



**FREDERICK RESEARCH CENTRE**

**Vulnerability of the narrow endemic *Cedrus brevifolia* from Cyprus: Detection of genes and phenotypic trait diversity linked to adaptation.**

Protocol No. DIDAKTOR/0609/13

### **Deliverable 9**



**Report of genes which will be tested in this project, responsible for phenotypic characteristics and physiological functions.**

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<sup>1</sup> The present report has been prepared by Ecologie des forêts Méditerranéennes, INRA, Avignon in the framework of the project DIDAKTOR/0609/13 entitled "Vulnerability of the narrow endemic *Cedrus brevifolia* from Cyprus: Detection of genes and phenotypic trait diversity linked to adaptation." The project is co-financed by the European Regional Development Fund and the Republic of Cyprus through the Research Promotion Foundation.

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## 1. Introduction

The current deliverable aims to provide an overview on candidate genes, which could be tested in *Work Package 5: Application and analysis of molecular markers – genes amplification and nucleotide diversity* (WP.5). It is noted that the present report is a preliminary work and cannot be the rule for later laboratory work. The present deliverable will serve as a tool on which the Scientific Committee (SC) will discuss and decide which of these candidate genes will be tested in WP.5, in order to determine the genes which will show successful amplified and polymorphic genes, and, hence, will be used for the whole sample size.

The majority of genomic research in Pinaceae family has been conducted in the *Pinus* subgenus *Pinus*, *Abies* and *Picea* species, mostly due to the high economic importance of these species. However, during the last decade, the need of knowledge on wild tree populations' adaptive variation has led to the expansion of genomic studies also for other species of Pinaceae family. One of the main research goals of the present study is to assess the diversity of candidate adaptive genes of *Cedrus brevifolia*. For this reason a careful and completed pre-evaluation of literature sources has been carried out through this document, where numerous adaptive candidate genes are presented. The literature sources were the:

1. Gene Banks (i.e. European Molecular Biology Laboratory –EMBL–, National Center for Biotechnology Information –NCBI–),
2. International bibliography (scientific books, scientific journals and scientific articles) and
3. Running research projects on relative issues.

## 2 Adaptive candidate genes

As mentioned above, the Pinaceae family includes a significant number of species with high economic importance, and, hence, a significant number of candidate genes on adaptive traits are nowadays available in international literature. It is characteristic that in GenBank over than 2.068 genes are reported for Pinaceae family, as well as 302.569 nucleotides (core subset nucleotide sequences) and 1.015.471 expressed sequences (EST). Therefore, the following criteria were adopted for the preliminary selection of genes which can be tested through the WP.5:

- The previous successful amplification and diversity of genes in *Cedrus spp.* and/or in Pinaceae family and
- The genes' function and their ability to adapt to stress resistance.

(A) A recent master thesis by Karam (2010)<sup>2</sup> is a significant work aiding genes selection for the current project. In this master thesis, the transferability of 132 candidate genes in *Cedrus spp.* from two projects (Fragments de gènes du projet du BRG 2005-2006 and Comparative Re-

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<sup>2</sup> Karam Marie-Joe (2010) Caractérisation du polymorphisme moléculaire de gènes candidats pour la résistance à la sécheresse dans le genre *Cedrus*. Université Saint-Joseph Année universitaire et Institut National de la Recherche Agronomique. Master thesis.

Sequencing in Pinaceae - <http://dendrome.ucdavis.edu/NealeLab/crsp/>) was evaluated, in order to assess the phylogenetic structure of cedar species (*Cedrus* spp.). Based on the quality of the first sequences obtained and the sequences algorithmic analysis, **nine genes** that are potentially related to drought resistance were selected (Table 1) by Karam (2010) for assessing the phylogenetic relationship among *Cedrus* spp.

- (B) Search in the GenBank found eight genes with successful amplification in the *Cedrus brevifolia* genome (<http://www.ncbi.nlm.nih.gov/nuccore/?term=Cedrus%20brevifolia>). **Three genes** out of the eight genes will also be tested (Table 2) in the present study.
- (C) A research project entitled Conifer Resequencing Initiative for European Conifers (CRIEC), under the framework of EvolTree programme (<http://www.evoltree.eu/>), had as a goal the transferability of candidate genes from maritime pine (*P. pinaster* Ait.) to 18 conifer species. Thus, CRIEC made available a large candidate gene set across several conifer species with contrasting life -and evolutionary- histories, opening the opportunity for extensive comparative studies at the DNA sequence level. Based on the above two criteria, the data set from CRIEC project was pre-evaluated and totally **187 candidate genes** (Table 3) out of the 300 were selected in order to be tested in the present study (after the relevant evaluation of those genes from SC).

It should be mentioned that the transfer of candidate genes information from model to non-model species is particularly challenging in conifers due to nearly-identical paralogs and large gene families, a consequence of their large genomes. However, the SC will be the corresponding body of the project for deciding the final number and type of genes which will be applied in the present study (see Deliverable 1). Finally, it must be pointed out that both the Young Researcher and the SC will continue to be updated about the running projects relevant to this study.

**Table 1: Candidate genes which showed successful transference to *Cedrus* spp. by Karam Marie-Joe (2010).**

ID	Fragment	Gene's name	Primer sequence		Function
			Forward (5' → 3')	Reverse (5' → 3')	
1.	0_8479	INT1	CTGGATTCAAAAATTTCCATC	TGTCATAGAAGTGCCAATGGT	Inositol transporter involved in root growth.
2.	0_16009	Argonaute7 (AGO7)	GAAATGGTAGGAGAGTTG	GATAATGGGTTGGTCTG	Micro RNAs involved in epigenetic mechanisms.
3.	2_1405	Methionine synthase: 5-methyltetrahydropteroyltriglutamate—homocysteine (MS1)	ATTGATATGGATGCCGATGT	ATGCAACCATGTTGGTCAAT	Changes in the growth rate in case of water stress.
4.	2_2973	ATP/ADP-antiporter	CATTCCAAGAGAAGACGAC	TTGCCAACTCCACTCCCTAC	Inhibit the palmitate-stimulated respiration in the controlled state and increase the membrane potential lowered by palmitate.
5.	2_9930	Transcription factor SHR (Short root)	CCCTAACATCATCAACAACATCATC	ACAACATCTCCACAAGCTCAAC	Root growth (root stem cell differentiation and development radial).
6.	CL_4354	Phosphatase 2A	AGAGATTCCCCATCCAC	TTACAGACCTTTTTGACTACTTCCC	Regulation of cell proliferation.
7.	CL_813	Sucrose synthase	CAGACAGAGTCATTAATCTCTCAG	TGAAATTATTGTGGATGGGG	Carbohydrate metabolism.
8.	UMN_5833	Methyltransferase	GATGTTGGTTGTGGAGTTG	AGAGGGGGTTTGGTATCTGG	Gene regulation without altering the original sequence.
9.	Gluc_C12	Precursor Glucan-endo-1,3-β-glucosidase	TCCCATCCATAAGTCGATGC	TGCGCTCTACAATAGGACCA	Maintaining osmotic balance under conditions of dehydration.

**Table 2: Three out of the eight GenBank pre-evaluated genes**

ID	Regions	Gene's name	Function	Reference
1.	trnC - trnD	PsbM	Photosystem II reaction centre M protein (PsbM). The photosystem II (PSII), a multi-subunit membrane protein complex, catalyzes oxidation of water to molecular oxygen and reduction of plastoquinon.	Qiao et al 2007 <sup>3</sup>
2.	trnC - trnD	PsbN	Hydrophobic protein, crucial for cytochrome b6-f complex assembly and/or stability	Qiao et al 2007
3.	rpL16 intron	Ribosomal protein S12	Component of the decoding center of the 30S ribosomal subunit and is involved in both tRNA selection and the response to streptomycin.	Qiao et al 2007

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<sup>3</sup> Qiao C Y, Ran J H., Li Y, Wang X Q (2007) Phylogeny and biogeography of *Cedrus* (Pinaceae) inferred from sequences of seven paternal chloroplast and maternal mitochondrial DNA regions. *Ann. Bot.* 100 (3): 573 – 580.

**Table 3: Pre-evaluated candidate genes from Conifer Resequencing Initiative for European Conifers (CRIEC) project.**

ID	Code of genes in GenBank <sup>4</sup>	Description of genes	Function (biological process)
1.	At1g12260	NAC domain-containing protein 7	Transcription regulation
2.	At1g09540	myb proto-oncogene protein	Regulation of secondary metabolism, in the control of cell shape and fate, and in responses to hormones, drought, and viral infection
3.	At2g01950	serine/threonine-protein kinase	Trans membrane receptor
4.	At3g20250	pumilio 5	Regulation of translation
5.	At1g70190	ribosomal protein L7/L12 domain-containing	Translation
6.	At1g16030	heat shock protein 70B	Response to stress (heat)
7.	At5g01890	leucine-rich receptor-like protein kinase	Protein phosphorylation
8.	At1g54990	protein auxin RESPONSE 4	Required for the auxin influx, response to auxin stimulus, response to mechanical stimulus
9.	AtCg00500	acetyl-CoA carboxylase beta subunit	Fatty acid biosynthesis, lipid synthesis, chloroplast
10.	At5g23860	tubulin beta-8 chain	Microtubules, response to salt stress
11.	At5g23860	tubulin beta-8 chain	Microtubules, response to salt stress
12.	At2g39940	Coronatine-insensitive protein 1	Required for jasmonate-regulated plant fertility and defense processes, and for coronatine and/or other elicitors perceptions/responses
13.	At4g22720	glycoprotease M22 family protein	Proteolysis
14.	At3g04380	histone-lysine N-methyltransferase SUV4	Methyltransferase, chromatin regulator
15.	At1g53730	STRUBBELIG-receptor family 6	Membrane protein, protein phosphorylation
16.	At1g20980	squamosa promoter binding-like protein	Transcription regulation, May play a role in plant development.
17.	At1g44760	adenine nucleotide alpha hydrolase-like	Response to stress
18.	At1g33560	disease resistance protein ADR1	Hypersensitivity, plant defense
19.	At5g54250	cyclic nucleotide-gated ion channel 4	Acts as cyclic nucleotide-gated ion channel, Might constitute a common downstream component of the signaling pathways leading to hypersensitive response (HR); plant defense
20.	At5g14760	L-aspartate oxidase	NAD biosynthetic process, oxidation-reduction process
21.	At5g66390	peroxidase 72	Removal of H <sub>2</sub> O <sub>2</sub> , oxidation of toxic reductants, biosynthesis and degradation of lignin, suberization, auxin catabolism, response to environmental stresses such as wounding, pathogen attack and oxidative stress.
22.	At1g67100	LOB domain-containing protein 40	Response to gibberellins stimulus
23.	At5g53130	cyclic nucleotide-gated ion channel 1	Ion transport
24.	At4g04970	callose synthase 11	Cell wall biogenesis and degradation
25.	At1g11870	Seryl-tRNA synthetase	Chloroplast and mitochondrion organization, ovule development, seryl-tRNA aminoacylation
26.	At2g18150	peroxidase 15	Oxidation-reduction process, hydrogen peroxyde catabolic process

<sup>4</sup> <http://www.ncbi.nlm.nih.gov/>

ID	Code of genes in GenBank <sup>4</sup>	Description of genes	Function (biological process)
27.	At5g57930	APO protein 2	May be involved in the stable assembly of several 4Fe-4S cluster-containing complexes of chloroplasts
28.	At1g58340	MATE efflux family protein	Regulation of organ formation, response to nematode
29.	At1g80870	protein kinase-like protein	Cell membrane, protein phosphorylation
30.	At2g32950	E3 ubiquitin-protein ligase COP1	Phytochrome signaling pathway, ubl conjugation pathway
31.	At5g26340	sugar transport protein 13	Mediates an active uptake of hexoses, probably by sugar/hydrogen sympor
32.	At1g30950	protein UNUSUAL FLORAL ORGANS	Floral development
33.	At3g16620	translocase of chloroplast 120	GTPase involved in protein precursor import into chloroplasts.
34.	At1g15080	Phosphatidic acid phosphatase (PAP2)	May play a general "housekeeping role" in lipid metabolism: abscisic acid signaling pathway
35.	At1g68530	3-ketoacyl-CoA synthase 6	Contributes to cuticular wax and suberin biosynthesis; response to cold and light stimulus, unidimensional cell growth
36.	At3g29360	putative UDP-glucose 6-dehydrogenase 1	Oxidation-reduction process
37.	At1g61040	plus-3 domain-containing protein	Histone modification, negative regulation of flower development
38.	At5g26340	sugar transport protein 13	Sugar transport
39.	At2g20190	CLIP-associated protein	Cell growth, mitosis, protein stabilization
40.	At5g05390	laccase 12	Lignin degradation and detoxification of lignin-derived products
41.	At3g14930	uroporphyrinogen decarboxylase 1	Chlorophyll and porphyrin biosynthesis
42.	At1g06800	phospholipase A1-Igama1	Lipid catabolic process, chloroplast, Could be involved in early wound response
43.	At1g58290	glutamyl-tRNA reductase 1	Chlorophyll and porphyrin biosynthesis
44.	At4g01370	mitogen-activated protein kinase 4	Plant defense, response to cold, fungus and many other things
45.	At2g20780	putative polyol transporter 4	Sugar transport
46.	At5g17630	Nucleotide/sugar transporter	Sugar transport
47.	At4g11660	heat stress transcription factor B-2b	Response to stress (heat)
48.	At1g02880	thiamin pyrophosphokinase1	Thiamine metabolic process
49.	At4g16700	phosphatidylserine decarboxylase	Phospholipid biosynthetic process
50.	At4g16566	protein histidine triad nucleotide-binding	Catalytic activity
51.	At1g02170	metacaspase 1	Hydrolase, protease, May be involved in the modulation of programmed cell death activated by oxidative stress
52.	At3g46980	putative anion transporter 4	Inorganic phosphate and probable anion transporter, chloroplast
53.	At2g37410	mitochondrial import inner membrane	Transmembrane protein transport, mitochondrion
54.	At4g24520	NADPH-ferrihemoprotein reductase	Oxidation-reduction process, response to abscisic acid stimulus, response to oxidative stress, phenylpropanoid metabolic process
55.	At3g10340	phenylalanine ammonia-lyase 4	Phenylpropanoid metabolism
56.	At3g15730	phospholipase D alpha 1	Abscisic acid signaling pathway, ethylene signaling pathway, lipid degradation; lays an important role in various cellular processes, including phytohormone action and response to stress, characterized by acidification of the cell.

ID	Code of genes in GenBank <sup>4</sup>	Description of genes	Function (biological process)
57.	At1g29340	U-box domain-containing protein 17	Apoptosis, defense response to fungus, incompatible interaction
58.	At3g09270	glutathione S-transferase TAU 8	Transferase, response to cadmium ion, toxin catabolic process
59.	At1g77380	amino acid permease 3	Amino acid transport
60.	At5g59570	myb family transcription factor	Regulation of secondary metabolism, in the control of cell shape and fate, and in responses to hormones, drought, and viral infection
61.	At3g48000	aldehyde dehydrogenase 2B4	Oxidation-reduction process, response to cadmium ion, mitochondrion
62.	At3g56640	putative exocyst complex component 6	Exocytosis
63.	At4g08810	calcium ion binding protein	Unknown
64.	At1g11050	putative receptor-like protein kinase	Protein phosphorylation
65.	At3g55980	zinc finger CCCH domain-containing protein 4	Stress response
66.	At2g42620	F-box protein ORE9	Promotes the senescence
67.	At3g02280	flavodoxin-like protein	Oxidation-reduction process
68.	At1g09840	Shaggy-related protein kinase kappa	May mediate extracellular signals to regulate transcription in differentiating cells
69.	At2g06925	Phospholipase A2-like protein	Lipid catabolic process, phospholipids metabolic process
70.	At1g21590	adenine nucleotide alpha hydrolases-domain	Response to stress, protein phosphorylation
71.	At2g06850	xyloglucan endotransglucosylase/hydrolase protein 4	Participates in cell wall construction of growing tissues
72.	At1g30220	putative inositol transporter 2	Signaling (symport, transport)
73.	At2g24820	translocon at the inner envelope membrane	Oxidation-reduction process, protein targeting to chloroplast
74.	At1g76160	SKU5 similar 5 protein	Oxidation-reduction process
75.	AtMg00510	dehydrogenase subunit 7	Electron transport respiratory chain (mito)
76.	At1g62750	elongation factor EF-G	Protein biosynthesis, chloroplast organization, seed germination
77.	At3g48950	glycoside hydrolase family 28 protein	Carbohydrate metabolic process, cellular cell wall organization
78.	At5g15470	alpha-1,4-galacturonosyltransferase	May be involved in pectin and/or xylans biosynthesis in cell walls
79.	AtCg00340	photosystem I P700 chlorophyll a apoprotein	Photosystem
80.	At4g16260	catalytic/ cation binding / hydrolase	Glycosidase, hydrolase, carbohydrate metabolic process, defense response to fungus, incompatible interaction, response to salt stress
81.	At1g03760	Prefoldin chaperone subunit family protein	Protein folding
82.	At1g32640	transcription factor MYC2	Light (involved in the regulation of ABA-inducible genes under drought stress conditions)
83.	At1g10050	glycosyl hydrolase and carbohydrate-binding	Carbohydrate metabolic process
84.	At5g62560	U-box domain-containing protein 41	Ubi conjugation pathway
85.	At5g49760	leucine-rich repeat protein kinase-like	Protein phosphorylation
86.	At1g24620	putative calcium-binding protein CML25	Potential calcium sensor, response to cold, root hair elongation
87.	At1g48830	40S ribosomal protein S7-1	Translation

ID	Code of genes in GenBank <sup>4</sup>	Description of genes	Function (biological process)
88.	At1g69390	bacterial MinE 1-like protein	Cell division, chloroplast fission, regulation of barrier septum formation
89.	At5g01020	protein kinase family protein	Protein phosphorylation
90.	At4g30440	UDP-D-glucuronate 4-epimerase 1	Carbohydrate metabolism; Involved in the synthesis of the negatively charged monosaccharide that forms the backbone of pectic cell wall components.
91.	At2g16570	amidophosphoribosyltransferase	Purine biosynthesis
92.	At5g35100	peptidyl-prolyl cis-trans isomerase	Isomerase, rotamase
93.	At4g31820	Phototropic-responsive NPH3 family protein	Response to light, stimulus apical protein localization, basipetal auxin transport, cotyledon development
94.	At2g20560	DNAJ heat shock protein-like protein	Reponse to stress, protein folding
95.	At1g22190	ethylene-responsive transcription factor ERF	Ethylene signaling pathway, Probably acts as a transcriptional activator; May be involved in the regulation of gene expression by stress factors and by components of stress signal transduction pathways
96.	At4g37320	cytochrome P450, family 81, subfamily D, polypeptide 5	Oxydation-reduction process
97.	At5g43280	delta(3,5),delta(2,4)-dienoyl-CoA isomerase	Faty acid catabolic process
98.	At2g47420	dimethyladenosine transferase	Transferase
99.	At2g20560	DNAJ heat shock protein-like protein	Response to stress, protein folding
100.	At1g08960	cation exchanger 11	Transmembrane transport
101.	At1g29150	26S proteasome regulatory subunit N6	Protein catabolic process, response to cadmium ion
102.	At1g13130	Cellulase (glycosyl hydrolase family 5)	Carbohydrate metabolic process
103.	At1g80730	zinc finger protein 1	Photomorphogenesis
104.	At1g20230	pentatricopeptide repeat-containing protein	Belong to the PPR family (not known function)
105.	At5g10770	aspartyl protease family protein	Proteolysis
106.	At4g24730	calcineurin-like phosphoesterase family protein	Hydrolase activity
107.	At5g06110	DnaJ and myb-like DNA-binding domain-contain	Response to stress, drought
108.	At1g61580	60S ribosomal protein L3-2	Translation
109.	At1g68020	alpha,alpha-trehalose-phosphate synthase	Trehalose biosynthetic process, Regulates plant architecture, shape of epidermal pavement cells and branching of trichomes
110.	At4g24210	F-box protein GID2	Gibberellin signaling pathway
111.	At5g07280	leucine-rich repeat receptor protein kinase	Protein phosphorylation
112.	At1g68750	phosphoenolpyruvate carboxylase 4	Carbon dioxide fixation, photosynthesis
113.	At2g28470	beta-galactosidase 8	Carbohydrate metabolic process
114.	At4g18640	putative LRR receptor-like serine/threonine	Protein phosphorylation, root hair cell differentiation
115.	At4g00150	scarecrow-like protein 6	Cell division, regulation of transcription, root hair cell tip growth
116.	At3g06580	Galactokinase	Galactose metabolic process
117.	At3g57430	pentatricopeptide repeat-containing protein	Belongs to the PPR family; chloroplast RNA processing
118.	At1g05140, At2g32480	-	Chloroplast organization, proteolysis

ID	Code of genes in GenBank <sup>4</sup>	Description of genes	Function (biological process)
119.	At3g57520	putative galactinol--sucrose galactosyltrans	Carbohydrate metabolic process, response to karrikin (plant growth regulators found in the smoke of burning plant material)
120.	At3g04670	putative WRKY transcription factor 39	Regulation of transcription
121.	At4g12420	Monocopper oxidase-like protein SKU5	Cell membrane, cell wall, May be a monocopper oxidase of unknown specificity. Involved in directional growth processes, possibly by participating in cell wall expansion.
122.	At2g28000	chaperonin-60alpha	Chloroplast organization, embryo development, protein refolding, This protein binds RuBisCO small and large subunits and is implicated in the assembly of the enzyme oligomer. Subunit structure Oligomer of probably six alpha and six beta subunits.
123.	At2g39770	mannose-1-phosphate guanylyltransferase	Cellulose biosynthesis process, defense response to bacterium, response to ammonium ion, response to heat, response to jasmonic acid stimulus, response to ozone, response to salt stress
124.	At3g13772	protein transmembrane nine 7	Cellular copper ion homeostasis, cellular zinc ion homeostasis
125.	At5g49890	chloride channel protein CLC-c	Ion transport
126.	At1g55250/At1g55255	E3 ubiquitin-protein ligase BRE1-like	Ubl conjugation pathway
127.	At1g06220	-	Protein biosynthesis
128.	At1g55150	DEAD-box ATP-dependent RNA helicase 20	Nonsense-mediated mRNA decay, ribosome biogenesis, rRNA processing
129.	At1g08250	arogenate dehydratase 6	Amino-acid biosynthesis, aromatic amino acid biosynthesis, phenylalanine biosynthesis
130.	At3g25140	Galacturonosyltransferase 8	Cell wall biogenesis/degradation, cell adhesion
131.	At5g41370	DNA repair helicase XPB1	DNA repeat, nucleotide-excision repair, response to UV, transcription
132.	At4g23650	calcium-dependent protein kinase 6	Abscisic acid mediated signaling pathway, protein phosphorylation, regulation of anion channel activity, regulation of stomata movement, response to salt stress
133.	At1g48030	dihydrolipoyl dehydrogenase 1	Cell redox homeostasis, oxidation-reduction process, response to cadmium ion
134.	At3g49090	small subunit ribosomal protein S9	Translation
135.	At2g46280	translation initiation factor 3 subunit I	Protein biosynthesis, response to salt stress, response to cadmium ion
136.	At3g17000	ubiquitin-conjugating enzyme E2 32	Ubl conjugation pathway
137.	At3g12290	amino acid dehydrogenase family protein	Folic acid -containing compound biosynthetic processes, oxidation-reduction process
138.	At5g58490	Rossmann-fold NAD(P)-binding domain-contains	Cellular metabolic process
139.	At3g10050	threonine dehydratase biosynthetic	Isoleucine biosynthetic process
140.	At3g53570	serine/threonine-protein kinase AFC1	Protein phosphorylation, regulation of transcription
141.	At1g15690	Pyrophosphate-energized vacuolar membrane	Proton transport
142.	At4g34050	putative caffeoyl-CoA O-methyltransferase	Plant cell wall (reinforcement and in response to wound or pathogens)
143.	At5g62790	1-deoxy-D-xylulose 5-phosphate reductoisomerase	Isoprene biosynthesis

ID	Code of genes in GenBank <sup>4</sup>	Description of genes	Function (biological process)
144.	At1g06290, At1g06300	-	Fatty acid beta-oxidation, medium-chain fatty acid metabolic process
145.	AtMg01360	cytochrome c oxidase subunit 1	Electron transport, respiratory chain, mitochondrion
146.	At3g46510	U-box domain-containing protein 13	Ubl conjugation pathway
147.	At1g70460	-	Protein phosphorylation
148.	At5g58230	histone-binding protein RBBP4	DNA replication, differentiation, flowering, transcription; Required for several aspects of plant development including normal leaf expansion, correct development of flowers, normal endosperm development, repression of parthenogenetic seed development and repression of floral homeotic genes in leaf tissue.
149.	AtCg00680	photosystem II 47 kDa protein	Photosystem
150.	At4g33210	F-box/LRR-repeat protein 15	Auxin homeostasis, organ formation
151.	At4g00150	scarecrow-like protein 6	Cell division, regulation of transcription, root hair cell tip growth
152.	At3g54140	peptide transporter PTR1	Peptide and protein transport
153.	AtCg00600	cytochrome b6/f complex subunit V	Photosystem
154.	At3g02360	6-phosphogluconate dehydrogenase	Pentose-phosphate shunt, response to salt stress
155.	At3g28180	xyloglucan glycosyltransferase 4	Cellular cell wall organization
156.	AtCg00540	cytochrome f	Photosystem
157.	AtCg00730	cytochrome b6/f complex subunit IV	Photosystem
158.	AtCg00680	photosystem II 47 kDa protein	Photosystem
159.	At3g47520	malate dehydrogenase	Cellular carbohydrate metabolic process, maltase metabolic process, response to cold, tricarboxylic acid cycle
160.	At4g37650	protein SHORT-ROOT	Asymmetric cell division, cell cycle, iron ion homeostasis, leaf development, radial pattern formation, regulation of hormone metabolic process, regulation of transcription DNA-dependent
161.	At3g47520	malate dehydrogenase	Acellular carbohydrate metabolic process, maltase metabolic process, response to cold, tricarboxylic acid cycle
162.	At3g26430	GDSL esterase/lipase	Lipid catabolic process
163.	At5g40540	protein kinase family protein	Protein phosphorylation
164.	At4g24660	ZF-HD homeobox protein	Transcription regulation
165.	At4g36990	heat stress transcription factor B-1	Stress response (heat)
166.	At5g40540	ipoxxygenase 5	Protein phosphorylation
167.	At1g69440	-	Defense response, gene silencing by miRNA, regulation of development, heterochronic, regulation of translation
168.	At1g64060	respiratory burst oxidase	ABA and ethylene mediated signaling pathway, defense response by calluses deposition, hydrogen peroxyde biosynthetic process, negative regulation of programmed cell death, oxidation-reduction process, regulation of stomata movement, respiration burst involved in defense response
169.	At2g16920	putative ubiquitin-conjugating enzyme E2	Post-translational protein modification
170.	At5g51300	splicing factor 1	RNA splicing
171.	At1g49760	-	Response to cadmium ion

ID	Code of genes in GenBank <sup>4</sup>	Description of genes	Function (biological process)
172.	At5g13290	-	Protein phosphorylation, regulation of flower development, regulation of root meristem growth
173.	At1g19250	putative flavin-containing monooxygenase 1	Plant defense; Required for the establishment of systemic acquired resistance (SAR)
174.	At5g60450	auxin response factor 4	Auxin signaling pathway, transcription
175.	At5g63780	RING/FYVE/PHD zinc finger-containing protein	Maintenance of shoot apical meristem identity
176.	At3g05260	-	Oxidation-reduction process
177.	At5g12190	pre-mRNA branch site protein p14	RNA splicing, mRNA processing
178.	At4g03390	STRUBBELIG-receptor family 3	Protein phosphorylation
179.	At3g48820	glycosyltransferase family 29	Protein glycosylation
180.	At5g11490	beta-adaptin-like protein A	Endocytosis, intracellular protein transport
181.	At3g07110	60S ribosomal protein L13a-1	Translation
182.	At5g13850	Nascent polypeptide-associated complex subunit	Protein transport, response to salt stress
183.	At1g25380	NAD <sup>+</sup> transporter 2	Transmembrane transport
184.	At1g20950	putative pyrophosphate-dependent phosphofru	Glycolyse, photosynthesis, response to fructose, glucose and sucrose stimulus
185.	At5g27030	Topless-related protein 3	Regulation of transcription
186.	At1g24510	T-complex protein 1 subunit epsilon	Protein folding
187.	At3g12400	protein ELC	Protein transport