

Messenger RNAs Mobile in *Salix Matsudana* Grafts Were in Association With Plant Rooting

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Research Article

Keywords: Salix matsudana, graft, mobile mRNAs, rooting, SNP

Posted Date: June 16th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-556961/v1>

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Abstract

Messenger RNAs exchanged between scions and rootstocks of grafted plants seriously affect their traits performance. The study goals were to identify the long-distance mRNA transmission events in grafted willows using a transcriptome analysis and to reveal the possible effects on rooting traits. The results showed that the *Salix matsudana* variety 9901 has better rooting ability than YJ, which reasonably improved the rooting performance of the heterologous grafts 9901 (scion) / YJ (rootstock). A transcriptome analysis showed that 2,948 differentially expressed genes (DEGs) were present in the rootstock of 9901/YJ grafted plants in comparison with YJ/YJ. Among them, 692 were identified as mRNAs moved from 9901 scion based on a SNP analysis of two parents. They were mostly 1,001–1,500 bp, had 40–45% GC contents, or had expression abundance values less than 10. However, mRNAs over 4,001 bp, having 50–55% GC contents, or having expression abundance values of 10–20 were preferentially transferred. Eight mRNAs subjected to long-distance trafficking were involved in the plant hormone pathways and may significantly promote the root growth of grafted plants. Thus, heterologous grafts of *Salix matsudana* could efficiently influence plant rooting since of the mRNAs transport from scion to rootstock. Thus, the grafting parents and grafting patterns would be much concerned in the breeding process to gain the expected results in future.

Introduction

Grafting is used for the asexual propagation of woody plants, allowing the rapid proliferation and preservation of improved lines [1], as well as the shortening of flowering plants' breeding periods, without altering genotypes [2].

Occasionally, grafting results in changes in plant traits. For example, *Siberian pine* (scion) grafted onto *Scots pine* (rootstock) (presented as scion/rootstock) grew faster and taller than *Siberian/Siberian pines* [1]. A wild-type (WT) tomato plant grafted on the mouse ear leaf mutant resulted in the scion leaves being phenotypically similar to the mouse ear mutant leaves [3]. The tomato grafts displayed leaf phenotype changes from the original multi-serrated angustifoliate leaves of the scion to the ovate leaves of the transgenic rootstock containing the *Cmgaip* gene (*Cucurbita maxima*) [4]. And, grafting a watermelon scion onto a *Cucurbit* rootstock effectively improved the plant's resistance to wilt disease [5], drought [6], cold [7], and heavy metal pollution [8].

Several studies had explored the possible mRNAs mobile mechanisms and revealed that the transcripts could travel long distances between scions and rootstocks, leading to variations in the grafted plants. For example, the *CmGA1* transcript has been readily detected in the WT scion grafted onto a *CmGA1* transgenic tomato rootstock [4]. In potato grafts, *BEL5* transcripts from the *BEL5*-overexpressing scion have been found in the WT rootstocks [9]. The transcriptome was analyzed to determine the transcript compositions in heterologous grafts using single nucleotide polymorphisms (SNPs). Large numbers of mRNAs were identified as having undergone long-distance movement. In grape [10], 1,963 mRNAs were transferred from scions to rootstocks, while 2,210 mRNAs were transferred from rootstocks to scions.

Evaluations of the mobile mRNAs showed that highly expressed genes might generate great quantities of mobile mRNAs and that ~ 10% of the mobile mRNAs showed large differences in their transmission ratio owing to different field conditions. This suggested the existence of complicated passive and selective mechanisms of mRNA movement. Genotypes, graft combinations and growth environments impacted the direction of the mRNA movement, as well as the numbers and species of mRNAs being exchanged. Transcriptome studies were also conducted in some other graft plants such as *Arabidopsis thaliana* (2,006 mobile mRNAs) [11], cucumber (3,546 mobile mRNAs) [12], and tobacco (1,163 mobile mRNAs) [13].

Salix matsudana is a widely planted willow species that has rich germplasm resources and plays an important role in greening, ecological protection, and conifer utilization. Grafting has been widely used in willow production. Here, the study goals were to identify the long-distance mRNA transmission events in grafted willows using a transcriptome analysis and to reveal the possible effects on rooting traits. The further characterization of transferred mRNA will provide insights into long-distance mobile mRNAs mechanisms and help improve grafting systems.

Results

9901 scion enhanced the rooting of YJ rootstock in 9901/YJ plants

During hydroponic culturing, the grafted willows started rooting at the bases of the rootstocks. Obviously, the 9901/9901 grafts rooted faster than the YJ/YJ plants (Fig. 1). The total root length of the 9901/9901 grafts was 2.66 times that of the YJ/YJ by the 22nd d after grafting, indicating that 9901 has a strong rooting potential than YJ (Fig. 2). The 9901/YJ plants rooted faster than YJ/YJ plants, and the total root length of the 9901/YJ grafts by the 22nd d after grafting was 1.93 times that of the YJ/YJ grafts. This revealed that the 9901 scions, with a fast rooting potential, had a certain promotive effect on the rooting of the YJ rootstocks.

Degs In Homologous And Heterologous Willow Grafts

A total of 49,425, 48,176 and 48,713 genes were identified in the rootstock tissues of 9901/9901, YJ/YJ, and 9901/YJ grafted plants, respectively (Fig. 3), using a transcriptome analysis. In total, 2,948 DEGs were identified between YJ/YJ and 9901/YJ, which probably resulted in their different rooting performances. Among them, 1,687 and 1,261 genes were significantly up- and down-regulated, respectively, in 9901/YJ compared with in YJ/YJ.

A total of 2,309 DEGs (S1 Fig) were annotated in the GO database. The DEGs related to biological processes were grouped in 21 terms, which were mainly involved in metabolic (1,100 genes), cellular (983 genes), and single-organism (916 genes) processes. The DEGS related to cellular component were grouped in 15 terms, which were mainly involved in cell (999 genes), cell part (975 genes), membrane (931 genes), and organelle (571 genes). The DEGS related to molecular function were grouped in 15

terms, which were mainly involved in catalytic activity (1,226 genes), binding (1,170 genes), and transporter activity (216 genes).

SNP analysis revealed 692 shoot-to-root mobile mRNAs in the 9901/YJ graft

SNP analysis was conducted between the homologous genes of two grafts (YJ/YJ, 9901/YJ), which showed 692 of 48,713 mRNAs in rootstock of 9901/YJ came from the scion. Among them, 536 mRNAs were annotated in the GO database (Fig. 4). In total, 16 annotated terms were related to biological processes, including metabolic processes (253 mRNAs), cellular processes (234 mRNAs), and single-organism processes (163 mRNAs). There were 14 annotated terms related to cellular component, including cell (240 mRNAs), cell part (239 mRNAs), and membrane (201 mRNAs), and there were 11 annotated terms related to molecular function, including binding (301 mRNAs) and catalytic activity (259 mRNAs).

An example was given in detail. The ABF (ABA responsive element binding factor) (K14432) gene was 966 bp in both the parents but displayed three SNPs at site of 135, 200, and 259 bp in the grafted plants (Fig. 5). The SNPs resulted in coding sequence changes in two amino acids, which further affected the secondary structure of the 9901-sourced homologous protein having less alpha helix and extension chain in comparison with the YJ-sourced protein, even far from the SNP site (Fig. 6). The polymorphisms in the proteins might really contribute to graft performance.

Characterization Of The Mobile Mrnas In Grafted Willows

The transfer ratio of 455 mobile mRNAs were estimated (the others, having less than 30 reads, were not considered), and they ranged from 7.14–68.75% with an average of 27.30%. Among them, 29.89%, 23.74%, and 20.88% of the mRNAs had transfer ratio of 10–20%, 20–30%, and 30–40%, respectively.

The maximum size of a mobile mRNAs was 10,710 bp and the minimum was 186 bp, with an average of 1,657 bp, which was 19.64% greater than the average 1,385 bp length of all willow transcripts. On the basis of mRNA length, the 455 mobile mRNAs were classified into several groups. The 1,000–1,500bp group contained the largest proportion, at 26.59%, of all the mobile mRNAs, followed by the 501–1,000 bp and 1,501–2,000 bp groups. However, a transfer ratio analysis revealed that mRNAs > 4,001 bp were preferred for transfer, accounting for 2.40% of the mobile mRNAs in the group, followed by the 3,501–4,000 and 2,501–3,000-bp mRNAs (Table 1).

Table 1
mRNA length and transfer ratio in the rootstock of 9901/YJ

mRNA length (bp)	Mobile mRNA amount	Total transcribed gene amount	Mobile mRNA ratio in total transcribed gene of the group (%) ^a	Mobile mRNA proportion in all mobile mRNA (%) ^b
0-500	44	4883	0.90	9.67
501–1000	96	12127	0.79	21.10
1001–1500	121	11219	1.08	26.59
1501–2000	65	6441	1.01	14.29
2001–2500	46	3444	1.34	10.11
2501–3000	35	1901	1.84	7.69
3001–3500	17	1151	1.48	3.74
3501–4000	11	558	1.97	2.42
4001–	20	835	2.40	4.40
^a A ratio between the mobile mRNAs amount in the group and the total transcribed gene amount in the group;				
^b A ratio between the mobile mRNAs amount in the group and the total mobile mRNAs (455) in the rootstock of 9901/YJ.				

The GC contents of all the transcripts in willow were calculated, and ranged from 28.70–67.84%, with an average of 44.37%. Comparably, the GC contents of the 455 mobile mRNAs ranged from 36.40–57.89%, with an average of 44.18%. The transcribed mRNAs were grouped on the basis of their GC content (Table 2). Among them, the mRNAs with GC contents of less than 35% were not transferred. The highest proportion, at 64.18%, of all the mobile mRNAs had GC contents of 40–45%, followed by mRNAs with GC contents of 45–50% and 50–55%. The transfer ratio calculation showed that the mRNAs with GC contents of 50–55% had the largest value at 1.20%, followed by the mRNAs with GC contents of 40–45% and 35–40%.

Table 2
GC content and transfer ratio in the rootstock of 9901/YJ

GC content (%)	Mobile mRNA amount	Total transcribed gene amount	Mobile mRNA ratio in total transcribed gene of the group (%)	Mobile mRNA proportion in all mobile mRNA (%)
25–30	0	2	0	0
30–35	0	72	0	0
35–40	13	1353	0.96	2.86
40–45	292	25776	1.13	64.18
45–50	128	13471	0.95	28.13
50–55	21	1752	1.20	4.62
55–	1	133	0.75	0.22

The expression abundances (presented as FPKM values) of the mobile mRNAs (Table 3) revealed minimum and maximum expression levels of 0.42 and 817.09, respectively, with an average of 19.81. Comparably, the average expression level of all the transcribed genes was 17.74% lower, at 16.83, than that of the mobile mRNAs. The mobile mRNAs were classified into several groups on the basis of the expression abundance. Among them, the mRNAs with expression value less than 10 formed the largest group, representing 63.30% of the mobile mRNAs, followed by the mRNAs with expression value of 10–20, representing 17.58% of the mobile mRNAs. The transfer efficiency evaluation showed that mRNAs with expression value of 10–20 accounted for 1.12% of the transcribed genes, followed by the mRNAs with expression values of 40–50.

Table 3
Gene expression abundance and transfer ratio in the rootstock of 9901/YJ

mRNA expression abundance (FPKM)	Mobile mRNAs amount	Total transcribed gene amount	Mobile mRNAs ratio in total transcribed gene of the group (%)	Mobile mRNAs proportion in all mobile mRNAs (%)
0–10	288	33241	0.87	63.3
10–20	80	7113	1.12	17.58
20–30	27	3168	0.85	5.93
30–40	12	1734	0.69	2.64
40–50	12	1077	1.11	2.64
50–60	4	631	0.63	0.88

In comparison with the previous reports, several mobile mRNAs were recognized in association with rooting such as ABCB29 [14], ARR5 [15], ERF9 [16], and ABF [17]. PCR tests showed them well expressed in 9901 rootstock of 9901/9901 plants, but less in YJ rootstock of YJ/YJ plants (Fig. 7). Obviously, these genes had more transcripts in YJ rootstock of 9901/YJ plants than in YJ rootstock of YJ/YJ plants, potentially gained from its 9901scion and resulted in their improved rooting ability.

KEGG pathways of the mobile mRNAs participate in root formation

A total of 142 (20.52%) mobile mRNAs were annotated to 85 pathways in the KEGG database. The main pathways included spliceosome, biosynthesis of amino acids, plant–pathogen interaction, and protein processing in endoplasmic reticulum (Table 4), which enriched with 11, 11, 10, and 10 mobile mRNAs, respectively.

Table 4
The main pathways of the mobile mRNAs involved

Pathway	ko_id	P_value	Mobile mRNAs amount
Spliceosome	ko03040	0.0606	11
Biosynthesis of amino acids	ko01230	0.1549	11
Plant-pathogen interaction	ko04626	0.0588	10
Protein processing in endoplasmic reticulum	ko04141	0.1816	10
Plant hormone signal transduction	ko04075	0.5378	8
RNA transport	ko03013	0.3316	7
Carbon metabolism	ko01200	0.7074	7
Ribosome	ko03010	0.9146	7
Fructose and mannose metabolism	ko00051	0.1093	4
Carbon fixation in photosynthetic organisms	ko00710	0.2043	4

Notably, the plant hormone signal transduction was enriched with eight mobile mRNAs (S2 Fig), which participated in auxin (AUX), cytokinin (CK), gibberellin (GA), abscisic acid (ABA), jasmonates(JAs), and salicylic acid(SA) metabolism, with transfer ratio of 14.72–68.29% (Table 5). They may directly or indirectly participate in root formation as previously reported.

Table 5
The mobile mRNAs involved in the plant hormone signal transduction pathway

Mobile mRNAs	Gene function	Expression abundance*			Transfer ratio
		9901/9901	YJ/YJ	9901/YJ	
AUX/IAA (K14484)	activation of the downstream transcription factor ARF	0.50(0)	0(0.14)	0.37(0.26)	58.73%
CRE1 (K14489)	transmembrane histidine kinase cytokinin receptor activity	0.29(0)	0(0.03)	0.12(0.12)	50.00%
B-ARR (K14491)	sequence-specific DNA binding	0.45(0)	0(0.11)	0.04(0.04)	50.00%
TF (K16189)	protein dimerization activity	0.10(0)	0(0.09)	0.04(0.06)	40.00%
ABF (K14432)	sequence-specific DNA binding	4.20(0)	0(0.84)	0.08(0.40)	16.67%
ABF (K14432)	sequence-specific DNA binding	0.20(0)	0(0.31)	0.03(0.18)	14.29%
JAZ (K13464)	transcription corepressor activity	0.80(0)	0(0.31)	0.28(0.13)	68.29%
NRP1 (K14508)	Regulatory protein	0.23(0)	0(0.38)	0.10(0.37)	21.28%
* The data outside the parentheses means the expression abundance of 9901 homologous gene in rootstock of grafts, while the data inside the parentheses means the expression abundance of YJ homologous gene in rootstock of grafts.					

Discussion

The number of mobile mRNAs varied vastly in different grafts

Long-distance mRNA movement events frequently occur in grafts, but the numbers of mobile mRNAs in different studies have varied greatly. For example, 422 and 441 mobile mRNAs were identified in roots and shoots of heterografts watermelon (WM)/bottle-gourd (LAG) and LAG/WM [18], respectively. Additionally, 138 mobile mRNAs were identified in *Nicotiana benthamiana*/*Arabidopsis* grafts [19], and 23 mobile mRNAs were identified in *Canola* /*Arabidopsis* grafts [13]. Thus, the numbers of the mobile mRNAs is correlated with the affinity between the scion and rootstock. Grafts involving two closely related varieties of a species could transfer more mRNAs than grafts involving more distantly related species. Our study here contributed the further evidence that more than 692 mobile mRNAs were identified in willow grafts, while both willow parents were bred from the same species of *Salix matsudana*.

Furthermore, the numbers of mobile mRNAs might also associate with the tissue conditions, tissue ages [10], and the sampling distance from the grafting site as the previous reports [11,12,13].

The Mobile Mrnas Efficiently Affacted Willow Grafts' Rooting

Long-distance mRNA movement events in grafts really affect plant traits performance. Here, the willow graft experiment showed that 9901 scion transmitted its strong rooting ability to the YJ rootstock, thereby improving rooting by as much as 1.93 times that of YJ/YJ. Some kind of hormones were frequently involved in this process and convinced in this study. For example, AUX/IAA may activate the downstream transcription factor ARF, which is involved in regulating root development [20,21,22]. Interestingly, the *AUX/IAA* gene was found mobile in various grafts [9,23,24]. In willow, its transfer ratio reached 74.41%. A cellular mechanism for the positive role of ABA in promoting root meristem maintenance and root growth has been demonstrated in *Arabidopsis*. Two *ABF* genes in the ABA metabolic pathway were determined mobile in willow grafts at ratio of 1.91% and 15.24%, respectively. An amino acid analysis showed their structures varied in the two parents, which might have resulted in their different rooting efficiencies. As a transcription factor, the *ABF* gene regulates downstream gene expression, such as basic leucine zipper transcription factor of *bZIP4* in maize (*Zea mays*). The *ZmbZIP4* over-expression lines have longer primary, seminal, and lateral roots in comparison with those of the WT plants. Immunoprecipitation sequencing revealed that *ZmbZIP4* positively regulates some target genes related to root growth, including *ZmLRP1*, *ZmSCR*, *ZmIAA8*, *ZmIAA14*, *ZmARF2*, and *ZmARF3* [25]. Additionally, the *ABF2* activity levels in the radicles and shoot meristem regions of *ABF2* transgenic plants' embryos are high. During subsequent seedling growth, the highest *ABF2* activity level, except the levels in the meristem regions and the elongation zones, was detected in lateral roots [26]. Thus, the mobile of the *ABF* gene in willow grafts may affect the rooting abilities of the grafts.

The mobile mRNAs in grafts are of some sequence characteristics

An association analysis showed that the mRNAs characteristics, such as mRNA length, GC content, and mRNA expression abundance, had effects on the mobile efficiency in grafts. Several studies, such as those in *Arabidopsis*, *N. benthamiana*, cucumber, grape, and willow, revealed that more than 70% of the mobile mRNAs in grafts were less than 2,000 bp. However, transfer ratio analyses revealed that larger mRNA fragments were preferentially transferred in heterologous grafts. For example in willow, the transfer ratio of mRNAs > 4,000 bp was 2.4%, which is 3.13 times that of mRNAs < 2,000 bp. In *Arabidopsis*, the transfer ratio of mRNAs > 4,000 bp reached 11.52%, which was 2.55 times that of mRNAs < 2,000 bp. Probably, the larger mRNA fragments may easily form certain stable spatial structures and suited for long-distance transfers.

A previous analysis using a computational diffusion-based model showed that mRNA abundance is an important factor in a mRNA's long-distance mobile [27]. Unfortunately, the correlation between mRNA

expression abundance and the transfer ratio was not perfectly defined in several experiments, For example, in the willow grafts, mRNAs with the expression abundances of 10–20 and 40–50 had high transfer efficiencies, being 1.62 and 1.61 times that of mRNAs with expression abundances of 30–40. In *N. benthamiana* grafts, only 3 of 183 mobile mRNA were highly ranked among all the transcribed genes on the basis of their expression abundance levels [13]. In the over-expression experiments, the over-expressed *GUS* and *GFP* genes under control of the 35S promoter [28,29], and even *AtAMT1* and *AtCHL1* under the control of the strong phloem-specific promoter SUC [13], did not undergo long-distance transfer. Thus, the effect of gene expression level on their mobile ratio in grafts might be in combination with some other mechanisms.

GC content is another factor that may influence mRNA mobile. In willow grafts, 95.16% mobile mRNAs had GC content between 30% and 50%. Among them, mRNAs with GC content of 50–55% were preferentially transferred with a transfer ratio of 1.20%, which was 1.60 times that of mRNAs with GC contents greater than 55% and 1.13 times that of mRNAs with GC contents less than 50%. Similarly, mRNAs with GC contents of 50–55% exhibited the highest transfer ratio of 8.45% in *Arabidopsis* grafts, which is 1.08 times that of mRNAs with GC contents > 55% and 1.54 times that of the mRNAs with GC contents < 50%. Therefore, the mRNA mobile in grafts is of complicated mechanism, in which sequence characteristics was much concerned and probably was of comprehensive effect. More details will be explored in the future.

Materials And Methods

Plant materials and grafting

The current shoot segments of the *Salix mandshurica* variety 9901 and Yanjiang (YJ) were used as sources to construct the homologous and heterologous grafts 9901/9901, YJ/YJ, and 9901/YJ by V-shaped grafting method. The grafted segments were grown in hydroponics condition (changed every other day) in a growth chamber of a 16/8 h light/dark cycle (2000lux) and relative humidity of 75–80% at 25°C. The total root length was measured for each plant starting from 10th day of grafting. Permission for collection, planting and grafting of the willow plants was obtained from Beijing Forestry University.

Extraction Of Total Rna

At 22th day of grafting, the bark tissue (containing phloems for organic substances transporting) of 9901/9901, YJ/YJ and 9901/YJ rootstocks were individually sampled for total RNA extraction by using polysaccharide polyphenol kit (TIANGEN company). The isolated RNA was treated with RNase-free DNase I (Takara) for 30 min at 37°C to remove the residual DNA. RNA quality was tested by using NanoDrop2000 spectrophotometer (NanoDrop, Thermo Scientific, Waltham, USA). RNA integrity was assessed using the RNA Nano 6000 Assay Kit of the Agilent Bioanalyzer 2100 system (Agilent Technologies, CA, USA).

Rna Library Construction And Sequencing

RNA sequencing libraries were generated using NEBNext Ultra™ RNA Library Prep Kit for Illumina (NEB, USA) following the manufacturer's instruction. The library was sequenced on an Illumina platform (Biomaker company) and the paired-end reads were generated. The clean data were obtained by removing adapter and low quality reads from the raw data. Q20, Q30, GC-content and sequence duplication level of the clean data were calculated. All the analyses were based on the high quality clean data.

Identification of the differentially expressed genes (DEGs) and function analysis

The reads per kilobase per million mapped reads (RPKM) were generated to represent the expression abundance of each mRNA. Differential expression analysis of two data sets (YJ/YJ and 9901/YJ) was performed using the edgeR. The $FDR < 0.01$ & $Fold\ Change \geq 2$ were as the threshold for significantly differential expression. Gene Ontology (GO) enrichment analysis of the DEGs was implemented by the GOseq R packages based Wallenius non-central hyper-geometric distribution, which can adjust for gene length bias in DEGs [30]. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses were performed using Blast2GO software (BioBam Bioinformatics SL) [31].

Determination Of The Transfer Rnas

All the clean reads of 9901/9901, YJ/YJ and 9901/YJ were compared by using HISAT2 software [32]. SNPs between two parents were identified with GATK software [33]. The reads (transcripts) in rootstocks of 9901/YJ having SNPs with YJ/YJ but homozygous with 9901/9901 were determined as the mobile mRNAs from 9901 scion to YJ rootstock in 9901/YJ grafts.

Estimation Of Transfer Ratio

Based on the expression abundance of the mobile mRNAs in 9901/YJ, the mobile mRNA transfer ratio from 9901 to YJ in 9901/YJ was estimated: [the normalized number of the 9901-sourced mobile mRNAs in the rootstock of 9901/YJ divided by the total normalized number of the 9901-sourced and YJ –sourced mobile mRNAs in the rootstock of 9901/YJ]. When SNPs were present in several mobile reads, the average value was used as the transfer ratio of the mobile mRNA. The mobile mRNA with less than 30 mapped reads in the graft was not considered for transfer ratio estimation so as to reduce the bias.

Declarations

Author contributions

Yin Peng and Xu Jichen wrote the main manuscript text. Yin Peng, Liu Xiao and Lan Baoliang prepared Figs. 1–7. Yin peng, Cui Yu and Wang Yan prepared tables 1–5. All authors reviewed the manuscript.

Acknowledgements

This work was supported by the National Natural Science Foundation of China (#31870648)

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Figures



9901/9901

YJ/YJ

9901/YJ

Figure 1

Rooting of the willow grafts 9901/9901, YJ/YJ, and 9901/YJ

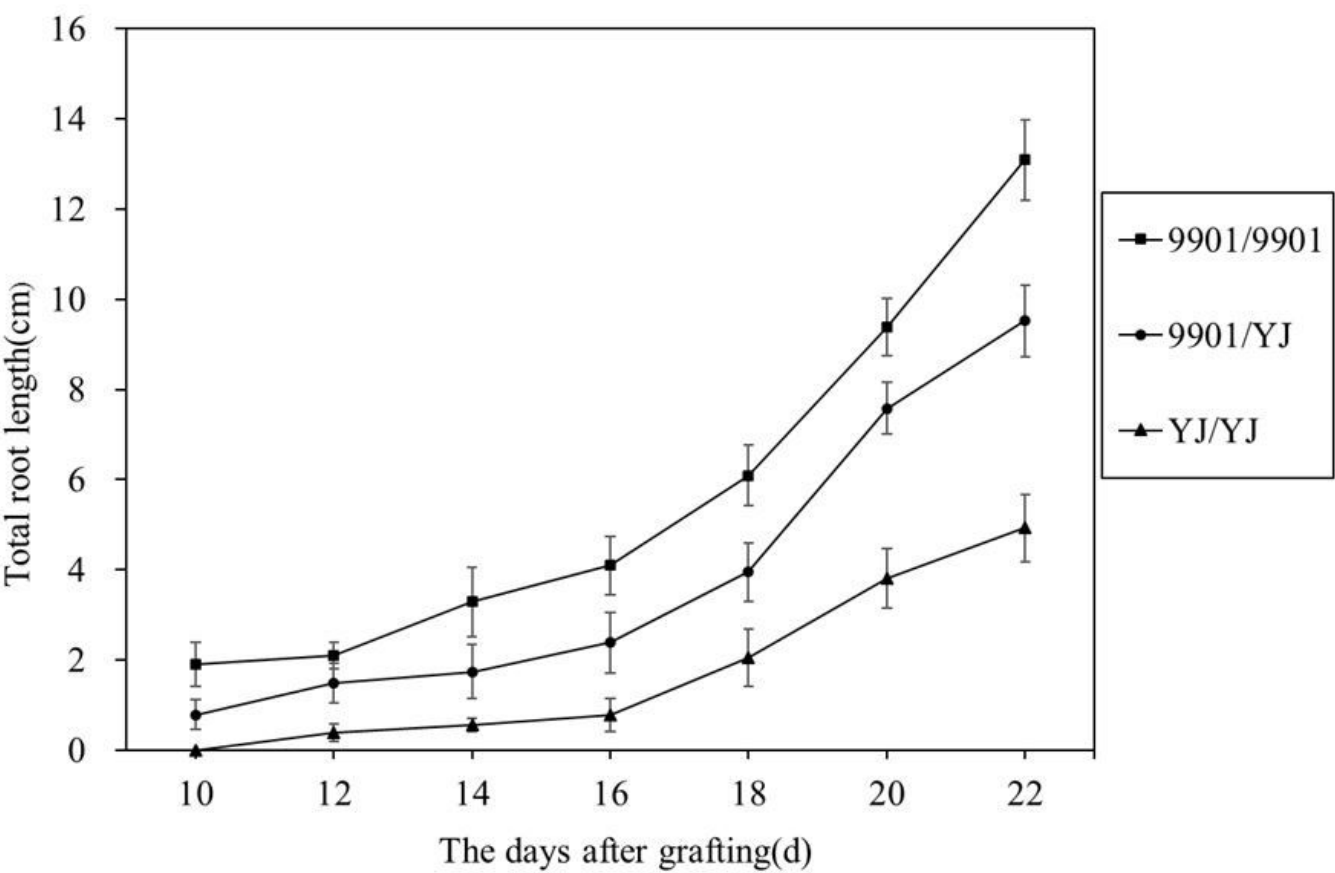


Figure 2

The total root length of willow grafts in hydroponics culture

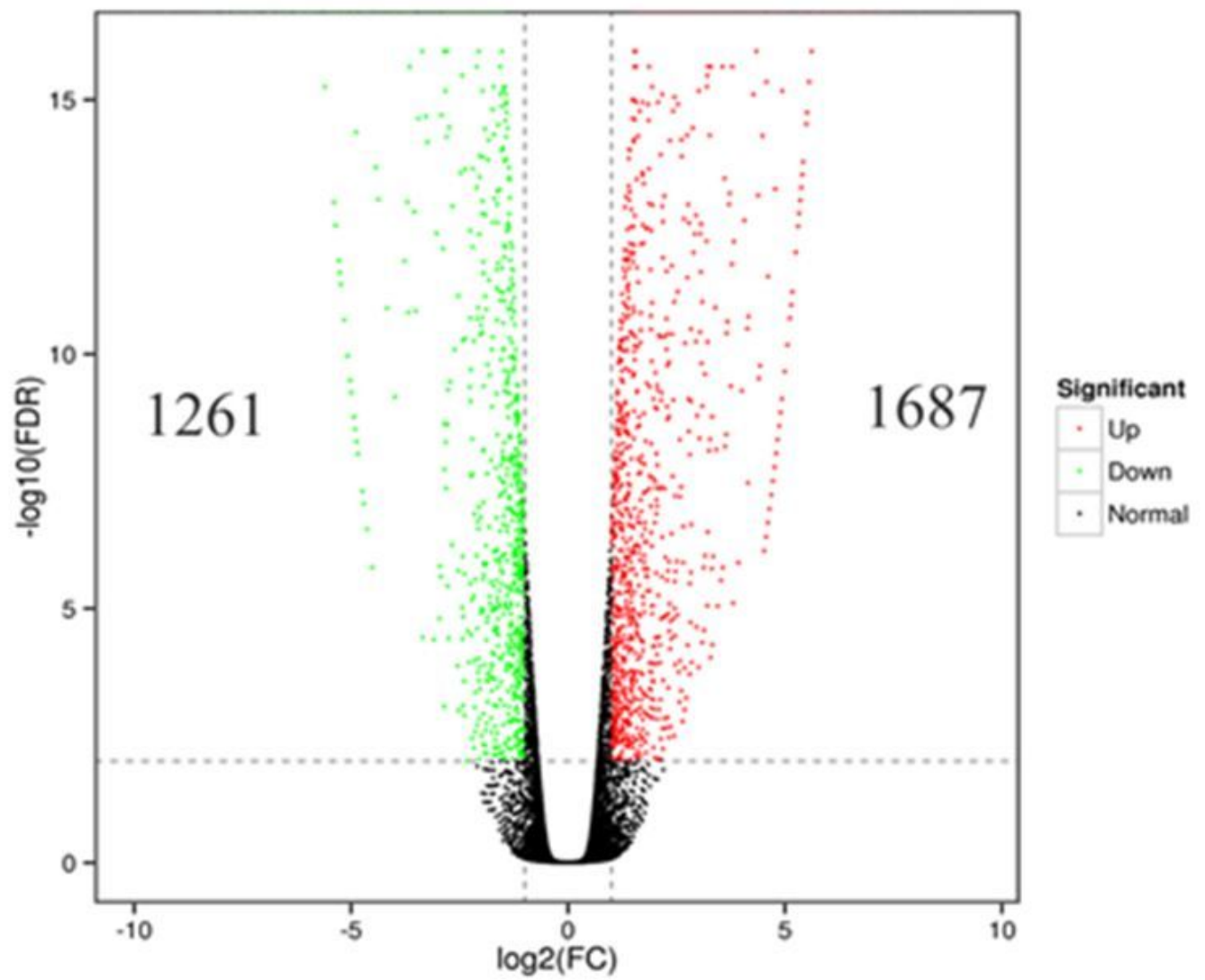


Figure 3

Volcano plot of DEGs in grafted willows of 9901/YJ comparing with YJ/YJ

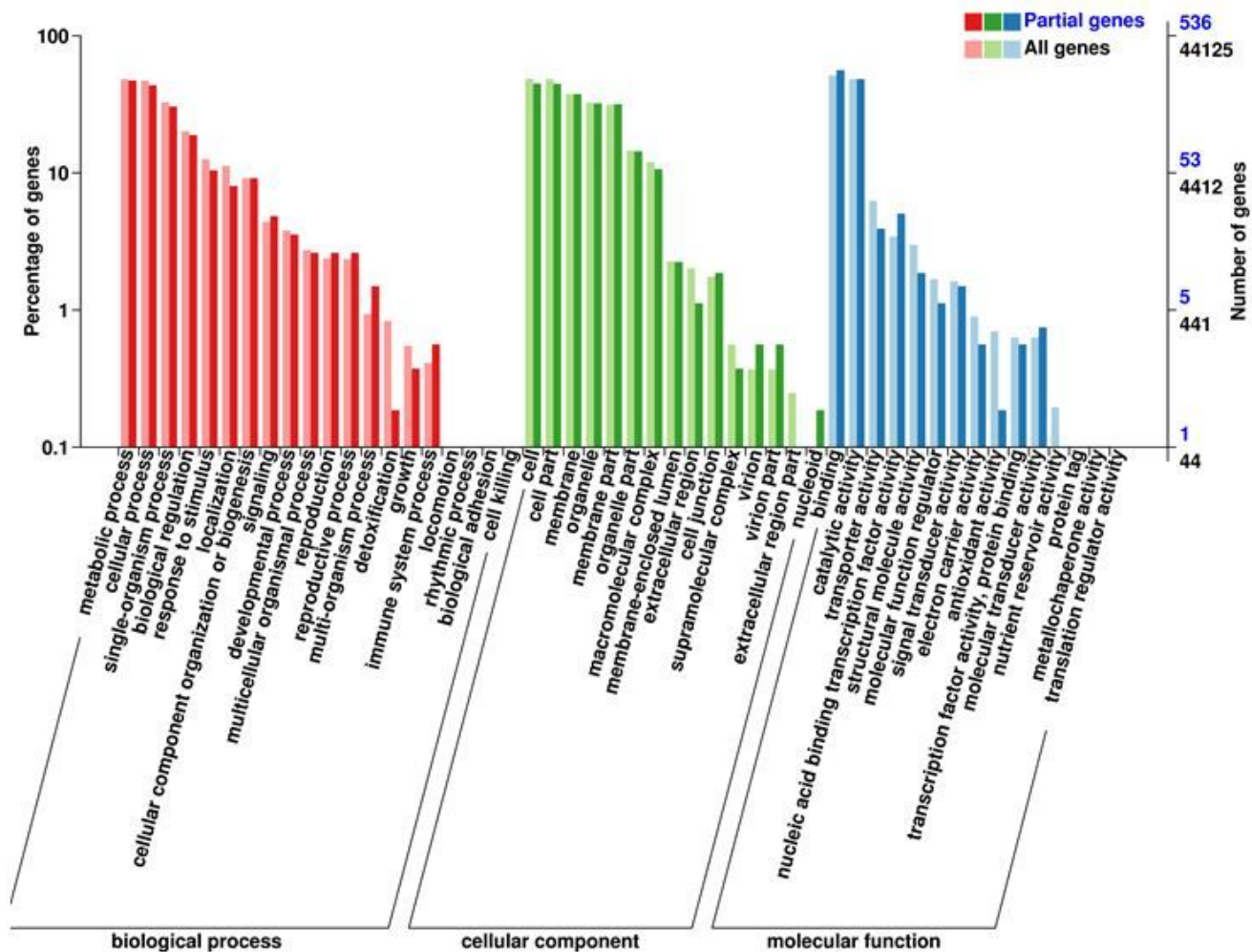


Figure 4

GO annotation of the transfer genes from scion to rootstock in 9901/YJ

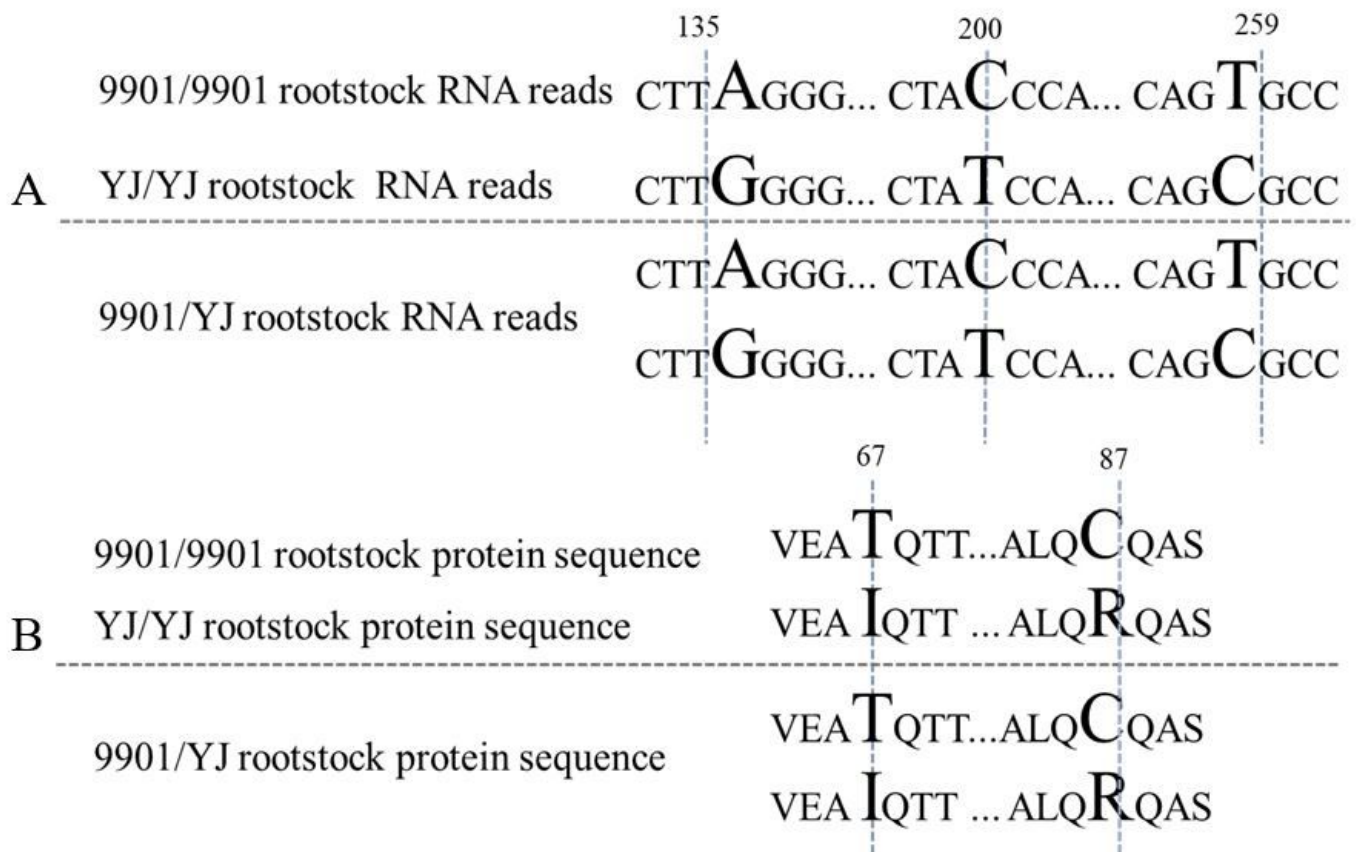


Figure 5

SNP analysis of the ABF gene (K14432) in the rootstock of 9901/YJ. A, nucleotide; B, amino acids

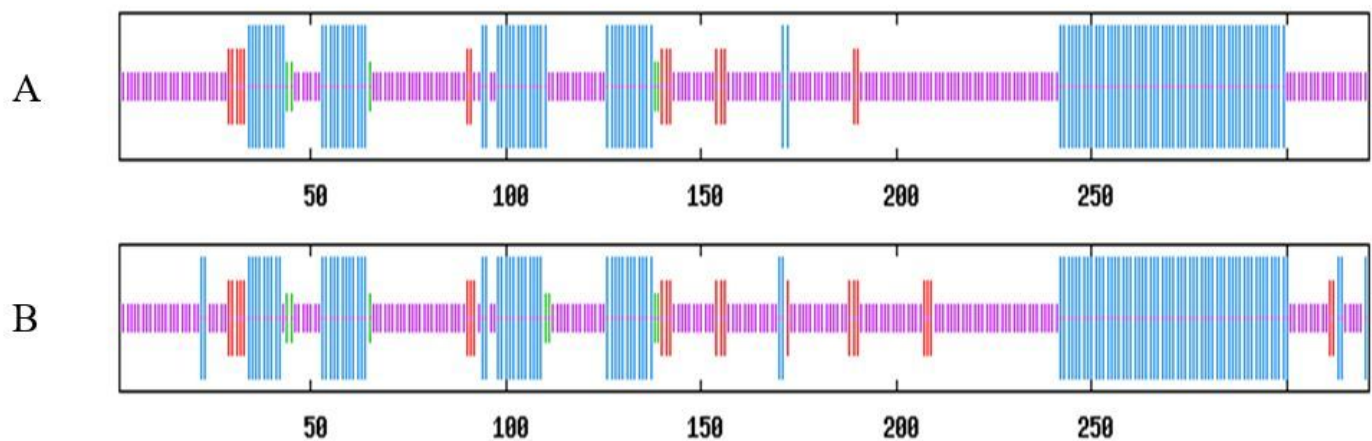


Figure 6

Secondary structure of the ABF (K14432) protein. A, 9901-sourced protein; B: YJ-sourced protein. The blue parts represent the alpha helix, the red parts represent the extension chain, the green parts represent the beta turn, and the purple parts represent the random coil.

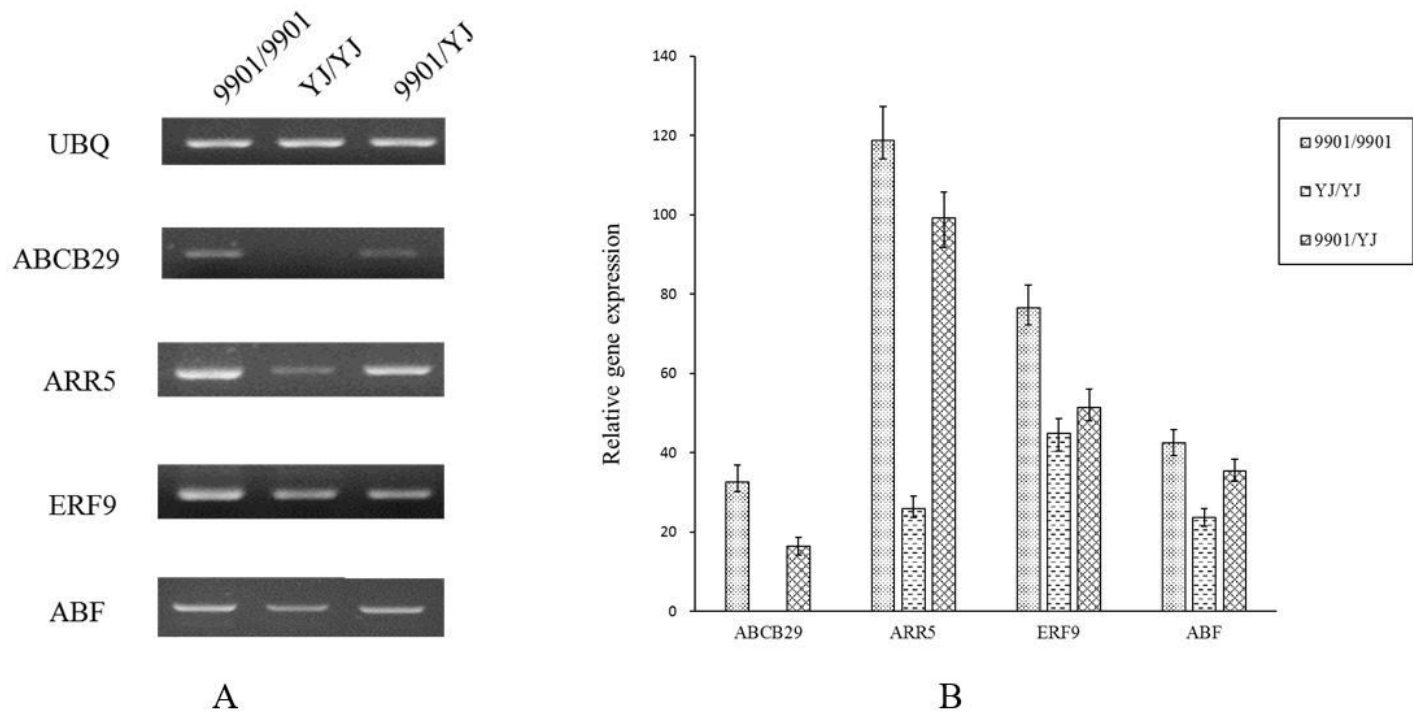


Figure 7

Expression tests of the mobile mRNAs in rootstock of the grafted plants. A, PCR results of four mobile genes (ABCB29, ARR5, ERF9, ABF) with UBQ as the reference; B, The quantitative PCR results

Supplementary Files

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