

Collection and Comparative Analysis of 1888 Full-length cDNAs from Wild Rice *Oryza rufipogon* Griff. W1943

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Abstract

A huge amount of cDNA and EST resources have been developed for cultivated rice species *Oryza sativa*; however, only few cDNA resources are available for wild rice species. In this study, we isolated and completely sequenced 1888 putative full-length cDNA (FLcDNA) clones from wild rice *Oryza rufipogon* Griff. W1943 for comparative analysis between wild and cultivated rice species. Two cDNA libraries were constructed from 3-week-old leaf samples under either normal or cold-treated conditions. Homology searching of these cDNA sequences revealed that >96.8% of the wild rice cDNAs were matched to the cultivated rice *O. sativa* ssp. *japonica* cv. Nipponbare genome sequence. However, <22% of them were fully matched to the cv. Nipponbare genome sequence. The comparative analysis showed that *O. rufipogon* W1943 had greater similarity to *O. sativa* ssp. *japonica* than to ssp. *indica* cultivars. In addition, 17 novel rice cDNAs were identified, and 41 putative tissue-specific expression genes were defined through searching the rice massively parallel signature-sequencing database. In conclusion, these FLcDNA clones are a resource for further function verification and could be broadly utilized in rice biological studies.

Key words: wild rice; *Oryza rufipogon*; full-length cDNA; transcriptome comparison; tissue-specific expression

1. Introduction

The wild rice species *Oryza rufipogon* Griff. (AA genome) is the most closely related ancestral species to Asian cultivated rice (*O. sativa* L.).^{1,2} It contains various valuable traits with regard to tolerance to cold, drought and salinity. It also contains many quantitative trait loci with agronomic important traits.^{3,4} However, cultivated rice, which feeds more than half of the world's population, is often threatened by multifarious environmental factors including drought,

salinity, cold and other factors. The *O. sativa* ssp. *japonica* cv. Nipponbare genome has been completely sequenced through a map-based sequencing strategy.⁵ The draft genome sequence of the *O. sativa* ssp. *indica* cv. 93-11 was also generated through a whole-genome shotgun sequencing approach.⁶ The Rice Full-Length cDNA Consortium collected over 28 000 full-length complementary DNA (FLcDNA) clones from cv. Nipponbare.⁷ Now, there are >47 000 cultivated rice FLcDNA sequences publicly available (<ftp://ftp.ncbi.nih.gov/>). There is also a collection of 10 096 FLcDNAs of *O. sativa* ssp. *indica* cv. Guangluai 4.⁸ Moreover, comparative genome analysis has been developed to decipher the similarity and diversity among rice varieties, using single nucleotide polymorphisms data in 21 rice genomes.⁹

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Comparative analysis with cultivated rice cDNA sequences has also been developed using the microarray method.¹⁰ In contrast, for wild rice, there are few batches of mRNAs and FLCDNAs in public databases, with the exception of 5211 leaf ESTs from the *O. minuta* (BBCC genome).¹¹

Oryza rufipogon has been classified into perennial and annual ecotypes.¹² W1943 is a perennial *O. rufipogon*. For the first time, a total of 1888 FLCDNAs of *O. rufipogon* W1943 were generated in the present study; most (>96.8%) were highly homologous with cultivated rice genome sequences. Furthermore, W1943 had greater similarity to *ssp. japonica* than to *ssp. indica*. Additionally, 1% of W1943 FLCDNAs was verified as novel rice genes not previously reported. We also discovered 41 putative tissue-specific expressed genes by applying the rice massively parallel signature-sequencing (MPSS) database.¹³

2. Materials and Methods

2.1. Plant materials and cDNA library construction

Two enriched FLCDNA libraries were constructed from wild rice *O. rufipogon* Griff. W1943. Seeds were germinated and seedlings were grown in a greenhouse with day/night of 13/11 h and 25/30°C. Three weeks after germination, some seedlings were exposed to 5°C and leaves were separately harvested after 0, 1, 12, 24, 48, 72 and 120 h of cold treatment. We constructed two cDNA libraries from 3-week-old rice leaves grown under normal and cold conditions, respectively. All samples were immediately frozen in liquid nitrogen and stored at -80°C.

We constructed two FLCDNA libraries according to the Cap-Tagging⁸ and Cap-trapper methods.¹⁴ The 5' cap-tagging method utilizes the 5' cap-capture technique through the combined treatments of calf intestinal phosphatase (CIP) and tobacco acid pyrophosphatase (TAP) so that only the FLCDNA was targeted for library construction. The cap-trapper method is based on chemical introduction of a biotin group into the diol residue of the cap structure of mRNA, which is followed by RNase I treatment to select FLCDNA. Total RNA was isolated using the TRIZOL reagents, and mRNAs were purified with the Oligotex mRNA kit (Qiagen). Double-stranded cDNA was digested with *EcoRI* (1 U) and *XhoI* (10 U) for 1 h at 37°C, and cDNA fraction of 0.6–2 kb was collected and pooled, with which ligated to the sites of *EcoRI* and *XhoI* of vector pBluescript SK+ (Stratagene) at 16°C overnight. Then, cDNA was transformed into competent *E. coli* DH10B cells (Invitrogen) by electroporation. We assessed the library quality by assaying ligations and carrying out 5'-end sequencing; the former procedure determined library titer, and the latter used

to evaluate cDNA full-length percentage as well as the proportion of empty vectors.

2.2. DNA sequencing and assembling

DNA sequencing was carried out on ABI3730 sequencers. The clones were sequenced from both ends by the dideoxy chain termination method using BigDye Terminator Cycle sequencing V2.0 Ready Reaction (Applied Biosystems). The *Phred* base-calling software was used to analyze sequence trace files and generate raw sequences.¹⁵ Peaks with *Phred* quality values of <20 were taken as ambiguous sequences and were presented by a universal placeholder 'N'. Vector sequences were filtered automatically. Then, all 5'-tagged sequences were selected by a Perl script for clustering, which used the TGICL program.¹⁶ These singletons and every representative clone from each contig were selected to be completely sequenced by bidirectional sequencing strategy. All processed sequences were assembled by *Phrap* software.

Accession numbers for submitted data in the EMBL database CT841557–CT841684; CT841686–CT841707; CT841710–CT841954; CT841956–CT842008; CU405560–CU405627; CU405629–CU405654; CU405656–CU405706; CU405708–CU405710; CU405712–CU405714; CU405716–CU405717; CU405719–CU405720; CU405722–CU405729; CU405731–CU405880; CU405882–CU405928; CU405930–CU406064; CU406066–CU406249; CU406251–CU406335; CU406337–CU406954 and CU861673–CU861883.

These W1943 sequences are available from our website (<http://202.127.18.228/ricd/dym/ftp.php>).

2.3. Comparative analysis of FLCDNA sequences

Similarity searches were performed with BLAST (version 2.2.14) program¹⁷ against sequence data as follows: NCBI GenBank nt DB (2007-12), nr DB (2007-12), est-other DB (2007-07), rice *japonica* genomic sequence (<http://rgp.dna.affrc.go.jp/IRGSP/>), the Institute for Genomic Research (TIGR) rice cDNA data (release 4.0), TIGR_*Oryza*_Repeats_v3.1, Knowledge-based *Oryza* Molecular Biological Encyclopedia *japonica* cDNA collection (<http://cdna01.dna.affrc.go.jp/cDNA>, 2006-10-11) and National Center for Gene Research (NCGR, <http://www.ncgr.ac.cn/ricd>) Rice *Indica* cDNA Database (RICD). We downloaded all above sequence data and used our 1888 clones as query sequences. The similarity threshold of E-value was lower than 1E-10. We searched InterPro database¹⁸ to compare the profiles of proteins encoded in W1943 FLCDNAs. Functional classification of cDNAs was referred to PFAM profiles.¹⁹

A similarity-based tool *sim4*²⁰ was used to align W1943 FLCdNA sequence with rice genomic sequence. It was also used to identify and discard redundant gene sequences. Open reading frames (ORFs) of cDNA sequences were determined by using *getorf* program of EMBOSS package.²¹ The rice MPSS database¹³ was used for quantitative expression analysis of these W1943 cDNAs in rice. The expression levels were calculated for rice different tissues or same tissues at different developmental stages by summing all expressed tags in the sense strand. To calculate synonymous divergence (Ks), program ClustalX 1.8²² and PAL2NAL (version: V11)²³ were applied.

Rfam database²⁴ (<http://www.sanger.ac.uk/Software/Rfam/>) and miRBase²⁵ (<http://microrna.sanger.ac.uk/>) data were downloaded for non-protein-coding transcripts analysis. Software mFOLD was applied to predict pre-miRNAs' secondary structure (<http://mfold.bioinfo.rpi.edu/>).²⁶

3. Results and Discussion

3.1. Overall description of W1943 FLCdNA sequences

Two full-length enriched cDNA libraries of *O. rufipogon* W1943 were constructed following the cap-tagging method.⁸ Each cDNA library was composed of 1×10^6 independent clones. The average cDNA sizes were 0.5–1.5 kb. In total, we randomly selected 8352 clones (6432 were from the normal rice leaf cDNA library and 1920 were from the cold-stressed rice leaf cDNA library) for 5'-end sequencing. In total, there were 4876 tagged potential FLCdNA clones of at least 100 continuous nucleotides with a *Phred* score of >20 , after removal of vector sequences and low quality reads. The TGICL program¹⁶ was used to cluster these 4876 cDNA clones. Thus, there were 2350 cDNAs, consisting of 454 representative unique clone contigs and 1896 singletons, generated for completely sequencing and assembling. Overlapping 5' and 3' reads were assembled to consensus sequences through the bidirectional sequencing strategy.

Up to now, we have successfully obtained 1888 non-redundant W1943 cDNA sequences. Of 1888 cDNA sequences, 1360 sequences matched to NCBI GenBank non-redundant database of proteins (nrDB) ($E < 1e-10$; $>70\%$ identity). Of 1360 sequences, 997 cDNAs could fully cover the protein N-terminal first amino acid sequence. Therefore, we estimated that $>70\%$ of the 1832 cDNA sequences were FLCDNAs. It should be pointed out that the efficiency of CIP and TAP treatments played a key role in constructing the FLCdNA library. On the other hand, it was also possible that some of the remaining 30% putative truncated cDNA sequences might be genuine FLCDNAs transcribed from alternative start sites. There are lots of alternative transcription start sites known in mammals.^{27,28}

3.2. Mapping of the 1888 W1943 FLCDNAs onto cultivated rice *O. sativa* genomic sequences

The 1888 FLCDNAs from *O. rufipogon* W1943 were mapped to *O. sativa* ssp. *japonica* cv. Nipponbare genomic sequence pseudomolecules (version 4.0) and compared with GenBank nrDB based on BLASTn ($E < 1e-10$) and BLASTx ($E < 1e-10$), respectively.⁵ Of the 1888 FLCdNA sequences, 1831 (97.0%) could be aligned to the *japonica* genomic sequences at $>80\%$ sequence identity over the entire length (Fig. 1). The remaining 57 cDNAs that did not match the ssp. *japonica* genomic sequences are discussed in the following analysis. Among 1831 W1943 cDNAs, 395 (21.6%) fully matched the ssp. *japonica* cv. Nipponbare genomic sequences with 100% identity at nucleotide level. However, among 1831 cDNAs, 487 fully matched to corresponding proteins in nrDB with 100% identity. Therefore, 35.8% of W1943 cDNAs had full identity to proteins from nrDB at amino acid level. In spite of relatively low full identity at nucleotide acid level (only 21.6%), it was more conservative at amino acid level ($>35.8\%$) between wild and cultivated rice. It was propitious to protect some key proteins from losing their conserved and vital functions.

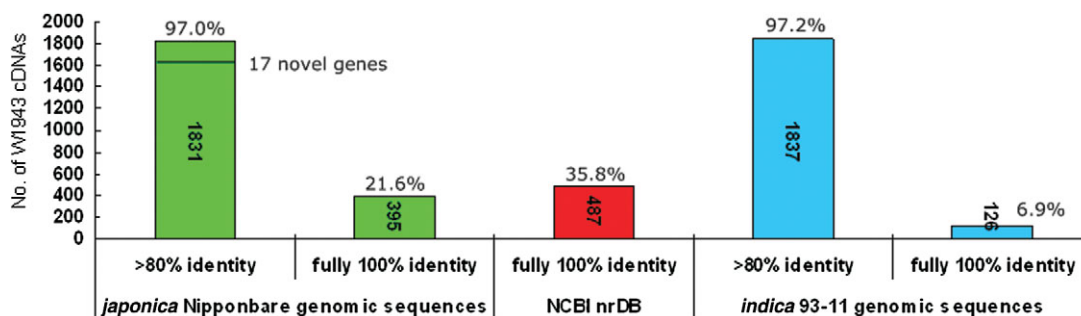


Figure 1. Mapping of the 1888 FLCDNAs onto *Oryza sativa* genomic sequences.

We also mapped the 1888 W1943 FLcDNAs to the *O. sativa* ssp. *indica* cv. 93-11 whole-genome shotgun sequences using BLASTn ($E < 1e-10$). A total of 1837 (97.2%) W1943 cDNAs could be aligned to the cv. 93-11 genome sequences at >80% sequence identity over the entire length (Fig. 1). Of these, 126 (6.9%) identically matched the cv. 93-11 genome sequences. These results indicated that the sequence of wild rice W1943 had a very high similarity with those of cultivated ssp. *japonica* (97.0%) and ssp. *indica* (97.2%) rice; and W1943 had greater similarity to *japonica* than to *indica* at nucleotide acid level. Monna et al.²⁹ surmised that W1943 was closer to *japonica* than to *indica*. It has been reported that *japonica* cultivars are closely related to the *O. rufipogon* perennial strains, and *indica* cultivars closely related to the *O. rufipogon* annual strains.³⁰ Our results confirmed this conclusion at transcriptional level.

In the case of 395 W1943 FLcDNAs that were 100% matched to the genomic sequences, we checked the splicing patterns by comparing with all rice ESTs or mRNAs in public databases. The results revealed that 15 W1943 cDNAs had alternative splicing patterns when compared with cultivated rice ESTs or mRNAs (Table 1). These alternative splicing patterns might be specific for W1943. Furthermore, the first introns of two genes (CT841942 and CU406810) had a distinct splice site with GC-AG and GT-TG. We concluded that cultivated rice had experienced some mutations including the intron region, and thus some genes were lost over the long evolutionary period. There were four typical alternative splicing patterns of these sequences (Fig. 2).

It should be pointed out that 10 of 1831 W1943 cDNAs had no hits to previously reported rice ESTs or mRNAs in GenBank database (Table 2). Another seven cDNAs had hits to rice ESTs or mRNAs at the sense-antisense pattern (Table 3). So these cDNA sequences offered novel rice transcripts to public database. As for the 17 W1943 cDNA sequences, they were either wild-rice-specific genes or cultivated rice co-owner genes. If the latter was the case, it may indicate that these genes are expressed at much lower levels in cultivated than in wild rice. Hence, it would be difficult to clone these cDNAs from cultivated rice in spite of a total of ~47 000 ssp. *japonica* and ssp. *indica* cDNAs available in the current public database (<ftp://ftp.ncbi.nih.gov/>). We used the rice MPSS database (<http://mpss.udel.edu/rice/>) to detect the expression level of these 17 putative novel W1943 cDNAs under different conditions.¹³ The results showed that 15 of 17 cDNAs were not detected having expressed tags with sense strand orientation in different tissues. Gene 'CU861721' was found only 18 times per million (tpm) in young leaves and gene 'CU406355' was found >100 tpm in young roots and germinating seedlings.

In addition, 57 W1943 cDNAs that could not be aligned to the ssp. *japonica* cv. Nipponbare genomic sequence were further analyzed. After comparing with other public databases, 14 of them matched the ssp. *indica* cv. 93-11 genomic sequences, 6 matched to rice ESTs in NCBI est-other database, 4 had similarity to *Sorghum bicolor*, *Triticum aestivum*, *Manihot esculenta* and *Spartina alterniflora* ESTs, 15 were homologs to *Gibberella moniliformis*, *Gibberella*

Table 1. List of 15 *Oryza rufipogon* W1943 genes with specific alternative splicing patterns

Accession Number	Length (bp)	Chromosome	Number of exon	Protein
CT841942	978	07	6 (1st intron: GC-AG)	
CU406810	958	06	6 (1st intron: GT-TG)	Dual-specificity phosphatase protein
CT841893	1011	01	6	Drought-induced protein
CT841874	1369	01	4	Vesicle transport protein
CU405853	1377	05	1	Dehydration-responsive protein
CU405923	639	07	1	IAA amidohydrolase
CU406279	648	05	1	
CU406025	839	02	1	
CT841561	740	06	2	
CU406579	468	09	2	
CU406935	1345	01	2	
CU406600	1107	01	2	
CU405570	952	01	2	
CU406091	893	01	3	
CU406134	665	10	3	

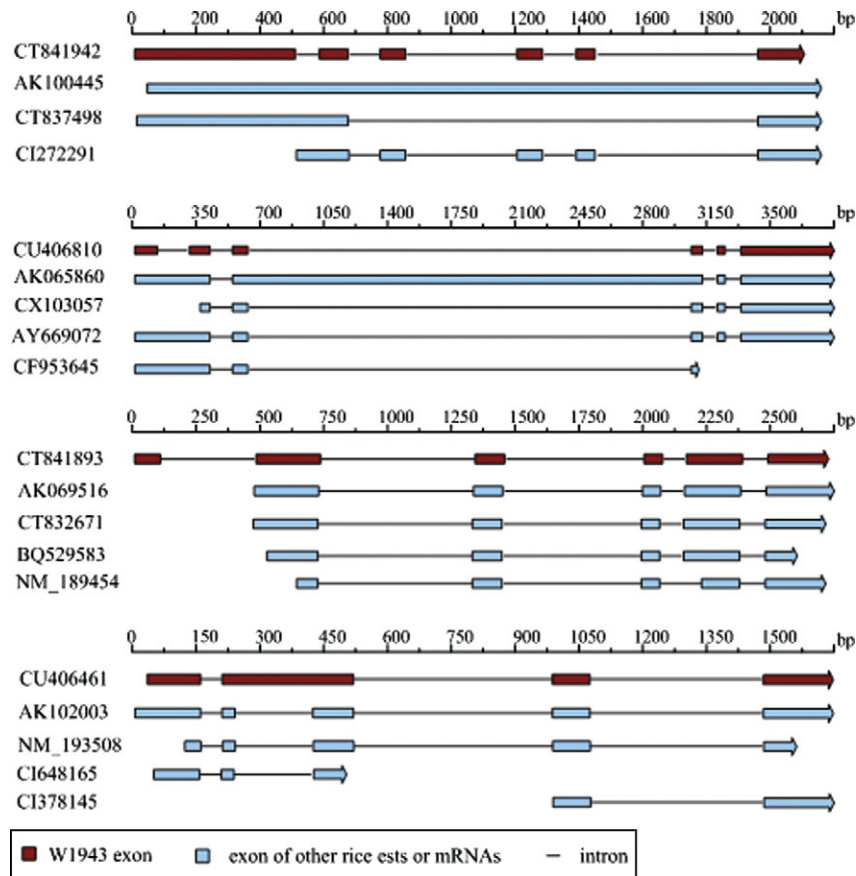


Figure 2. Total 17 W1943 cDNAs had alternative splicing patterns different from previous ESTs or mRNAs in public database. It revealed four typical splicing patterns in wild rice species.

Table 2. List of 10 novel cDNA transcripts of *Oryza rufipogon* W1943

Accession Number	Protein	Length (bp)	Chromosome	Identity (%)
CU405785	—	727	05	99
CU406138	—	568	02	99
CU406022	—	543	12	99
CU405757	—	477	04	100
CU406921	—	414	02	100
CU406535	—	389	02	100
CU406832	—	530	10	92
CU406871	—	458	01	84
CU861804	—	383	06	99
CU861721	—	554	01	100

zeae and *Magnaporthe grisea*, and the remaining 18 had no hits. Table 4 listed 24 W1943 cDNAs' information after excluding 15 possible contamination clones and 18 no any hits clones. Several W1943 cDNAs that did not match to the cv. Nipponbare genomic sequence might be located in the gap of genomic sequence or might be related to wild rice W1943-specific genes.

3.3. Comparative analysis with cultivated rice cDNA sequences in public databases

The 1888 W1943 cDNAs were compared with cultivated rice cDNA sequences. The large-scale rice ssp. *japonica* cv. Nipponbare cDNA sequences have been released to public databases.⁷ Recently, another batch of rice ssp. *indica* cv. Guangluai 4 cDNA sequences was released to public databases (<ftp://ftp.ncbi.nih.gov/>; <http://www.ncgr.ac.cn/RICD>).⁸ We compared these two major cultivated rice varieties' cDNAs with 1888 W1943 cDNA sequences. For convenience, here we named cv. Nipponbare cDNA sequences as KOME (knowledge-based oryza molecular biological encyclopedia) and cv. Guangluai 4 cDNA sequences as NCGR (National Center for Gene Research, CAS). At present, there are 35 187 ssp. *japonica* FLcDNA sequences in KOME, and 10 096 ssp. *indica* FLcDNA sequences in NCGR.

Initially, we identified chromosomal distributions of the three different rice cDNAs along the cv. Nipponbare chromosomal pseudomolecules (Fig. 3). Though there were relatively small quantities of W1943 cDNAs, there were similar trace trends and no visible large bias comparing KOME and NCGR

Table 3. List of seven sense–antisense cDNA transcripts of *Oryza rufipogon* W1943

Accession Number	Length (bp)	Protein	Location (chr)	Identity (%)	Antisense gene	Location (chr)	Protein
CU405785	727	—	05	99	CA764081	01	DNA-directed RNA polymerase 3
CU861795	475	—	09	79	CT858901	unsure	Unknown
CU406355	837	—	12	97	AK107125	12	AP2 domain, putative
CU406396	520	—	02	99	AK103485	02	Hypothetical
CT841800	941	—	11	99	AK121962	11	Patatin, putative
CU861688	693	—	08	99	AK109182	08	Hypothetical
CT841937	1552	—	08	98	AK106713	08	Unknown

Table 4. List of 24 no-hit *Oryza sativa* ssp. *japonica* genome sequences

Number	Accession Number	<i>japonica</i> chromosome	93–11 location	ESTs or mRNA hits	Protein
1	CT842002	—	Contig005912	AK241925.1	—
2	CT842007	—	Contig008507	CT856206	—
3	CU405940	—	Contig001402	AK103326	Unknown protein
4	CU406172	—	Contig014596	AK242967.1	—
5	CT842006	—	Contig000383	AK111647	GTP-binding protein
6	CU861753	—	Contig000750	AK099287	Ring-box protein
7	CU406308	—	Contig000444	AK070131	Unknown protein
8	CT841996	—	Contig002576	CT834800	Unknown protein
9	CU406568	—	Contig003848	AK064050	Bowman Birk trypsin inhibitor
10	CU406582	—	Contig000444	AK107776	Unknown protein
11	CU406596	—	Contig001277	AK242711.1	Hypothetical protein
12	CT842008	—	Contig008507	CT856206	Unknown protein
13	CU406895	—	Contig003011	CT859459	Hypothetical protein
14	CU861744	—	Contig000750	AK099287	Ring-box protein
15	CU405657	—	—	CT856885	—
16	CT841712	—	—	CA766528	—
17	CU405768	—	—	CT836656	60S ribosomal protein L7A
18	CU405675	—	—	CA756235	60S ribosomal protein L17
19	CU406202	—	—	NM_001063334	Unknown
20	CU406924	—	—	AC145809	—
21	CU405898	—	—	CN130755.1 (<i>Sorghum bicolor</i>)	Ribulose-bisphosphate carboxylase
22	CU406778	—	—	BE429292.1 (<i>Triticum turgidum</i>)	Hydrophobin
23	CU861677	—	—	FF534517.1 (<i>Manihot esculenta</i>)	Hypothetical protein
24	CT841912	—	—	EH277383.1 (<i>Spartina alterniflora</i>)	Unknown protein

cDNAs. So the 1888 W1943 cDNAs can give clues to the entire W1943 genome.

A Perl script known as MISA (<http://pgrc.ipk-gatersleben.de/misa/>) was used to identify simple sequence repeats (SSRs) in these cDNA sequences. We described all SSR motifs of 1–6 nucleotides in

size. The minimum repeat unit was prescribed as follows: 10 repeats for mononucleotides, 6 for di-nucleotides and 5 for all the other motifs such as tri-, tetra-, penta- and hexa-nucleotides. We detected the five highest frequencies of SSR motifs of the overall cDNA sequences, 5'-UTR sequences, ORF

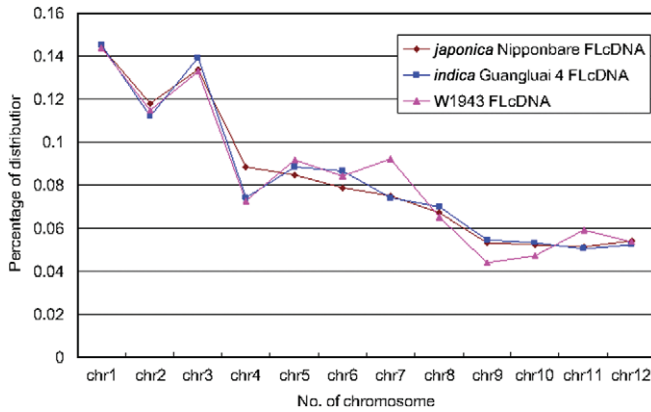


Figure 3. Chromosomal distributions of the three different rice cDNAs (W1943, KOME, NCGR) along the *ssp. japonica* cv. Nipponbare chromosomal pseudomolecule sequences. Though relative small quantities of W1943 cDNAs, it had about similar trace trends and no visible large bias comparing with KOME and NCGR (KOME, *Oryza sativa* ssp. *japonica* Nipponbare cDNAs; NCGR, *Oryza sativa* ssp. *indica* Guangluai 4 cDNAs.).

sequences and 3'-UTR sequences, respectively (Fig. 4). The highest frequencies of the SSR motifs in the three different rice cDNAs were identical in 5'-UTR, ORF or 3'-UTR regions. First, the motif CCG/CGG has the highest frequencies in 5'-UTR and ORF regions, but the SSR motif A/T has the highest frequency in 3'-UTR region. Second, all kinds of motif types were unevenly distributed in the FLcDNA sequences. The motifs CCG/CGG and A/T were more frequent in the ORF and 3'-UTR regions, respectively, with frequencies >50%. However, in 5'-UTR regions, the most frequent SSR motifs were ≤28%. In addition, scanning showed that the three most frequent SSR motif-types in ORF regions were all triplets that differed from those in UTR regions. This difference was very important for coding sequence because tri-nucleotide SSR motif-types could effectively prevent amino acid from frame shifting. Furthermore, the five most frequent SSR motifs were all triplets; the only exception was the fourth most frequent SSR type of NCGR, which was A/T (7.19%). In the process of evolution, relative higher frequency of mononucleotide SSR motifs of NCGR ORF was likely to be one key factor that led to divergence of *ssp. indica* and *ssp. japonica*. This

could partly explain why W1943 was closer to *japonica* than to *indica*.

We carried out transcripts comparisons between W1943 and the other two cultivated rice subspecies (Fig. 5). A total of 823 W1943 cDNAs were detected according to their homology with both KOME and NCGR (≥95% identity and non-redundant hit to KOME and NCGR). We extracted the ORF of each cDNA sequence using the *getorf* program.²¹ The amino acid levels in a total of 194 ORF groups were all identical (Fig. 5A), 143 ORF groups were specifically identical between W1943 and KOME, 87 ORF groups were specifically identical between W1943 and NCGR, and 64 ORF groups were specifically identical between KOME and NCGR. Consequently, 40.9% of transcripts were conserved in wild rice W1943 and cultivated rice *ssp. japonica* cv. Nipponbare; 34.1% were conserved in W1943 and cultivated rice *ssp. indica* cv. Guangluai 4 and 31.3% were conserved in cvs. Nipponbare and Guangluai 4.

The nucleotides of 194 identical ORF groups were extracted for further calculation of synonymous substitution rates. The results showed that 106 of 194 (54.6%) groups were also completely identical at nucleotide level. So the remaining 88 groups were used to calculate synonymous divergence (Ks) (Fig. 5B). Of 88 groups, 42 groups had no synonymous substitution between W1943 and KOME; 9 groups had no synonymous substitution between W1943 and NCGR; 15 groups had no synonymous substitution between KOME and NCGR and another 22 groups had synonymous substitutions among the three species and subspecies. That is, at nucleotide level, 76.2% of 194 identical ORF groups had no changes in W1943 and cv. Nipponbare, and 59.2% for W1943 and cv. Guangluai 4.

It was reported²⁹ that the rates of polymorphisms in predicted intergenic regions of rice were 0.302 (W1943/Nipponbare), 0.653 (W1943/Guangluai 4) and 0.630 (Nipponbare/Guangluai 4), respectively. These were similar to results in coding sequence regions in the present study. Thus, the hypothesis that *O. rufipogon* W1943 was closer to *ssp. japonica* than to *ssp. indica* was further validated.

	W1943	NCGR	KOME	W1943 5'-UTR	NCGR 5'-UTR	KOME 5'-UTR	W1943 ORF	NCGR ORF	KOME ORF		W1943 3'-UTR	NCGR 3'-UTR	KOME 3'-UTR	
1st 2nd	CCG/CGG	0.3114	0.3000	0.3504	0.2578	0.2514	0.2716	0.5282	0.5307	0.5167	A/T	0.5088	0.6113	0.5899
3rd	A/T	0.1828	0.2455	0.2336	0.1289	0.1596	0.1512	0.0536	0.0719	0.0248	AG/CT	0.0833	0.0463	0.0693
4th	AG/CT	0.1133	0.0864	0.1028	0.2200	0.1914	0.1842	0.0080	0.0134	0.0116	AT/AT	0.0702	0.0919	0.0500
5th	AGG/CCT	0.1029	0.0787	0.1081	0.1511	0.1047	0.1165	0.1206	0.1039	0.1280	AC/GT	0.0526	0.0444	0.0455
	AGC/CGT	0.0495	0.0506	0.0719	0.0422	0.0360	0.0410	0.0831	0.0909	0.1193	AAG/CTT	0.0526	0.0260	0.0257
	AAG/CTT	0.0333	0.0324	0.0328	0.0333	0.0549	0.0406	0.0268	0.0160	0.0223	CCG/CGG	0.0219	0.0355	0.0383
	ACC/GGT	0.0400	0.0314	0.0443	0.0333	0.0332	0.0380	0.0697	0.0485	0.0602				
	ACG/CTG	0.0429	0.0443	0.0518	0.0311	0.0355	0.0292	0.0612	0.0693	0.0749				

Figure 4. The first five highest frequency SSR motifs in the overall cDNA sequences, 5'-UTR sequences, ORF sequences and 3'-UTR sequences, respectively.

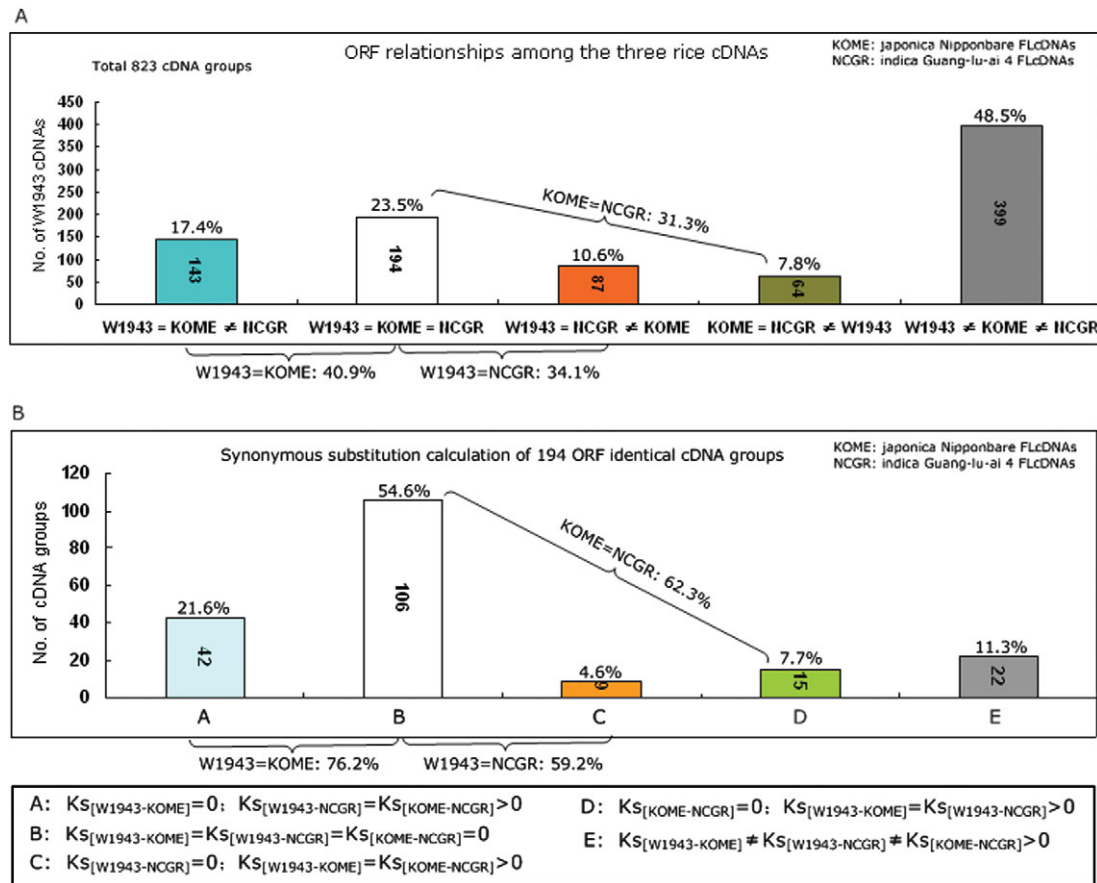


Figure 5. Comparative analysis with *Oryza sativa* cDNA sequences in public databases. (A) The relationships of ORFs among 823 W1943, KOME and NCGR co-cDNA groups at amino acid level. (B) The synonymous divergent (Ks) relationships of 194 ORF identical cDNA groups.

Table 5. List of 4 miRNAs

Accession Number	Gene length (bp)	Pre-miRNA length (bp)	Hit-miRNA	miRNA seq	Chromosome
CU406292	1416	262 (220–490)	osa-MIR159a	uuuggauugaaggagcucug	01
CU405943	1511	101 (160–280)	osa-MIR156j	ugacagaagagagugagcac	06
CU861819	561	80 (390–470)	osa-miR818e	aaucuuuuuuuugggacgg	04
CU861752	727	150 (325–475)	osa-miR446	aucaauugaauugggaaau	10

3.4. miRNAs identification

After searching against NCBI nrDB using BLASTx, 432 sequences of 1888 W1943 cDNAs found no hits in the database. Of 432 sequences, 71 were predicted as ORFs > 100 amino acid in length, so the remaining 361 were assumed to be putative non-protein-coding transcripts. Searching against Rfam database and miRBase, four cDNAs matched to four miRNA families; the osa-MIR159a, osa-MIR156j, osa-MIR818e and osa-miR446 families, respectively (Table 5). Using the mFOLD program, all four sequences could be predicted to pre-miRNA secondary structure and identified as miRNAs according to folding results.

3.5. Expression analysis by searching against the rice MPSS database

We used the rice MPSS database (<http://mpss.udel.edu/rice/>) to detect the expression level of W1943 cDNAs under different conditions.¹³ To define tissue-specific genes, we demarcated the qualifications as follows: (i) the expression level of every gene should >100 tpm of at least one tissue; (ii) if the gene expressed in several diverse tissues, then the highest expression level should be >75% among all tissues and (iii) the ratio of the first two highest expression levels should be >10. Thus, we identified 41 putative tissue-specific genes (Table 6). There were 16 W1943 cDNAs expressed remarkably highly in leaves,

Table 6. List of *Oryza rufipogon* W1943 tissue-specific genes (unit: tpm)

Clone Acc.	Leaf	Root	NGS	NCA	NGD	NME	NPO	PFAM Acc.	Description	E-value
CU406902	44 199	0	101	0	19	0	0	PF07207	Lir1	4.8e-85
CU405979	36 785	0	894	0	256	9	0			
CT841733	25 112	41	120	0	241	0	0	PF00101	RuBisCO_small	2.5e-45
CU405975	15 421	1278	0	0	650	223	0			
CT841994	9140	0	10	0	18	0	0			
CU406521	3504	6	0	0	0	0	0	PF01070	FMN_dh	2.8e-31
CU405996	3069	0	27	0	28	15	0	PF00430	ATP-synt_B	3.4e-28
CU405670	2653	0	11	5	21	4	23	PF00085	Thioredoxin	7.8e-43
CU406006	2337	0	0	0	0	0	10			
CU406668	2126	3	17	0	16	0	0			
CT841650	1997	0	0	0	0	0	0	PF00112	Peptidase_C1	6e-109
CT841731	1942	0	0	0	12	0	0	PF02507	PSI_PsaF	0
CT841902	1486	0	24	0	31	0	0			
CU405952	1253	7	110	5	2	5	0			
CU406199	1235	0	16	0	0	0	0			
CU406624	1012	0	60	58	0	3	5	PF05899	DUF861	2.1e-37
CU406431	0	189	0	0	0	18	17			
CU405706	1456	15 907	0	183	803	0	0	PF01439	Metallothio_2	2.7e-32
CU406330	0	358	4	0	0	1	31			
CT841629	217	2721	157	36	80	25	86	PF01124	MAPEG	3.1e-63
CU406513	18	230	0	0	0	0	0	PF01439	Metallothio_2	1.6e-34
CU406576	0	231	0	11	0	0	0			
CU406281	29	449	0	0	0	14	0			
CT841966	15	520	0	0	0	0	0	PF00188	SCP	5.7e-55
CU405942	0	185	0	5	0	0	0	PF00967	Barwin	3e-84
CU406520	5	1209	0	0	0	0	0			
CU406670	0	189	0	0	0	0	0	PF00280	Potato_inhibit	1.4e-20
CU406238	41	0	987	33	31	0	0	PF04398	DUF538	4.9e-41
CT841875	16	0	0	162	3	3	15			
CT841950	119	135	76	3079	107	19	0			
CT841815	107	135	76	3087	107	19	0			
CU406940	59	68	19	31	1393	4	0	PF02065	Melibiose	3.5e-13
CU406598	565	0	606	757	16 965	0	0	PF00234	Tryp_alpha_amyl	1.6e-31
CU406533	7	0	14	30	4662	119	0	PF00234	Tryp_alpha_amyl	5.5e-33
CU406609	0	0	0	0	143	0	0			
CU406264	0	0	0	0	237	0	0			
CU405759	0	0	0	0	779	0	0			
CU406038	14	14	0	0	247	0	0			
CU405951	0	25	0	0	13	1347	0	PF01439	Metallothio_2	6.5e-22
CU406698	13	0	0	0	0	0	289	PF00481	PP2C	2.4e-14
CU406351	103	4	36	66	48	42	3228			

NGS, 3 days—Germinating seed; NCA, 35 days—Callus; NGD, 10 days—Germinating seedlings grown in dark; NME, 60 days—Crown vegetative meristematic tissue; NPO, mature pollen.

11 cDNAs specifically in roots, 1 in germinating seed, 3 in callus, 7 in germinating seedlings, 1 in meristematic tissue and 2 in mature pollen. Searching against the PFAM protein database, we found that gene

'CU406902' was predicted as 'Lir1, light regulated protein Lir1'. Lir1 mRNA can accumulate in the light, reaching maximum and minimum steady-state levels at the end of the light and dark periods.³¹ Another

Table 7. List of seven cDNAs preferentially expressed under cold-stress, drought-stress and salinity in leaf (unit: tpm)

Clone Acc.	Normal leaf	NCL	NDL	NSL	PFAM Acc.	Description	E-value
CU406310	96	2872	3	255	Null	Null	Null
CT841781	96	3089	3	257	Null	Null	Null
CT841558	102	2404	2	365	Null	Null	Null
CU406554	11	568	0	83	Null	Null	Null
CT841576	303	0	3435	68	PF00234	Tryp_alpha_amyl	4.6e-33
CU406485	0	0	1477	0	Null	Null	Null
CU405946	0	113	0	591	PF00257	Dehydrin	2.2e-54

NCL, 14 days—Young leaves stressed in 4°C cold for 24 h; NDL, 14 days—Young leaves stressed in drought for 5 days; NSL, 14 days—Young leaves stressed in 250 mM NaCl for 24 h.

gene 'CT841733' was predicted as 'RuBisCO_small' (ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit). Although the RuBisCO large subunit is coded for by a single gene, the small subunit is coded for by several different genes, which are distributed in a tissue-specific manner. They are transcriptionally regulated by light receptor phytochrome, which results in RuBisCO being more abundant during the day when it is required.³²

In the similar restricted conditions as above, there were seven W1943 cDNAs with distinct expression level in leaves exposed to cold, drought or salinity stresses (Table 7). Of the seven cDNAs, four genes were up-regulated by cold stress, two genes were up-regulated by drought and one gene was up-regulated by salinity. It should be pointed out that gene 'CU405946' matched to PFAM protein annotated as 'Dehydrin'. This protein is produced by plants that experience water-stress.³³

3.6. Conclusions

In this research, we collected and completely sequenced 1888 putative FLCDNAs of wild rice *O. rufipogon* Griff. W1943. A total of 17 novel rice cDNAs and 41 putative tissue-specific expression genes were identified. The comparative analysis between wild rice and two cultivated rice subspecies indicated that *O. rufipogon* W1943 had greater similarity to *O. sativa* ssp. *japonica* than to ssp. *indica* cultivars. It is reported that W1943 is primarily distributed in Dongxiang (26°14'N, 116°36'E) of Jiangxi Province in China.³⁴ It is found to be the northern most distribution of *O. rufipogon* at present time.³⁵ Both cultivated rice *O. sativa* ssp. *japonica* and *indica* have distributions in this area. The geological distribution of W1943 can also provide some clues for further analysis between wild and cultivated rices.

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