Gns1*) to rice indicated increase of resistance to blast infection [Nishizawa et al. 2003]. Similar effect was observed for another glucanase gene – *OsGLN2* [Akiyama et al. 2004]. Moreover, combined introduction of chitinase and glucanase genes leads to higher fungal resistance. Zhu et al. [2007] designed Super Hybrid rice. They introduced two chitinase genes (*RCH10, RAC22*) from rice, glucanase gene (β-Glu) from alfalfa and a ribosome inactivating protein gene (B-RIP) from barley. Significant increase of resistance to rice blast disease was observed. Another study indicated that expression of rice chitinase (chi11) and tobacco β-1,3-glucanase genes caused resistance to sheath blight disease in rice [Sridevi et al. 2008].

Other dangerous plant pathogen is *Ustilago maydis* that causes huge losses in maize crops. Van der Linde et al. [2012] show that in maize, the resistance can be obtained by silencing of a gene encoding a putative cystatin (CC9), which is induced upon penetration by *U. maydis* wild type. Silencing of cc9 resulted in a strongly induced maize defense gene expression and a hypersensitive response to *U. maydis* wild-type infection.

Another target for development of transgenic cereals is resistance to insects. This approach is based on toxin that was found in soil bacteria – *Bacillus thuringiensis*. Many proteins from this bacterium were recognized as toxic for insects and they were commonly used in agriculture and forestry as sprays. After years of studies, development of molecular biotechnology and microbiology leaded to expanding knowledge about these toxins and now genes responsible for their biosynthesis are widely isolated from *Bacillus thuringiensis* and introduced into the crops. The first research was performed on the corn borer (*Ostrinia nubilalis*), a lepidopteran pest of maize. Gradually, another *Bacillus* genes were identified and isolated that were useful to design plants tolerant to other pests (coleopteran species, corn root worm) [Narva et al. 2013]. On the USA market there are maize varieties with several *Bt* genes sometimes combined with herbicide tolerance genes [Edgerton et al. 2012]. Single variety can contain even eight transgenes [Tabashnik et al. 2013]. One of the most important tool for insect pest protection is MON810 maize carrying the *Bt* gene (*Cry1Ab*) developed by Monsanto. That maize line is highly resistant to European corn borer by production of delta endotoxin [Ostry et al. 2010]. Tests of insect resistance genes had additional positive side-effects in crops. In GM maize with expression of *Bt* gene encoding resistance to corn root worm, the enhanced nitrogen uptake and improvement of nitrogen use efficiency was observed [Haegel and Below 2013]. Those results can be useful in agronomical approaches. Next studies indicated that maize with *Bt* gene had higher microbial activity and nitrogen mineralization [Velasco et al. 2013]. Moreover, transgenic rice showed reduction of the methane emission flux. However, that study proved reduction of bacterial communities in paddy soil [Han et al. 2013].
One of the major tasks for scientists is to design a transgenic plant without resistance development in the target insects. Previous studies indicated that after prolonged application of any compound the resistance was developed. After marketed the first GMO products, researchers suggested a strategy of areas with non-transgenic plants called refugia. That could limit incidence of insects with mutant resistance gene. Unfortunately, some farmers did not adopt this strategy. It is presumed that now about five pests developed such resistance [Tabashnik et al. 2013].

The maize ribosome-inactivating protein (MRIP), which was found in mature kernels and cleaves part of the ribosome, provides resistance to maize pests as well. Expression of this protein in leaves of different species of plants has resulted in increased resistance to both insects and fungi. Another food crop protein that has antinsect and antifungal activities is wheat germ agglutinin (WGA), which appears to affect insects by disrupting the peritrophic membrane. Dowd et al. [2012] investigated higher level of resistance to two major maize insect pests, the corn earworm (Helicoverpa zea) and fall armyworm (Spodoptera frugiperda) caused by these two proteins which were transgenically expressed in maize leaves. Additionally, resistance for fungus Fusarium verticillioides, which produces mycotoxins in maize was also tested.

Latest study concerns introduction of synthetic avidin gene into spring wheat (Triticum aestivum L.) cv. Giza 168 using a biolistic bombardment protocol [Abouseada et al. 2015]. Avidin as a glycoprotein that is able to bind biotin what is needed for insects to carboxylation reactions. For this fact, plants containing avidin are toxic to a wide range of insects. Therefore, transgenic wheat plants had improved resistance to Sitophilus granarius.

Biotic stress is also related with attacks by some bacteria or viruses. In this field of science, corresponding to GM cereals, some achievements are reported as well. In rice a silencing of the dominant allele Xa13 leads to improve rice bacterial blast resistance [Li et al. 2012]. For virus resistance approach in wheat an expression of the artificial microRNA was performed. As a results wheat streak mosaic virus resistant plants were obtained [Fahim et al. 2012]. Expression of dsRNA- specific endoribonuclease gene provided resistance to maize rough dwarf disease [Cao et al. 2013]. In rice an expression of RNAi construct that contains CP (coat protein) gene and SP (specific proteins) gene from RSV (rice stripe virus) caused enhance resistance [Zhou et al. 2012]. Similar strategy was observed for RGDV (rice gall dwarf virus) [Shimizu et al. 2012] or for rice grassy stunt virus [Shimizu et al. 2013].

TRANSGENIC CEREALS WITH ENHANCED TOLERANCE TO ABIOTIC STRESS

Tolerance to abiotic stress is much more difficult approach for the researches. Nevertheless, the knowledge of plants response to changes of environmental condition is very important. Plants are intensively tested under different stress factors like drought, salt or nutrition deficiency and some results are presented below. Plant responds to environmental stresses through numbers of biological and biochemical processes. The biggest effort
has to be made for identification of stress protective genes or adaptation of genes that can be active during abiotic stress.

SALINITY

Both salinity and drought induce osmotic stress. According to reports GM plants showed 4–11% losses in yield. In contrast, non-transgenic control showed more than 56% losses [Dunwell 2014]. Study on wheat demonstrated that overexpression of TaOPR1 gene cause increase tolerance on salinity [Dong et al. 2013]. That suggests this gene is a part of signaling pathway combined with regulation of the ABA-mediated signaling network. Studies with barley indicated that mitogen activated protein kinase HvMPK4 is involved in higher saline tolerance [Abass and Morris 2013]. It was proved that transgenic rice with overexpression of TaSIP gene (wheat gene encoding a salt tolerance protein) [Du et al. 2013] and LeSin1 (sheepgrass) gene [Li et al. 2013] presented improved tolerance to salinity. Overexpression of Arabidopsis CBF3 gene in GM oat enhanced salt stress tolerance. Additionally, it was noticed that even during salt stress condition, transgenic plants showed maintenance of leaf area, chlorophyll content, photosynthetic and transpiration rate as well as relative water content [Oraby and Ahmad 2012].

DROUGHT

It was proved that expression of molybdenum cofactor sulfurase from Arabidopsis in maize caused enhance of the drought tolerance [Lu et al. 2013]. Other study shows that OsPIL1 gene in GM rice promotes internode elongation and reduces plant height by cell-wall-related genes in response to drought. That data suggests plant growth can be improved under stress conditions [Todaka et al. 2012]. However, there are more reports consisted transgenic rice and drought tolerance. Overexpression of OsZIP16 [Chen et al. 2012a], OsHsfA7 [Liu et al. 2013], γ-glutamylcysteine synthetase [Choe et al. 2013], MIOX [Duan et al. 2012] improved drought resistance as well. Zhang et al. [2012] suggested that overexpression of Oshox22 gene leads to ABA biosynthesis which regulates drought response by ABA-mediated signal transduction pathways. Another approach indicates that transgenic maize with expression of Bacillus subtilis cold shock protein B revealed drought tolerance [Beazley et al. 2012].

COLD

In transgenic spring barley it was demonstrated that TaCBF14 and TaCBF15 wheat genes caused improvement of frost or other abiotic stress tolerance [Soltész et al. 2013]. Similar results were obtained for transgenic barley with overexpression of Osmyb4 rice gene under the control of cold inducible AtCOR15α promoter [Soltész et al. 2011] or TaDREB3 gene from wheat [Hackenberg et al. 2012, Kovalchuk et al. 2013] that
also survived low temperatures. Shou et al. (2004) showed that freezing tolerance in maize can be improved by constitutively expressing the active version of a tobacco MAPKKK gene, \textit{NPK1}, which is an activator of the oxidative signaling pathway. Two NPK1-transgenic maize events were able to withstand up to 2°C lower freezing temperature compared with their nontransgenic siblings. The 2°C improvement in the freezing tolerance would dramatically minimize yield loss due to frost damage that often occurs in spring and fall seasons, thereby stabilizing the productivity of maize. In this study, the transgene used for engineering maize, \textit{NPK1}, was involved in an H$_2$O$_2$ signaling pathway and modified maize plants expressing this gene displayed enhanced freezing tolerance. That result proved that the oxidative signaling pathway is one of the multiple pathways regulating plant response to stress. Additionally, that study showed that at least two genes (\textit{GST} and \textit{HSP17.8}), documented in the oxidative signaling pathway were up-regulated in both of the NPK1-transgenic events studied. Those results indicate that a dicotyledonous MAPKKK is able to activate the oxidative signaling pathway in a monocotyledonous plant. This activation, in turn, provided protection to plants from freezing damage.

**NUTRIENT DEFICIENCY**

Studies focused on improving crop under nutrient deficiency are mostly based on the maize overexpression of \textit{Thellungiella halophila} H – pyrophosphate gene [Pei et al. 2012]. In fact, under phosphate sufficient condition, transgenic plants indicate more vigorous growth of roots compared to non-GM control. However, stress of phosphate deficit caused development of more robust root systems. That result suggests transgenic plants subsequently accumulated more phosphorus. It was also proved that \textit{Pht1} gene promotes phosphate uptake in rice [Sun et al. 2012]. Moreover, in wheat overexpression of \textit{Ta-PHR1} gene leads to increase yield [Wang et al. 2013].

Another problem is presence of metals ions in soil. One of the most common ions is aluminum that causes inhibition of plant development, reduction of root growth and leads to decrease of water and nutrient uptake. For barley, potential candidate that can modulate Al tolerance is wheat \textit{ALMT1} gene that encodes a membrane-bound protein which is responsible for Al-activated malate efflux [Ryan et al. 1997, Zhang 2001]. Overexpression of that gene in tobacco cells caused enhance tolerance to aluminum [Sasaki et al. 2004]. Studies on transgenic barley proved development of root growth, shoot biomass and grain yield [Delhaize et al. 2004]. Moreover, overexpression of \textit{HvYS1} gene in barley indicated higher tolerance and improvement of crop in alkaline soil. Another study was based on this approach. GM rice with overexpression of this \textit{HvYS1} gene showed enhance growth and yield compared to the wild-type [Gómez-Galera et al. 2012]. Other studies consisted transgenic rice as well, indicated that overexpression of the protein from thermophilic archaea improved tolerance to mercury [Chen et al. 2012b] and \textit{OSHMA2} gene is involved in accumulation of cadmium [Takahashi et al. 2012].
HERBICIDE TOLERANCE

The main problem with using herbicides is the fact that some of them are non-selective, which means those herbicides are able to kill not only weed but also all crops. Transgenic researches are focused on identification, isolation and transfer resistance genes into crop. The first organic, systemic, selective herbicide was dichlorophenoxyacetate (2,4-D). Along with the green revolution, this herbicide has helped to increase the cereal production on the decades after 1950. Studies on soil bacteria have identified \textit{rdpA} gene from \textit{Sphingobium herbicidivorans} MH, which encodes the enzyme ariloxylalkanoate-dioxygenase-1 (AAD-1); which is able to degrade 2,4-D and other herbicides. Corn plants containing the gene \textit{rdpA} is tolerant to 2,4-D but also to the ariloxypheoxypropionate (AAPP) herbicides [Queiroz et al. 2014].

Another well known strategy is using glyphosate that is commonly applied by commercial companies. Identification of bacterial resistance genes and introduction into maize cells contributed to widely selling those plants by company. Second major trail of herbicide resistant was performed on glufosinate [Dunwell 2014]. Glyphosate is active ingredient of the herbicide Roundup produced by Monsanto. Roundup inhibits EPSP (5-enolpyruvylshikimate-3-phosphate) synthase, which is absolutely required for the survival of plant. Roundup Ready plants are genetically modified developed by Monsanto and carry the gene coding for a glyphosate-insensitive form, obtained from \textit{Agrobacterium} sp. strain CD4. The gene product, \textit{CP4 EPSP} synthase, contributed to crop resistance to glyphosate. Current Roundup Ready crops include soy, corn, canola, alfalfa, cotton or sorghum [Funke et al. 2006; http://web.mit.edu/demoscience/Monsanto/about.html].

CONCLUSION

Compared to dicotyledonous species, technology of cereal modification still faces significant hurdles. However, technology for transformation of major cereals is developed and well described. Current successful achievements are a base for next studies. That will enable to perform tests for basic and applied studies. The significant progress made in cereal transformation is promising for the future prospects and opportunities that can bring successful GM products. However, there are some issues, like regulatory aspects and especially public perception, which can limit scientific development of this approach. For this reason, it should be remembered that proper balance has to be maintained to make society feel safe.

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Genetic modifications as a future prospect in the improvement...
Streszczenie. Postęp w zakresie transformacji zbóż, jaki miał miejsce przez ostatnie dwie dekady, ma ogromne znaczenie dla nauki oraz rolnictwa. Dotychczas w transformacji zbóż posługiwano się głównie technikami bezwektorowymi, przede wszystkim bezpośrednią metodą transferu genów, tzw. strzelbą genową (gene gun). Osiągnięcia z zakresu agrobioro-technologii umożliwiły transformację zbóż przy użyciu bakterii glebowej Agrobacterium tumefaciens, która do niedawna nie była wykorzystywana w doświadczeniach na zbóżach, gdyż rośliny jednośmiernie nie stanowią dla niej organizmu gospodarza i nie wykazują objawów choroby guzowatości korzenia powodowanej. Obecnie pięć gatunków zbóż o najwyższym znaczeniu gospodarczym – ryż (Oryza sativa L.), kukurydza (Zea mays L.), pszenica (Triticum aestivum L.), jęczmień (Hordeum vulgare L.) i sorgo (Sorghum bicolor L.) – jest powszechnie poddawanych transformacji z udziałem A. tumefaciens. Wykorzystanie narzędzi genetyki molekularnej pozwala na uzyskanie zbóż o nowych, polepszonych cechach. W niniejszej pracy skupiono się na możliwości rozwoju rolnictwa poprzez wdrażanie genetycznie zmodyfikowanych zbóż odpornych na stresy biotyczne i abiotyczne oraz podsumowano najważniejsze osiągnięcia ostatnich lat z zakresu transformacji zbóż.

Słowa kluczowe: transformacje, Agrobacterium tumefaciens, zbóż, tolerancja na stresy, genetycznie modyfikowane zbóż