Plant biomass increase: recent advances in genetic engineering

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Introduction. Plants are photoautotrophic organisms which using light energy can transform inorganic carbon dioxide to carbohydrates and then to other compounds and in this manner form their biomass. We use plants for food and in different fields of our activity such as construction, textile, pharmaceutical and chemical industries. Plant biomass has also been considered as an important renewable source of biofuels [1, 2]. Enhancing plant height, growth rates and total biomass retains a principal demand due to the growing of the world population.

Considerable efforts of the plant scientists have been aimed at the problem of plant biomass increase. Plant growth markedly depends on availability of essential nutrients such as nitrogen and phosphorus which modulate a number of aspects of the plant development including root and shoot branching and enlargement, leaf growth, flowering time, and regulate expression of many genes involved in nitrogen and carbon metabolism [3, 4]. Genetic engineering investigations on nitrogen assimilation for the improvement of nitrogen efficiency have recently been deeply reviewed [5, 6].

Engineering of photosynthesis in crop species can significantly increase agricultural productivity. Summarizing the results obtained in the model objects on improvement of photosynthetic electron transport chain, rubisco activity and specificity, Rubisco activation state, photorespiration, sedoheptulose-1,7-bisphosphatase/fructose-1,6-bisphosphatase activity, Peterhansel et al. focused their attention on necessity to test elaborated approaches in true crops under conditions of agricultural production [7].

The regulation of carbon allocation between photosynthetic source – leaves and sink tissues – is an important factor controlling plant yield [8]. Plant organs are initiated as primordial outgrowths, and require controlled cell division and differentiation to achieve their final size and shape. Plant hormones thinly regulate plant growth and affect total biomass and yield production [9–12]. Transgenesis allows identification of the mechanisms of complex resistance to stresses and thus leads to an increase in production of plant biomass in non-optimal conditions [13].

The aim of this review was to show the last achievements in genetic engineering and perspectives of some approaches (different promoters, fused genes) for opti-
mization of ectopic gene expression for crop biomass increase under field.

**Biomass increase in optimal growth conditions.** Changes in the plant biomass accumulation can be achieved by regulation of the carbohydrate metabolism [14–16]. Simultaneous upregulation of UDP-glucose pyrophosphorylase, sucrose synthase and sucrose phosphate synthase resulted in enhanced primary growth; for example, for tobacco *Nicotiana tabacum* L. in some cases an increase in height growth was over 50 % [17]. Due to the increased sucrose phosphate synthase activity the total *Arabidopsis* (*Arabidopsis thaliana* L.) biomass was 2-fold higher in *AtPAP2* (purple acid phosphatase) overexpressed plants than in wild-type [18]. The RNAi-mediated down-regulation of glucan water-dikinase (the primary enzyme required for starch phosphorylation) under the control of an endosperm-specific promoter led to a decrease in starch phosphate content in common wheat ( *Triticum aestivum* L.) [19]. Consistent increase in vegetative biomass, grain size and grain yield was observed in subsequent generations in both greenhouse and field trials. Overexpression of sucrose synthase (*SusA1*) gene from a superior quality fiber germplasm line 7235 in cotton *Gossypium hirsutum* increased fiber length and strength [20]. Increasing *GhSusA1* transcript abundance in vegetative tissues led to elevated seedling biomass.

Many biotechnological systems have been established to advance enhancing plant height, growth rates and total biomass with emphasis on increasing the concentration of the plant hormones or on their signalling. Overexpression of the most studied gibberellin biosynthesis enzyme, GA 20-oxidase gene, resulted in an excessively high activity of gibberellin deactivating enzyme, GA 2-oxidase. It was shown that silencing the gibberellin deactivating enzyme in tobacco plants resulted in a dramatic improvement of their growth characteristics, compared with the wild type and GA 20-oxidase over-expressing plants [21]. Suppression of *PtGA2ox4* and *PtGA2ox5* genes belonging to the poplar C19 gibberellin 2-oxidase (GA2ox) gene subfamily which primarily expressed in aerial organs led to significant increase of leaf size (+ 50 %), stem height (+ 20 %), diameter (+ 10 %) and biomass (+ 30 %) in *Populus*. It had no effect on the root development [22]. Transplastomic tobacco plants expressing β-glucosidase (*Bgl-1*), as compared with untransformed plants, have shown 2-fold higher gibberellin (of both GA1 and GA4 levels) in leaves but not in other organs. The elevated levels of other plant hormones, including zeatin and indole-3-acetic acid, are observed in BGL-1 lines. These plants flowered 1 month earlier with an increase in biomass (1.9-fold), height (1.5-fold), and leaf area (1.6-fold) in comparison with untransformed plants [13].

The increase in organ size due to enhanced cell proliferation, without contribution from cell expansion was observed in *Arabidopsis* and tobacco plants expressing ARGOS (full-length cDNA from Chinese cabbage and *A. thaliana* leaves, respectively) gene [23, 24].

Significant axillary bud outgrowth at all nodes on the main stem with the pronounced branch development from the more basal nodes was observed in narrow-leaved lupin (*Lupinus angustifolius* L. cv Merrit) transgenic lines with isopentenyl transferase (*ipt*) gene from *Agrobacterium tumefaciens* coupled to a flower-specific promoter (TP12) from *N. tabacum* [25]. *IPT* expression increased cytokinin levels in flowers, meristem tissues and phloem exudates in a form specific manner. The total number of pod set in some transgenic lines was increased and grain size was not significantly altered compared to control. In transgenic tobacco expressing fused *AOC-ipt* gene, cytokinins increased only two to three fold, and the plants grew more vigorously than the AOC (the allene oxide cyclase gene from the salt-tolerant plant *Bruguiera sexangula*, which displays salt tolerance) transgenic plants lacking the *ipt* gene [26]. It was reflected in rapid plant growth, longer flowering period, greater number of flowers, more seed product, and increased chlorophyll synthesis. Total dry weight increased in *AOC-ipt* tobacco up to 1.27-fold in comparison with control ones and retained at the control level in *AOC* plants in nonstress greenhouse conditions.

In our experiments *cyp11A1* canola (*Brassica napus* L.) plants expressing cytochrome P450<sub>scC</sub> from bovine adrenal cortex mitochondria produced increased fresh weight (+ 33 %) and total soluble proteins (+ 71 %) in comparison with the control ones in non-stress aseptic conditions [27]. In animals cytochrome P450<sub>scC</sub> catalyzes cholesterol oxidation with formation of pregnenolone [28]. Superoxide radicals are formed during these reactions. We detected SOD activity increase in leaves
of some cyp11A1 canola plants in optimal growth conditions when it was compared with untransformed ones.

The enhanced initial seminal root growth in transgenic rice (Oryza sativa L.) seedlings expressing sheep serotonin N-acetyltransferase (NAT) matched their increased root biomass [29]. NAT is believed to be a rate-limiting enzyme in the melatonin biosynthesis in animals. It has previously been shown that exogenous melatonin application enhances plant growth [30]. Among a number of actions, melatonin is a direct free radical scavenger and an indirect antioxidant [31].

Agrobacterium rhizogenes-mediated transformation technique can be used for the plant biomass improvement. The increased dry weight was observed in rolA-transformed blue grama grass (Bouteloua gracilis (H. B. K.) Lag. ex Steud.) plants under greenhouse conditions, it was mainly related to shoot growth [32]. Several liquorice Glycyrrhiza glabra L. hairy root clones bearing rolB gene were more branched and showed about 8 fold higher root biomass on solid medium than untransformed ones [33].

Arabidopsis lines overexpressing pdx2 gene which is involved in the de novo vitamin B6 biosynthesis pathway in plants have considerably larger vegetative and floral organs and it is related to a general increase in total protein, lipid and carbohydrate content [34].

The STOREKEEPER (STK) family of DNA-binding proteins works as transcription factors and the ectopic expression of two stk-like genes from Arabidopsis, stk01 and stk03, in tobacco increased the number of vegetative internodes and promoted plant and leaf size, stem diameter and sturdiness [35].

Selective genes neither created significant unintended pleiotropic effects on gene expression nor led to increased biomass formation [36, 37]. In some experiments the plants bearing vector with only selective gene were used as control ones. Any observations about biomass increase were fixed ([13] – nptII gene,[38] – bar gene). We did not also detect differences in biomass production between untransformed and transgenic canola plants simultaneously expressing nptII and promoterless bar genes [39].

Genetic engineering approaches allow reaching more than 2-fold biomass increase in model as well as in crop plants under both optimal controlled (greenhouse or growth chamber) and field conditions (Table 1).

**Advantages under stress conditions.** The expression of majority of genes which are mentioned in this chapter gives the advantages for transgenic plants under stress growth. These plants often do not differ from control ones in the optimal conditions. Both transgenic and initial plants reduce biomass production under stress influences. Transgenesis leads to new mechanisms of complex resistance to stresses of different origin and this knowledge provides creating the plants with high productivity under unfavorable conditions.

The rate of photosynthesis declines at moderately high temperatures. This can be attributed to a reduced ability of Rubisco activase to achieve optimum activation of Rubisco, which causes lower Rubisco activity. Transgenic Arabidopsis lines expressing chimeric activase (Rubisco recognition domain in more thermostable tobacco activase was replaced with that from Arabidopsis) showed higher rates of photosynthesis than the wild type after a short exposure to higher temperatures [44]. They also formed higher biomass and seed yield when compared with the wild type plants exposed to moderately elevated temperature.

Tobacco chloroplast engineering of β-alanine pathway by over-expression of the Escherichia coli panD gene, which catalyzed decarboxylation of l-aspartate to generate β-alanine and carbon dioxide, enhances thermostolerance of photosynthesis and biomass production following high temperature stress [45].

Limited availability of phosphate ion (P) and nitrogen reduces plant growth in natural ecosystems. Compared with wild-type plants, the transgenic canola over-expressed barley alanine aminotransferase (AlaAT) driven by canola root specific promoter (btg26), had increased biomass (FW 1.98 fold, DW 1.75 fold) and seed yield in both laboratory and field under low nitrogen conditions, whereas no differences were observed under high nitrogen [46]. These changes resulted in a 40 % decrease in the amount of applied nitrogen fertilizer required under field conditions to achieve the yields equivalent to wild-type plants.

Phosphorus (P) is an essential nutrient for the plant growth and development, but is generally unavailable and inaccessible in soil, since applied P is mostly fixed to aluminium (Al) and ferrum (Fe) in acidic soils and to calcium (Ca) in alkaline soils. Increased organic acid excretion is one of the mechanisms by which plants use
to enhance P uptake. Overexpressing the mitochondrial malate dehydrogenase (MDH) gene from the mycorrhizal fungi *Penicillium oxalicum* transgenic tobacco lines which showed the highest level of MDH activity and malate exudate were characterized by a significant increase in growth over wild-type [47]. The construction of a new citrate synthesis pathway by simultaneous overexpression of own citrate synthase and a mutant (with reduced sensitivity to organic acid inhibition) phosphoenolpyruvate carboxylase from *Synechococ-
“cus vulcanus” in the cytoplasm of transgenic tobacco leaves led to an enhanced Al resistance in plants [48].

The biomass of several MtPHY1 (phytase, under control of the root-specific MtPHY1 promoter) alfalfa (Medicago sativa L.) lines was three times that of the control when plants were grown in sand supplied with phytate as the sole P source and two times when the plants were grown in natural soils without additional P supplement [49]. Over-expression of GmEXP2 (a soybean b-expansin) gene resulted in 28% increase in soybean (Glycine max (L.) Merr.) fresh weight at low P [50].

Protein dephosphorylation mediated by protein phosphatases plays a major role in signal transduction of plant responses to environmental stresses. The fresh weight increase in transgenic Arabidopsis lines bearing Faseolus vulgaris phosphatase (PvPs2:1) was significantly larger than that in wild type plants at low and high P levels, especially at the latter, accompanying by the upper of total P content and total root length [51]. AtPAP18 (Arabidopsis purple acid phosphatase encoding gene) tobacco plants exhibited significant increase in the acid phosphatase activity leading to an improved biomass production in both P$_r$-deficient and P$_r$-sufficient conditions [52].

Transgenic canola, expressing the gene for the enzyme 1-aminocyclopropane-1-carboxylate (ACC) deaminase, and/or untransformed canola treated with Pseudomonas putida UW4, which expressed the same gene, had greater shoot biomass compared to the untransformed canola under the low flood-stress conditions [53].

Inositol polyphosphate kinase (IPK) participates in inositol metabolism, calcium signaling, stress response, gene transcription and other physiological and biochemical processes. Transgenic soybean plants with the ThIPK2 gene (IPK from Thellungiella halophila) displayed water deficit-, salt- and oxidative-tolerance compared to untransformed controls [54]. Furthermore, the expression of ThIPK2 altered the ratio of fatty acid components in soybean seeds, resulting in an increase of oleic acid (C18:1). The seed size was also increased in the transgenic plants.

The ectopic antioxidant gene expression leads to an increased plant resistance to stress of different origin that is accompanied by the formation of a larger plant biomass. The first enzyme in the detoxifying process of reactive oxygen species which were generated as by-products of fatty acid β-oxidation, photosynthesis, and environmental conditions such as extreme temperatures and/or water stress, especially in combination with high light intensities is superoxide dismutase (SOD). It converts superoxide radicals to hydrogen peroxide. Some independent transgenic alfalfa (M. sativa) plants heterologously expressing Mn-SOD in mitochondria or chloroplasts had twice the herbage yield of the control plants after one winter period of growth [55]. The transgenic canola which overexpressed wheat Mn SOD3.1 produced more vigorous seedlings under both normal and stress conditions [56].

In our experiments cyp11A1 canola plants expressing cytochrome P450$_{sec}$ from bovine adrenal cortex mitochondria formed larger biomass during different ontogenetic stages compared with untransformed control [27, 57]. Some of transgenic lines formed seedlings with longer roots (by 50%) and hypocotyls (by 85%) during germination at high temperature (Figure) [57].

Dehydroascorbate reductase (DHAR) maintains redox pools of ascorbate (AsA) by recycling oxidized AsA to reduced AsA. OsDHAR1 rice significantly increased photosynthetic capacity and antioxidant enzyme
activities under paddy field conditions [58]. It also improved grain yield and biomass due to the increase of culm and root weights and enhanced panicle and spikelet numbers.

Ascorbate oxidase is an apoplastic enzyme, which also controls the redox ascorbate pool. Tomato *Solanum lycopersicum* plants with decreased ascorbate oxidase activity due to RNA-interference formed a larger fruit yield under limited water and leaf removing [59]. The ascorbate oxidase plants also showed increase in stomatal conductance and leaf and fruit sugar content, as well as an altered apoplastic hexose:sucrose ratio.

Glycine betaine is an osmoprotectant that plays an important role and accumulates rapidly in many plants during salinity or drought stress. Choline monooxygenase (CMO) is a major catalyst in the synthesis of glycine betaine. The seed cotton yield of the *AhCMO* (choline monooxygenase from *Atriplex hortensis*) plants was lower under normal conditions, but was significantly higher than that of non-transgenic plants under the salt-stressed field conditions [60]. Common wheat lines that were transgenic for the *betA* gene encoding choline dehydrogenase from *E. coli* were less injured and exhibited greater root length and growth compared with the wild type under drought stress [61].

Glutathione (GSH), a low-molecular-weight tripeptide molecule, that plays an important role in cell function and metabolism as an antioxidant, is synthesized by γ-glutamylcysteine synthetase (γ-ECS) and glutathione synthetase (GS). The transgenic rice plants expressing the *ECS* gene from *Brassica juncea* L. under the regulation of a stress-inducible *Rab21* promoter displayed a moderate increase in biomass (up to 1.2 times in total FW and 1.1 fold in root FW) and rice grain yield (up 1.2 fold in total seed weight) under general paddy field conditions [62].

*AlsAP* (stress-associated protein from the halophyte grass *Aeluropus littoralis*) durum wheat (*Triticum durum*) of the commercial cv. Karim exhibited improved germination rates and biomass production under salinity and osmotic stress conditions [63]. Following long-term salt or drought stress greenhouse trials, *AlsAP* lines produced normally filled grains whereas wild-type plants either died at the vegetative stage under the salt stress or showed markedly reduced grain filling under the drought stress.

Isopentenyltransferase (IPT) is a critical enzyme in the cytokinin biosynthetic pathway. The *ipt* expression under the control of a maturation- and stress-induced SARK promoter delayed stress-induced plant senescence that resulted in an enhanced drought tolerance in peanut (*Arachis hypogaea* L.) in both laboratory and field conditions [64]. The transgenic peanut plants maintained 2 fold higher photosynthetic rates and transpiration than wild-type plants under the reduced irrigation conditions. More importantly, the *ipt* peanut plants produced significantly higher yields than wild-type plants in the field dryland (50 and 29 g/plant, respectively) while at high irrigation no significant yield differences were observed between the transgenic and initial plants (42 and 40 g/plant, respectively).

The *AOC* gene plays a role in salt tolerance. When the *ipt* gene transcriptionally fused with *AOC* in the frame of *AOC-ipt*, slight cytokinin increases were obtained in these transgenic plants which played a positive role in improvement of plant growth. Dry weight was increased in the *pVKH35S-AOC* and *pVKH35S-AOC-ipt* up to 1.12 times and 1.39 fold, respectively, in comparison with the control plants under drought in a greenhouse. It was more prominent under high salinity when plants were watered by sea water and increase in the plant dry weight reached up to 1.59 and 1.37 times (*pVKH35S-AOC-ipt* and *pVKH35S-AOC*, respectively) [26].

As an innate and adaptive response to water deficit, land plants avoid potential damage by rapid biosynthesis of the abscisic acid (ABA), which triggers stomatal closure to reduce transpirational water loss. Recent genetic studies have pinpointed protein farnesyltransferase as a key negative regulator controlling ABA sensitivity in the guard cells. Conditional and specific down-regulation of farnesyltransferase in canola using the *Arabidopsis* hydroxypyruvate reductase promoter driving an RNAi construct resulted in yield protection against drought stress in the field [10]. There was no significant difference in growth and agronomic performance between the genetically engineered transgenic canola and its wild-type control in optimal conditions. However, under the moderate drought stress conditions at flowering, the transgenic plants produced significantly higher seed yield.

High ectopic expression of the tomato abscisic acid-induced *myb1* (*SLAIM1*) gene encoding the R2R3MYB
### PLANT BIOMASS INCREASE: RECENT ADVANCES IN GENETIC ENGINEERING

#### Table 2
**Transgenic plant advantages in biomass production in different stress conditions**

<table>
<thead>
<tr>
<th>Species</th>
<th>Gene(s)</th>
<th>Conditions</th>
<th>Increase, up fold</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Arabidopsis <em>Arabidopsis thaliana</em> L.</td>
<td><em>Phaseolus vulgaris</em> phosphatase (<em>PvPs2:1</em>)</td>
<td>High P level</td>
<td>1.2 (total FW)</td>
<td>[51]</td>
</tr>
<tr>
<td>Tobacco <em>Nicotiana tabacum</em> L.</td>
<td>Arabidopsis purple acid phosphatase encoding gene, AtPAP18</td>
<td>In both P-deficient and P-sufficient conditions</td>
<td>1.41 (total FW)</td>
<td>[52]</td>
</tr>
<tr>
<td></td>
<td>Mitochondrial malate dehydrogenase (<em>MDH</em>) gene from the mycorrhizal fungi <em>Penicillium oxalicum</em></td>
<td>Al-phosphate medium</td>
<td>1.49 (total FW)</td>
<td>[47]</td>
</tr>
<tr>
<td></td>
<td>The same</td>
<td>Fe-phosphate medium</td>
<td>1.29 (total FW)</td>
<td>[47]</td>
</tr>
<tr>
<td></td>
<td>The same</td>
<td>Ca-phosphate medium</td>
<td>1.28 (total FW)</td>
<td>[47]</td>
</tr>
<tr>
<td>Alfalfa cv. Regen SY-4D</td>
<td><em>AOC</em>-ipt-isopentenyl transferase gene (ipt) downstream transcriptionally fused with <em>AOC</em> (allene oxide cyclase gene from <em>Bruguiera sexangula</em>, which displays salt tolerance) gene</td>
<td>Drought stress</td>
<td>1.39 (total DW)</td>
<td>[26]</td>
</tr>
<tr>
<td>Alfalfa</td>
<td>Phytase (<em>M PHY1</em>) gene from <em>Medicago truncatula</em> under the root-specific MtPT1 promoter</td>
<td>In natural soils without additional Phosphorus supplement</td>
<td>2 (total FW)</td>
<td>[49]</td>
</tr>
<tr>
<td></td>
<td>The same</td>
<td>With phytase as the sole P source</td>
<td>3 (total FW)</td>
<td>[49]</td>
</tr>
<tr>
<td>Rice cv. Ilimi</td>
<td><em>Mn-SOD</em> in mitochondria or chloroplast</td>
<td>Cold stress</td>
<td>2 (total FW)</td>
<td>[49]</td>
</tr>
<tr>
<td>Rice cv. Nipponbare</td>
<td><em>Brassica juncea</em> γ-glutamylcysteine synthetase (<em>BrECS</em>) gene under the regulation of a stress-inducible Rab21 promoter</td>
<td>Osmotic stress (100 mM NaCl)</td>
<td>1.2 (total FW); 1.1 (root FW); 1.2 (total seed weight)</td>
<td>[62]</td>
</tr>
<tr>
<td>Durum wheat (<em>Triticum durum</em>) commercial cv. Karim</td>
<td>Arabidopsis <em>HARDY</em> (<em>HRD</em>) gene, an AP2/ERF-like transcription factor</td>
<td>Drought stress</td>
<td>1.5 (total FW) in greenhouse</td>
<td>[41]</td>
</tr>
<tr>
<td>Common wheat (<em>Triticum aestivum</em> L.) cv. Jinan 17</td>
<td><em>AISAP</em> (stress-associated protein) gene from the halophyte grass <em>Aeluropus littoralis</em></td>
<td>Osmotic stress (50 mM NaCl)</td>
<td>3 (leaf DW)</td>
<td>[63]</td>
</tr>
<tr>
<td>Canola cv. Westar</td>
<td><em>beta</em> encoding choline dehydrogenase from <em>Escherichia coli</em></td>
<td>Drought stress</td>
<td>1.36 (total DW)</td>
<td>[61]</td>
</tr>
<tr>
<td></td>
<td>Barley alanine aminotransferase (<em>AlaAT</em>) under canola root specific promoter (<em>bg26</em>)</td>
<td>Low nitrogen</td>
<td>1.98 (total FW); 1.75 (total DW)</td>
<td>[46]</td>
</tr>
<tr>
<td></td>
<td><em>1-Aminocyclopropane-1-carboxylate (ACC) deaminase</em> from <em>Pseudomonas putida</em> UW4 under control of the rolD promoter from <em>Agrobacterium rhizogenes</em></td>
<td>Low flood stress</td>
<td>1.34 (total DW) in field conditions</td>
<td>[53]</td>
</tr>
</tbody>
</table>
transcription factor resulted in reduced plant growth compared with the control plants under normal growth conditions [65].

However, the 35S:SIAIM1 plants grow significantly better than the wild-type controls under high salinity, and only marginally lower than the 35S: SIAIM1 plants grown without salt stress.

Different plants exhibit different, sometimes opposite, response to the same foreign gene introduction. Expression of Δ1-pyrroline-5-carboxylate synthetase (P5CS) from mothbean (Vigna aconitifolia L.) under the control of a stress-inducible promoter led to stress-induced overproduction of the P5CS enzyme and proline accumulation in the transgenic rice plants [66]. Second-generation plants showed an increase in biomass under salt- and water-stress conditions as compared to the untransformed plants. But biomass increase in chickpea (Cicer arietinum L.), which accumulated proline (up to 6-fold) due to mutagenized P5CS expression, was not documented [67]. Authors supposed that the enhanced proline level had little bearing on the components of yield architecture that are significant in overcoming the negative effects of drought stress in chickpea.

The transformation of dicots with the rolA gene results in the shortened internode length, green darkened leaves, reduced apical dominance, leaf wrinkling, decreased length-to-width leaf ratio, shortened styles, larger flower size, reduced flower number, condensed inflorescences, male sterility, and retarded onset of flowering [68]. The rolA B. gracilis (the important forage grass) lines showed a 2-fold reduced root system, but they produced up to twice as much foliage as control plants due to enhanced height (up 1.3 fold) and increased tillering and leaf number (up to 1.7 and 1.5 fold, respectively) [32].

Transgenesis allows reach up to 2 fold biomass increase versus the untransformed (wild type or tissue culture) plants in stress (Table 2).

### Table 2

<table>
<thead>
<tr>
<th>Species</th>
<th>Gene(s)</th>
<th>Conditions</th>
<th>Increase, up fold</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Canola cv. Westar</td>
<td>1-Aminocyclopropane-1-carboxylate (ACC) deaminase + <em>Pseudomonas putida</em> UW4, which also expresses ACC deaminase</td>
<td>Low flood stress</td>
<td>1.38 (control total DW)–1.31 (transgenic total DW) in field conditions</td>
<td>[53]</td>
</tr>
<tr>
<td>Canola doubled haploid line DH-12075</td>
<td>Wheat mitochondrial Mn superoxide dismutase (<em>Mn SOD3.1</em>)</td>
<td>Cold, drought, high temperature (field and in vitro)</td>
<td>1.4 (total FW)</td>
<td>[56]</td>
</tr>
<tr>
<td>Canola cv. Mariia</td>
<td><em>cyp11A1</em> gene encoding cytochrome P450&lt;sub&gt;sec&lt;/sub&gt; from bovine adrenal cortex mitochondria</td>
<td>Osmotic stress (500 mM mannitol) in vitro</td>
<td>2 (total FW)</td>
<td>[27]</td>
</tr>
<tr>
<td>Canola cv. Youyan N 9</td>
<td><em>Brassica napus</em> heme oxygenase (<em>BHO-1</em>)</td>
<td>Hg stress</td>
<td>1.41–1.50 (total DW)</td>
<td>[69]</td>
</tr>
<tr>
<td>Tomato (<em>Solanum lycopersicum</em>) cvs CastlemarII and Micro-Tom</td>
<td>The tomato abscisic acid-induced <em>myb1</em> (<em>SIAIM1</em>) gene encoding an R2R3MYB transcription factor</td>
<td>Osmotic stress (200–250 mM NaCl)</td>
<td>1.1 (total FW)</td>
<td>[65]</td>
</tr>
<tr>
<td>Sugar beet (<em>Beta vulgaris</em> L.) cv. Heitian N 1</td>
<td>An <em>Arabidopsis thaliana</em> vacuolar Na&lt;sup&gt;+&lt;/sup&gt;/H&lt;sup&gt;+&lt;/sup&gt; antiporter gene, <em>AtNHX3</em></td>
<td>Osmotic stress (500 mM NaCl)</td>
<td>2 (total DW); 2.2 (total FW); 2.2 (storage root DW)</td>
<td>[70]</td>
</tr>
<tr>
<td>Soybean (<em>Glycine max</em> (L.) Merr.) cv. HN89</td>
<td>A soybean β-expansin (<em>GmEXPB2</em>) gene</td>
<td>Low P level</td>
<td>1.28 (total FW)</td>
<td>[50]</td>
</tr>
<tr>
<td>Peanut (<em>Arachis hypogaea</em> L.) New Mexico Valencia A</td>
<td>Isopentenyltransferase (<em>IPT</em>) under the control of a maturation- and stress-induced promoter (<em>P&lt;sub&gt;cav&lt;/sub&gt;</em>)</td>
<td>Drought stress</td>
<td>1.84–1.61 (shoot FW-DW); 2.88–2.24 (root FW-DW) in growth chamber</td>
<td>[64]</td>
</tr>
</tbody>
</table>
Conclusions. Genetic engineering approaches allow reaching more than 2-fold biomass increase in model as well as in crop plants under optimal conditions. Transgenesis can reveal the new mechanisms of complex resistance to stresses of different origin and this knowledge may be used to create plants with high productivity under unfavorable conditions. It leads to reduced biomass losses under stress nearly 2-fold. Overexpression of some genes of phosphorus and nitrogen metabolism offers an effective approach for reducing the consumption of chemical fertilizers through increased acquisition of soil nutrients and mobilization of internal resources. In recent years the significant amount of studies have been focused at crops such as canola, rice and wheat under field conditions. It should facilitate the introduction of these developments in the agriculture practice.

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