ORIGINAL PAPER

Hui-Wen Wang · Jin-Song Zhang · Jun-Yi Gai Shou-Yi Chen

Cloning and comparative analysis of the gene encoding diacylglycerol acyltransferase from wild type and cultivated soybean

Received: 8 September 2005 / Accepted: 28 December 2005 / Published online: 24 January 2006 © Springer-Verlag 2006

Abstract Diacylglycerol acyltransferase (DGAT), as an important enzyme in triacylglycerol synthesis, catalyzes the final acylation of the Kennedy pathway. In the present study, the GmDGAT gene was cloned from Glycine max by using AtDGAT as a query to search against the soybean EST database and the rapid amplification of cDNA ends (RACE) method. Allelic genes were also isolated from 13 soybean accessions and the divergence of the deduced amino acid sequences were compared. The comparison reveals that although GmDGAT is a highly conserved protein, several differences of insertion/deletion were identified in the N-terminal region of the GmDGATs from various soybean accessions. In the C-terminal regions, a single amino acid mutation specific to both G. max and G. soja was also found. The GmDGAT genomic sequences were further cloned and the number and size of exons in the DGAT genomic sequence were very similar among different plant species, whereas the introns were more diverged. These results may have significance in elucidating the genetic diversity of the GmDGAT among the soybean subgenus.

Communicated by F. J. Muehlbauer

H.-W. Wang · J.-S. Zhang (⊠) · S.-Y. Chen
The National Key Laboratory of Plant Genomics, Institute of
Genetics and Developmental Biology, Chinese Academy
of Sciences, 100101 Beijing, China
E-mail: jszhang@genetics.ac.cn
Tel.: + 86-10-64886859
Fax: + 86-10-64873428
E-mail: sychen@genetics.ac.cn

H.-W. Wang Graduate School of the Chinese Academy of Sciences, 100039 Beijing, China

J.-Y. Gai

National soybean Institute for Improvement, Nanjing University, 210095 Nanjing, China

Keywords Diacylglycerol acyltransferase gene \cdot *Glycine max* \cdot Diversity

Introduction

Soybean is one of the most important crops, accounting for 48% of the world market in oil crops (Singh and Hymowitz 1999). China is the place of origin for soybean (Glycine max L. Merr) and it has rich soybean germplasm. Our laboratory has been focusing on soybean genomic research for years and several genes related to agronomic traits have been cloned and characterized (Zhang et al. 1997; Liu et al. 2000; Wu et al. 2001; He et al. 2002, 2003; Tian et al. 2004a, b; Wang et al. 2005; Luo et al. 2005). Oil content is the major trait of soybean. Triacylglycerol (TAG) is the main component of soybean oil whose content ranged from 13 to 22% in the soybean cultivars (Singh et al. 1999). In plants, TAG biosynthesis mainly contributes to the accumulation of seed oil. TAG is an important agricultural commodity and acts as a major energy source for the growth of new seedling (Lu and Hills 2002). TAG synthesis is via the Kennedy pathway, a biochemical process of the acylation of the glycerol backbone (Kennedy 1961). Diacylglycerol acyltransferase (DGAT) is a membrane-bound enzyme that transfers an acyl group from acyl-coenzyme-A to the sn-3 position of 1,2-diacylglycerol in the final acylation step of the Kennedy pathway. It is the only step that is unique to TAG synthesis. DGAT-catalyzed esterification of TAG was proposed to be a rate-limiting step in the control of plant TAG synthesis (Settlage et al. 1998). A strong positive correlation was found between the rate of oil accumulation and DGAT activity in mature seeds of soybean (Settlage et al. 1998) and rape (Perry and Harwood 1993). In the Arabidopsis thaliana mutant line AS11, which has an insertion mutation in the DGAT, the DGAT activity and seed TAG content were reduced (Jako et al. 2001). Over-expression of the AtDGATcDNA in wild-type A. thaliana enhanced oil deposition and average seed weight (Jako et al. 2001).

The first reported sequence of a DGAT gene was from mouse (AF078752) (Cases et al. 1998). Then homologous DGAT genes have been cloned from various plants, such as A. thaliana (AJ131831) (Hobbs et al. 1999), Brassica napus (AF164434) (Nykiforuk et al. 1999) and Ricinus communis (AY366496) (He et al. 2004). Several DGATs were purified from various plants and the acyl-CoA-dependent DGAT activity was tested (Hobbs et al. 1999; Triki et al. 2000; Hobbs and Hills 2000; Jako et al. 2001). The DGAT was proved to be a component of the endoplasmic reticulum (Cao and Huang 1986; Settlage et al. 1995; Lacey and Hill 1996). Transcript levels of the DGAT were also examined. The DGAT was highly expressed in maturing seeds (Kaup et al. 2002; Lu et al. 2003) and its expression was also found in flowers and germinating seeds (Zou et al. 1999). Investigation of the DGAT gene would allow us to ascertain the role of the DGAT in regulating the plant TAG synthesis.

Soybean is an important oil crop and its DGAT gene has not been identified. To understand the features of this gene and compare the phylogenetic relationship of the DGAT between wild type and cultivars of soybean, the full-length cDNA of GmDGAT was cloned from cultivated soybean accession using the rapid amplification of cDNA ends (RACE) method (Frohman 1993). The DGAT cDNA sequences were further amplified from different accessions of soybean. The phylogenetic relationships of these DGAT proteins and the exon/ intron structure of the DGAT genomic sequences between plant species were analyzed.

Materials and methods

Plant materials and DNA and RNA extractions

Soybean (Glycine max L. Merr.) cultivar 8904 and 17 other accessions from the subgenera Soja and Glycine were used in this study (Table 1). The bulked soybean seeds, which were harvested in the experimental station last year, were grown in the experimental station from May to September in Beijing. Leaves, flowers and pods were harvested at the indicated stages and stored at -70°C for RNA isolation. RNA was extracted according to the method of Zhang et al. (1996). The tissues were ground to fine powder in liquid nitrogen. Isolation of total RNA was performed using guanidine thiocyanate, and then purified with phenol-chloroform extraction. Mature leaves were harvested and DNA extraction was performed as described previously (Chen et al. 1991). Genomic DNA was extracted with SDS extraction solution and then purified with phenol-chloroform extraction and ethanol precipitation.

Cloning of the full-length cDNA of GmDGAT

Five µg total RNA from pods of 8904 at 20 days after flowering (DAF) was reverse-transcribed into

first-strand cDNAs with the cDNA synthesis kit (Promega, Madison, WI, USA) in a 20 µl reaction volume. For screening of the *GmDGAT* from soybean, the cDNA sequence of AtDGAT was used as a query for a Basic Local Alignment Search Tool (BLAST) search against soybean ESTs in the GenBank, and two putative GmDGAT ESTs were obtained. The PCR primers, DGAT P1 and DGAT P2 (Table 2, Fig. 1), were designed according to the two EST sequences obtained above. The total volume of the PCR reaction mixture was 25 µl, containing 1 µl cDNA, 0.5 µM of each primer, 1×PCR buffer, 0.4 mM dNTPs, and 1 unit of long and accurate (LA) DNA polymerase (Takara, Kyoto, Japan) which is a proofreading enzyme; hence the fidelity is significantly better than that of rTag polymerase (Takara). The reaction was denatured at 94°C for 5 min, and then followed by 30 cycles of 1 min at 94°C, 1 min at 56°C and 2 min at 72°C, then 10 min at 72°C. PCR reaction was performed by using a Gene-Amp PCR System 9600 (Perkin Elmer, Boston, MA, USA). The partial GmDGAT fragment was purified using DNA Purification Kit (Dingguo, Beijing, China), cloned into pMD18-T vector (Takara) and sequenced.

For cloning of the full-length of GmDGAT from *G. max*, a SMARTTM RACE cDNA Amplification Kit (Clontech, Mountain View, CA, USA) was used. RACE is a method widely used to isolate the cDNA of unknown 5' or 3' flanking sequences. One μ g total RNA from pods of 8904 at 20 DAF was used to synthesize cDNA as described in the protocol. The RACE primers (Table 2, Fig. 1) were designed based on the sequence of the partial *DGAT* fragment described above. The PCR reaction was performed as the protocol.

Based on the full-length sequence of the GmDGATgene obtained above, the full length ORF of the DGATgene from other accessions was amplified from corresponding cDNAs, with the primers DGAT F-P1 and DGAT F-P2 (Table 2, Fig. 1). The PCR reactions were performed as described above and three individual clones were selected and sequenced. The putative LcD-GAT and OsDGAT ESTs from Lotus corniculatus and Orvza sativa, respectively, were obtained by searching GenBank, and the complete sequence of LcDGAT and OsDGAT were assembled by ContigExpress, a component of Vector NTI Suite 6.0 (InforMax Inc., Carlsbad, CA, USA). The alignments of the DNA or amino acid sequences were performed with MegAlign of DNAS-TAR (DNASTAR Inc., Madison, WI, USA) by using clustal method.

Southern hybridization analysis

About 10 μ g of genomic DNA was digested with 50 units of restriction enzyme *Taq*I in a final volume of 50 μ l at 37°C for 18 h. The cleaved DNA fragments were run on a 0.8% (w/v) agarose gel and transferred to Hybond-N+ membranes (Amersham Pharmacia, Little Chalfont, Buckinghamshire, England). The membranes

1088

Accessions	Latin name	Seed color	Origin area ^a	Oil content (% w/w)	Usage in this study
8904	G. max	Yellow	-	21.50	Cloning the cDNA and genomic sequence. Analysis of <i>GmDGAT</i> expression
Xiangchundou15	G. max	Yellow	Hunan	15.98	Cloning the cDNA sequence
DianYD028	G. max	Yellow	Yunnan	18.25	Cloning the cDNA sequence
Jidou12	G. max	Yellow	Heibei	17.14	Cloning the cDNA sequence
Jilin30	G. max	Yellow	Jilin	16.61	Cloning the cDNA sequence
Heilong38	G. max	Yellow	Heilongjiang	19.60	Cloning the cDNA sequence
Wandou16	G. max	Yellow	Anhui	17.30	Cloning the cDNA sequence
ZYD4617	G. soja	Black	Jiangxi	11.50	Cloning the cDNA sequence
ZYD3708	G. soja	Black	Shanxi	9.65	Cloning the cDNA sequence
ZYD4174	G. soja	Black	Jiangsu	11.70	Cloning the cDNA sequence
ZYD4433	G. soja	Black	Zhejiang	10.48	Cloning the cDNA sequence
ZYD3235	G. soja	Black	Shandong	9.54	Cloning the cDNA sequence
PW0063	G. tomentella	Black	-	-	Cloning the cDNA and genomic sequence
PW0031	G. latifolia	Black	_	_	Cloning the cDNA and genomic sequence. Analysis of <i>GmDGAT</i> expression
Heihuangdou	G. max	Black	-	22.00	Cloning the genomic sequence
PI547844	G. max	Yellow	-	22.10	Cloning the genomic sequence
y43	G. gracilis	Black	_	_	Cloning the genomic sequence
y74	G. gracilis	Black	_	_	Cloning the genomic sequence

^aOrigin area is the province name of China

were hybridized with $[\alpha^{-32}p]dCTP$ -labeled (Amersham Pharmacia) 0.8 kbp *GmDGAT* fragment mentioned above. The hybridization procedures followed the standard protocols (Chen et al. 1991). The membrane was washed once with 2×SSC plus 0.1% (w/v) SDS at 65°C for 15 min, then 1×SSC plus 0.1% (w/v) SDS at 65°C for 8 min and exposed to FUJI Medical X-ray film at -70°C.

Cloning of the DGAT genomic sequences

Partial genomic sequences containing the *DGAT* gene from the genomic DNAs of six accessions, *G. max* PI547844, *G. max* Heihuangdou, *G. gracilis* y43, *G. gracilis* y74, *G. latifolia* PW0031 and *G. tomentella* PW0063, were amplified with a pair of primer (DGAT P1 and DGAT PG-2) (Table 2). The full-length

 Table 2 Primers used in this study

Name	Sequence $(5' \rightarrow 3')$	Usage in this study
DGAT P1	TCA ACC TCT GTA TAG TAG TC	Cloning the partial <i>GmDGAT</i> cDNA
DGAT P2	GAA CAG GCA TAT TCC ACA TC	Cloning the partial <i>GmDGAT</i> cDNA and genomic DNA
5'RACE-GSP1	GGA AAT ACC ACA AGA GAA AGA CAA CAC	RACE
5'RACE-GSP2	CCA GTC TCT CAA TGA CTT TGA GC	RACE
3'RACE-GSP1	TTA CGC CAT CGA GAG AGT TCT GAA GC	RACE
3'RACE-GSP2	GAG CTT CTT CGA TTT GGT GAT CGT G	RACE
DGAT F-P1	GTT AGT AAA CAC GCT CGC TCG GTC	Cloning the full-length GmDGAT cDNA
DGAT F-P2	CTG CCA TGG TAG ATG AAA GTA CTC GTG	Cloning the full-length GmDGAT cDNA
DGAT PG-2	TT CCA CAT CAA AGA TAT ATG	Cloning the partial <i>GmDGAT</i> genomic DNA
G-primer1	TGA GTT AGT AAA CAC GCT CGC TCG GTC	Cloning the <i>GmDGAT</i> genomic sequence
G-primer1'	CCA GTC TCT CAA TGA CTT TGA GC	Cloning the <i>GmDGAT</i> genomic sequence
G-primer2	GAT TAT TCA ACC TCT GTA TAG TAG TC	Cloning the <i>GmDGAT</i> genomic sequence
G-primer2'	GAA CAG GCA TAT TCC ACA TC	Cloning the <i>GmDGAT</i> genomic sequence
G-primer3	CAA GAG CTT AGC ATA TTT CCT GGT TGC	Cloning the <i>GmDGAT</i> genomic sequence
G-primer3'	CAG CCA ACC CTT TCG AAT ATA AGG TGT GCG AG	Cloning the <i>GmDGAT</i> genomic sequence
G-primer4	CAT TGT ACA AAA TTC ACA GCA TC CTC	Cloning the <i>GmDGAT</i> genomic sequence
G-primer4'	ATG GAA AAT ATA GGT GGC GGA TCA TCC	Cloning the <i>GmDGAT</i> genomic sequence
G-primer5	CAC CTA TAT TTT CCA TGT TTA AGG CAC	Cloning the <i>GmDGAT</i> genomic sequence
G-primer5'	AAT ATA GCA GTA CGC ACA TAG GTT GAC	Cloning the <i>GmDGAT</i> genomic sequence
GmDGAT-RT-P-1	GTG GAG AAG TTG GCA CAG CAG AAG TG	Analysis of GmDGAT expression
GmDGAT-RT-P-2	GTG GCA AGG AAC AGC GAT GCA CAG CTC	Analysis of GmDGAT expression
β -Tubulin P1	AAC CTC CTC CTC ATC GTA CT	Analysis of GmDGAT expression
β -Tubulin P2	GAC AGC ATC AGC CAT GTT TCA	Analysis of GmDGAT expression

DGAT F-P1 1 GAA GAG AAG ACT GAG TTA GTA AAC ACG CTC GCT CGG TCT TCT TTT CCA ATG GCG ATT TCC 60 MAIS 61 GAT GAG CCT GAA ACT GTA GCC ACT GCT CTC AAC CAC TCT TCC CTG CGC CGC CGT CCC ACC 120 D E P E T V A T A L N H S S L R R R P T 121 GCC GCT GGC CTC TTC AAT TCG CCC GAG ACG ACC ACC GAC AGT TCC GGT GAT GAC TTG GCC 180 A A G L F N S P E T T T D S S GDDLA 181 AAG GAT TCC GGT TCC GAC GAC TCC ATC AGC AGC GAC GCC GCC AAT TCG CAA CCG CAA CAA 240 K D S G S D D S I S S D A A N S Q P Q Q 241 AAA CAA GAC ACT GAT TTC TCC GTC CTC AAA TTC GCC TAC CGT CCT TCC GTC CCC GCT CAT 300 K Q D T D F S V L K F A Y R P S V P A H 301 CGC AAA GTG AAG GAA AGT CCG CTC AGC TCC GAC ACC ATT TTC CGT CAG AGT CAC GCG GGC 360 420 421 TTA ATG AAG TAT GGT TGG TTC AAA TCT GGC TTT TGG TTT AGC TCA AAG TCA TTG AGA L M K Y G W L I K S G F W F S S K S L R 481 <u>GAC TGG</u> CCC CTC TTC ATG TGT TGT CTT TCT CTT GTG GTA TTT CCT TTT GCT GCA TTT ATA 540 D W P L F M C C L S L V V F P F A A F I 541 GTG GAG AAG TTG GCA CAG CAG AAG TGT ATA CCC GAA CCA GTT GTT GTT GTA CTT CAT ATA 600 V E K L A Q Q K C I P E P V V v v L н 601 ATC ATT ACC TCA GCT TCA CTT TTC TAT CCA GTT TTA GTA ATT CTC AGG TGT GAT TCT GCT 660 v т S ASL F Y P ьv ILRCDSA т т 661 TTT CTA TCA GGT GTT ACG TTA ATG CTA TTT GCT TGT GTT GTA TGG TTA AAA TTG GTG TCT 720 LSGVTL MLF ACVVW L K L V S 721 TAT GCA CAT ACA AAC TAT GAT ATG AGA GCA CTT ACC AAA TCA GTT GAA AAG GGA GAA GCT 780 Y A H T N Y D M R A L T K S V E K G E A 781 CTG CCC GAT ACT CTG AAC ATG GAC TAT CCT TAC AAT GTA AGC TTC AAG AGC TTA GCA TAT 840 L P D T L N M D Y P Y N V S F K S L A Y 841 TTC CTG GTT GCC CCT ACA TTA TGT TAC CAG CCA AGC TAT CCT CGC ACA CCT TAT ATT CGA 900 F L V A P T L C Y Q P S Y P R T P Y I R 901 AAG GGT TGG CTG TTT CGC CAA CTT GTC AAG CTG ATA ATA TTT ACA GGA GTT ATG GGA TTT 960 K G W L F R Q L V K L I I F T G V M G F 961 ATA ATA GAA CAA TAC ATT AAT CCC ATT GTA CAA AAT TCA CAG CAT CCT CTC AAG GGA AAC 1020 I I E Q Y I N P I V Q N S Q H P L K G N 1021 CTT CTT TAC GCC ATC GAG AGA GTT CTG AAG CTT TCT GTT CCA AAT TTA TAT GTG TGG CTC L L Y A I E R V L K L S V P N L Y V W L 1081 TGC ATG TTC TAT TGC TTT TTC CAC CTT TGG TTA AAT ATA TTG GCA GAG CTT CTT CTA ATT 1080 1140 C M F Y C F F H L W L N I L A E L L R Б 1141 GGT GAT CGT GAA TTC TAC CAG GAT TGG TGG AAT GCC AAA ACT GTT GAA GAT TAT TGG AGG G D R E F Y Q D W W N A K T V E D V W P 1200 1201 ATG TGG AAT ATG CCT GTT CAC AAA TGG ATG ATC CGC CAC CTA TAT TTT CCA TGT TTA AGG DGAT P2M W N M P V H K W M I R H L Y F P C L R 1260 1261 CAC GGT ATA CCA AAG GCC GTT GCT CTT TTA ATT GCC TTC CTG GTT TCT GCT TTA TTC CAT H G I P K A V A L L I A F L V S A L F H 1320 1321 GAG CTG TGC ATC GCT GTT CCT TGC CAC ATA TTC AAG TTG TGG GCT TTC GGT GGA ATT ATG 1380 ELCIAVPCHI F K L W A G 1381 TTT CAG GTT CCT TTG GTC TTC ATC ACT AAT TAT CTG CAA AAT AAA TTC AGA AAC TCG ATG 1440 FQVPLVFITNYLQNKFRNSM 1441 GTT GGA AAT ATG ATT TTT TGG TTC ATA TTC AGT ATT CTT GGT CAA CCT ATG TGC GTA CTG 1500 V G N M I F W F I F S I L G Q P M C V L 1501 CTA TAT TAC CAT GAC TTA ATG AAT AGG AAA GGC AAA CTT GAC TGA AGG TGC ACG TGG ATA 1560 L YHDLMNRKGKLD* Y 1561 AGC TTT TCT GTT TTT GGA GTG TAT AAT TGA TGT CGA TAT GTT GAT CAA TAT TGG TTT CCA 1620 1621 CGA GTA CTT TCA TCT ACC ATG GCA GTG GCT GCT CTG AAG GAT TTC CAC CTG ATA TAC CAG 1680 1681 GTC GCG AGG CTA ATT CAT CTT GAT CTA TGT ACT TAA TCA ACT CTC CTC TGG CAA TTG TAT 1740 1741 CGA TAT ATG CAA TTT TGA GAG CCA TAC ACT GGC ATT GAT AAC TGC CAA GGA ACA GTG NTA 1800 1801 GCT GTT TTT CTG TTA AAT GTT AAT TAG TAG AGA GCT AGA TGT AAA TAA ATT TAT GCT CAA 1860 1861 ААА ААА ААА ААА ААА ААА 1880

B

A

Fig. 1 *GmDGAT* gene sequence and predicted protein structure. **a** Nucleotide and deduced amino acid sequence of the *GmDGAT*. The deduced amino acid sequence was presented under the DNA sequence in *bold capital letters* and the stop codon was marked with an *asterisk*. The positions of the potential transmembrane domains

are indicated by *black lines*. The *broken lines* under the nucleotide sequence indicate the position of primers. **b** Schematic representation of the GmDGAT structure. The *black rectangles* represent the potential transmembrane domains predicted by SMART

1090

fragment of *DGAT* was amplified from the genomic DNA of *G. max* 8904 and *G. tomentella* PW0063 respectively with five pairs of primers (Table 1). The total volume of the PCR reaction mixture was 25 μ l, containing 100 ng of the genomic DNA, 0.5 μ M of each primer, 1×PCR buffer, 0.4 mM dNTP, and 1 unit of LA DNA polymerase (Takara, Kyoto, Japan). The reaction was denatured at 94°C for 5 min, and followed by 35 cycles of 1 min at 94°C, 1 min at 56°C, 2 min at 72°C and then 10 min at 72°C. The amplified fragments of the *DGAT* genomic sequence were recovered, cloned into pMD18-T vector (Takara, Kyoto, Japan) and three individual clones were selected and sequenced.

Analysis of GmDGAT expression

Five microgram of the total RNA isolated from young leaves, mature leaves, flowers, and pods from the cultivar 8904 or wild-type *G. latifolia* PW0031 was used for cDNA synthesis by using a first strand cDNA synthesis kit (Promega, Madison, WI, USA) in a 20 µl reaction volume. The first strand cDNA mix was used as template for RT-PCR.

The *GmDGAT*-RT-P-1 and *GmDGAT*-RT-P-2 were used as primers (Table 2). The total volume of the PCR reaction mixture was 25 µl, containing 1 µl cDNA, 0.5 µM of each primer, 1×PCR buffer, 0.4 mM dNTP, and 1 unit of rTaq enzyme (Takara). The reaction was denatured at 94°C for 2 min, and then followed by 30 cycles of 1 min at 94°C, 1 min at 56°C, 1 min at 72°C and concluded with one step of 10 min at 72°C.

Amplified fragments were separated on a 1% (w/v) agarose gel and stained with ethidium bromide. The agarose gel was scanned by using Gel Doc GS670 (Bio-Rad, Hercules, CA, USA). A soybean β -Tubulin gene, amplified with primers β -Tubulin P1 and β -Tubulin P2 (Table 2), was used as a control in the experiments.

Results and discussion

Cloning and structural analysis of the soybean *DGAT* gene

Arabidopsis AtDGAT gene was used as a query to search against the soybean EST database and two homologous ESTs were identified. The two putative GmDGAT ESTs were 559 bp (BM178620) and 572 bp (BM309669) in length, respectively, and non-overlapping, possibly representing the 5'- and 3'- sequence of GmDGAT when compared with other plant DGATs. Two specific primers (DGAT P1 and DGAT P2) were thus designed from these two ESTs and a 0.8 kbp fragment of the GmDGAT gene were obtained from soybean cultivar 8904. Using the RACE method, the 5'- and 3'- ends of the GmDGAT cDNA were further cloned from soybean pod cDNAs, and the full-length cDNA of GmDGAT was obtained under the accession number of AY496439. The full-length cDNA of GmDGAT was 1,880 bp in length containing 48 bp of the 5'- leader sequence and 335 bp of the 3'- untranslated region. The complete open reading frame (ORF) of 1,497 bp encoded a protein of 498 amino acids (Fig. 1a), with a predicted molecular weight of 57.3 kDa and a calculated isoelectric point of 8.89 (Protparam: http://www.expasy.ch). By BLAST against the ESTs in the GenBank, we also assembled the complete ORF of *LcDGAT* (AY859489) from *L. corniculatus* and *OsDGAT* (AY858584) from rice.

In plants, DGAT has been shown to localize in the endoplasmic reticulum (Cao and Huang 1986; Settlage et al. 1995; Lacey and Hill 1996) where the Kennedy pathway mainly occurs. Using SMART program (Simple Modular Architecture Research Tool: http:// www.smart.embl-heidelberg.de/), nine potential transmembrane domains were identified in the GmDGAT, suggesting that the protein is also localized in the membrane systems (Fig. 1a, b). A putative signal peptide peptidase domain (amino acids 10-232) and an acid phosphatase homolog region (amino acid 108-216) were also recognized. However, these domains may not be active since some of the required catalytic sites were not detected in these regions. A WWE domain (amino acid 214-279) was predicted, which is named after three of its conserved residues and is predicted to mediate specific protein-protein interactions in ubiquitin and ADP ribose conjugation systems (Aravind 2001). By comparing the soybean DGAT with other plant DGATs, an MBOAT (membrane bound O-acyltransferase) domain (amino acid 204-489) was identified in the GmDGAT (Fig. 2a). This domain is possibly involved in acyl transfer (Hofmann 2000). Compared with other proteins, the full-length GmDGAT exhibited 78.2% similarity to LcDGAT from L. corniculatus (AAW51456) and 66.3% to AtDGAT (AAF19262). The highest similarity was mainly within the C-terminal region, which contained the MBOAT domain. The MBOAT domains shared a similarity of 91.9% between GmDGAT and LcDGAT, and 78.4% between GmDGAT and AtD-GAT. The N-terminal region showed a high degree of variation among the DGATs compared (Fig. 2a). Cluster analysis was also performed and the GmDGAT was grouped with that of L. corniculatus, a legume plant, and it also appeared to be closely related to the DGATs from Arabidopsis and Brassica. However, the GmDGAT may be more divergent when compared with the proteins from tobacco and rice (Fig. 2b).

Comparative analysis of the DGATs from 14 soybean accessions

Soybean germplasm is abundant and highly diversified in China, where several wild *Glycine* species are native. There are many differences between wild-type species and cultivated soybean with regard to traits such as oil content, seed color, and plant morphology. It would be



Conserved sequences were shaded in *black*. The *bold line* under the sequence represents the MOBAT domain in different plants. **b** The phylogenetic tree of different plant DGATs. The length of each pair branches represents the distance between sequence pairs. The units at the bottom of the tree indicate the number of substitution events

interesting to know if there is any difference in the amino acid sequence of the DGAT protein from different soybean accessions. The full length of the DGAT cDNA was cloned from 13 accessions and compared with the GmDGAT gene of accession 8904. Among these 14 accessions, 7 were from G. max, 5 were from G. soja, 1 was from G. latifolia (PW0031) and 1 was from G. tomentella (PW0063) (Table 1). Alignment of the deduced amino acid sequences of these DGATs revealed that the C-terminal regions were almost the same except for a few amino acid changes, whereas a number of differences in the N-terminal region were identified among these proteins (Fig. 3a, b). Seven DGATs from G. max showed similarities from 98.2 to 100% among the members. When compared with the five DGATs from G. soja, the DGATs from G. max showed similarities from 97.8 to 100% (Fig. 3b). The DGATs from cultivar 8904 and Xiangchundou15 were the same as those in accessions ZYD4174 and ZYD3235 from G. soja. The DGATs from the two wild-type accessions, PW0031 (G. latifolia) and PW0063 (G. tomentella), showed a distinct divergence in comparison with the other proteins. The high similarity of the DGATs between members from both G. max and G. soja indicates that G. soja is an ancestor of G. max. The G. latifolia and G. tomentella have a more distant relationship to G. max and G. soja. Other cytological, morphological and molecular evidence also suggest that G. soja is the ancestor of G. max (Hymowitz 1970; Doyle and Beachy 1985; Shoemaker et al. 1986; Doyle 1988).

In the N-terminal region, four locations were recognized where amino acid residues were missing when a comparison was made between the soybean accessions. The first difference occurred in the 26th residue where three residues (Thr-Ser-Ala) were missing in the 12 accessions of subgenus Soja in comparison with other wild-type accessions PW0031 and PW0063. The second was found at the 58th position where one or two residues were missing in all accessions of subgenus Soja but not in G. latifolia (PW0031) and G. tomentella (PW0063). The third occurred in the 63rd amino acid where an Asn was missing in all subgenus Soja accessions and wildtype accessions PW0031. The last difference at the 101th position showed an interesting variation (Fig. 3a). Both cultivars DianYD028 and Wandou16 had the same sequence Gln-Leu-Gln as that of the wild type PW0031 (G. latifolia), although they were from different subgenus, whereas the other 11 accessions have a single Gln residue at this position. Moreover, there were 20 single amino acid changes in at least one of these 14 accessions of soybean (Fig. 3). Considering the properties of polarity and charge of the changed amino acids, ten changes are synonymous and ten changes are nonsynonymous.

In the C-terminal regions, only five single-residue changes were found (Fig. 3). There are two synonymous single amino acid changes and three non-synonymous single amino acid changes. The amino acid change at the 371th position should be noted. In the two wild-type accessions, PW0063 and PW0031, this position is a Lys whereas in the other 12 accessions, 7 from G. max cultivar and 5 from G. soja, a Gln is present instead of Lys (Fig. 3a). In DGATs from other plants such as Lotus corniculatus, Ricinus communis, Brassica napus, Nicotiana tabacum, Olea europaea, Arabidopsis thaliana and Oryza sativa, there is also a Lys at this position (Fig. 2a), which is the same as the ones in the two wild-type soybean accessions. It seems that Gln³⁷¹ is specific for G. max and G. soja but not for G. latifolia and G. tomentella and the other plant species examined. It is possible that the DGATs from the accessions of G. max and G. soja are derived from the Lys to Gln mutation, and it might be additional molecular evidence that the cultivated soybean is derived from G. soja. The other functions of this mutation need to be further investigated.

We further examined if the protein sequence variation accounts for different oil levels between the soybean accessions. We find that although the DGATs from these 14 accessions are highly homologous, the oil contents in these accessions are more variable (Table 1). Transcript abundance of the DGAT between the soybean accessions had no significant difference (data not shown). This may indicate that the DGATs do not directly correlate with the oil content in soybean seeds. Other factors may play roles in determination of the oil content.

Genomic architecture of the *GmDGAT* gene in various soybean accessions

We further investigated the difference in the genomic architecture of the DGAT gene between soybean accessions. The genomic DNAs from 27 accessions were digested with TaqI and subjected to Southern analysis. The 0.8 kbp GmDGAT fragment derived from two original ESTs was used as a probe. The results are shown in Fig. 4. It can be seen that the hybridization patterns are the same in all accessions from the subgenus Soja, with two major bands and a few weaker bands. It is also possible that minor variations in fragment length existed among these different accessions. However, the hybridization pattern was completely different in the subgenus *Glycine* genomes, with some accessions having two bands and others having up to seven bands. Therefore, the genomic architecture of the DGAT gene is very similar among the accessions in the subgenus *Soja*, but is more diversified among the accessions in subgenus Glycine.

Comparison of the *DGAT* genomic sequences from various soybean accessions

Although the amino acid sequences of the soybean DGATs are highly similar, their genomic architectures are more varied between subgenus *Soja* and *Glycine*. It probably suggests that there are major differences in the introns of the genomic sequence of the *DGAT* genes.

Fig. 3 Comparison of the deduced amino acid sequence of the DGATs from different accessions of soybean. a Alignment of the soybean DGAT sequences. The names of accessions are shown on the *right* and amino acid sequence numbers are show on the *left*. Differences in amino acids are shaded in *black*. b The percent divergence and similarity between the soybean DGATs

1	MAISDEPENVATALNHSSLERRENA AGLENSETTTDSSGERLAKDSGSDDSISSRAADNSOPCOKODTDSSVLKFAYRPSVPAHRKVKESPLSSDT	Xiangchundou15
1	MATSDEPPEVATALNHSSLERRPPA-AGLENSETTTDSSGDDLAKDSGSDDSTSSDAA-NSOPO-CKODTDSVLKFAYRPSVPAHRKVKESPLSSDT	DianYD028
1		Hoilong29
-	PAISDEPENVALAURSSENARTA - AREPNOSETTEDSSEDELARDSGSDDSESEARA NSVEC AREDIDSVERTATRESVERTRAVRESEESSET	nerrongso
1	MAISDEPENVATALNHSSLRRRPWATTAGLFNSETTTDSSGDDLAKDSGSDDSISSDAATNSOPOTOKODTDSVLKFAYRPSVPAHRKVKESPLSSDT	Jidoul2
1	MAISDEPETVATALNHSSLRRPTAAGLFNSSETTTDSSGDDLAKDSGSDDSISSDAAANSOPC-CKQDTDESVLKFAYRPSVPAHRKVKESPLSSDT	Jilin30
1	MAISDEPP VATALNHSSLERREWAAGLENSETTTDSSGD#LAKDSGSDDSISSDA-NSOPO-CKODTD SVLKFAYRPSVPAHRKVKESPLSSDT	Wandou16
1	MATSORDAUATALNESSLER BUD WAAFLENSETTTOSSCOLAKOSSORDSTSSDALSSOPC SKOTTOSSUKFAVESVDAHEKVKFSUSSOT	8904
2		0904
T	MAISDEPPIVATALNHSSLNRRPWA - ARLPNSETTTDSSGLDLAKDSGSDDSISSDAAANSOPCEKKDTDSSVLKFAYRPSVPAHRKVKESPLSSDT	ZYD461/
1	MAISDEPETVATALNHSSLRRRPTAAGLFNSEETTTDSSGDDLAKDSGSDDSISSDAA-NSOPC-CKODTDESVLKFAYRPSVPAHRKVKESPLSSDT	ZYD3708
1	MAISDEPENVATALNHSSLERRETA-A-AGLENSETTTDSSGDDLAKDSGSDDSISSDAA-NSOPC-CKODTDSVLKFAYRPSVPAHRKVKESPLSSDT	ZYD4174
1	MATSORDAWATALNESSLOW DWAAFLENSSTTTTDSSCOLAKOSODISTSSCOLAKOSODIC & KONTOSVIKEAVDSVDAHDKVKESULSSOT	7VD4433
-		80999995
T	MAISDEPENVATALNHSSLARRPNA - ABLPNSETTTDSSGLDLARDSGSDDSISSDAA - NSOPL-OKODTDSVLKPATRPSVPAHRKVKESPLSSDT	ZYD3235
1	MAISDEPESVATALNHSSLRRRPSATSAAGLFNSEETTTDSSGDDLAKDSGSDDSINSDAAADNSOPCNEKRDTDLSVLKFAYRPSVPAHRKVKESPLSSDT	PW0063
1	MAISDEPPTVATALNHSSLRHRPTATSAASLFNSETTTDSSGDDLAKDSGSDDSISSAAAAANSHPC-CKODTDSSVLKFAYRPSVPAHRKVKESPLSSDT	PW0031
07		Vi
97	1FRO SHAGLENICIVVLVAVNSKLITENLMKIGWLIKSGEWESSKSLKUWPLFMCCLSLVVEFFAAFIVEKLAQUKCIPDVVVVLHITITSASLEIPPL	Alangenundouls
97	IFF <mark>QLC</mark> SHAGLFNLCIVVLVAVNSRLIIENLMKYGWLIKSGFWFSSKSLRDWPLFMCCLSLVV <mark>DE</mark> FAAFIVEKLAC <mark>OK</mark> CIPE <mark>F</mark> VVVVLHIIITSASLF <mark>Y</mark> PVL	DianYD028
98	IFR-CSHAGLFNLCIVVLVAVNSRLIIENLMKYGWLIKSGFWFSSKSLRDWPLFMCCLSLVVFLFAAFIVEKLAQOKCIPPEVVVVLHIIITSASLFYPVL	Heilong38
97	TERO SHAGLENLCTVVLVAVNSELTENIMKYGWLTKSGEWESSKSLENDELEMCCLSLVVEEFAAFTVEKLAGKCTPE	Jidou12
00		7111-20
98	1PR CSHAGLPNLCIVVLVAVNSRLIIENLMKIGWLIKSGEWESSKSLKUWPLPMCCLSLVVEEFAAPIVEKLAQUKCIPDEVVVVLHIIIISASLEPPPL	J111N30
97	IFROLOSHAGLFNLCIVVLVAVNSRLIIENLMKYGWLIKSGFWFSSKSLRDWPLFMCCLSLVVDEFAAFIVEKLAQOXCIPEEVVVVLHIIITSASLFYPVL	Wandou16
97	IFRO-SHAGLFNLCIVVLVAVNSRLIIENIMKYGWLIKSGFWFSSKSLRDWPLFMCCLSLVVFEFAAFIVEKLACOKCIPPEVVVVLHIIITSASLFYEVL	8904
98	TER - OSHAGLENLCTV///WAVNSRLTENL/WAVNSRLTENL/WAVGWLTKSGEWESSKSLRDWPLEMCCLSLV//SEFAAFTVEKLACOBCTPEW//WULHTTNSASLEVEW/	ZVD4617
		BUD 1017
98	1FR CSHAGLFNLCIVVLVAVNSRLIIENLMKYGWLIKSGFWFSSKSLRUWPLFMCCLSLVVVFFAAFIVEKLAQ	ZYD3708
97	IFRO SHAGLFNLCIVVLVAVNSRLIIENIMKYGWLIKSGFWFSSKSIRDWPLFMCCLSLVVEFAAFIVEKLACOKCIPE	ZYD4174
98	IFF-CSHAGLFNLCIVVLVAVNSRLIIENLMKYGWLIKSGFWFSSKSLRDWPLFMCCLSLVVFEFAAFIVEKLAQOKCIPPEVVVVLHIIITSASLFYEVL	ZYD4433
97	TERO SHACLENI CTUULUAUNSDI TENI MKYCHI IKSCENESSKSI DONDI EMCCI SUMEREA FTUEKLAGKCI DEMUMULITI TESA SI EMDUL	7703235
200		DIDO200
103	IFF CSHAGLFNLCIVVLVAVNSRLIIENIMKYGWLIKSGFWFSSKSLRDWPLFMCCLSLVVFFFAAFIVEKLAQRCIPDSVVVVLHIIIIISASLFYPIL	PW0063
102	IFR <mark>OLC</mark> SHAGLFNLCIVVLVAVNSRLIIENLMKYGWLIKSGFWFSSKSLRDWPLFMCCLSLVV <mark>FF</mark> FAAFIVEKLAC <mark>OK</mark> CIPE <mark>F</mark> VVVVLHIIITSASLF <mark>Y</mark> FVL	PW0031
197	VILCOSA FEGUTI MILFACUAWI, KUNSYA HINYDWRALTKSVEKCEAL, FITIAMDY PYNYSEKSLAYFU VA PTLCYOPSY PRIVERKOULFROUWL. IF	Xiangchundou15
1.00		niangenandours
199	VILRCDSAFTSGVTLMLFPCVVWLKLVSYAHTNYDMRALTKSVEKGEALFTTLMMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRRGWLPRQLVKLIIF	DianiD028
198	VILRCDSAFTSGVTLMLFRCVVWLKLVSYAHTNYDMRALTKSVEKGEALFTLNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLFRQLVKLIIF	Heilong38
197	VILRCDSAFTSGVTLMLFACVVWLKLVSYAHTNYDMRALTKSVEKGEALETINMDYPYNVSFKSLAYFLVAPTLCYOPSYPRTPYTRKGWLFROLVKLITF	Jidou12
100	UT DODO A DOCUMENT AND A DOWNARD A DOWN AND A DOWN	Tilin20
190	VIIKODARENGVIIMILEECVWILKIVOTARINIIMALIKOVEKGEALEETIMUDIFINVOFKSLATELVAFILLIQESIFKIFIIKOWLEKQUVKLIIF	01111130
199	VILRCDSAFHSGVTLMLFACVVWLKLVSYAHTNYDMRALTKSVEKGEALHHTLNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLFRQLVKLIIF	Wandoul6
107	VILECDSAFUSGVTLMLEACVVWLKLVSYAHTNYDMBALTKSVEKGEALEPTLNMDYPYNVSEKSLAYFLVAPTLCYOPSYPRTPYTEKGWLEBOLVKLTTE	0004
191	Theorem Boot manage of the state of the stat	8904
198	VILRODSAFLSGVTIMLERCVVWLKUSVAHTNYDMRALTKSVEKSPALETINNDYPYNVSFKSLAVFLVAPTLCYOPSYPRTPYTRKGULFROUVKLITF	8904 ZYD4617
197	VIIRCDSAFISGVTIMIERCVWIKLVSYAHTNYDMRALTKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTICYQPSYPRTPYIRKGWLFRQUVKLIF VIIRCDSAFISGVTIMIERCVWIKLVSYAHTNYDMRALTKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTICYQPSYPRTPYIRKGWLFRQUVKLIF	8904 ZYD4617
197 198 198	VIIRCDSAFIGGVTIMLERCVVWLKLVSYAHTNYDWRALIKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLFRQLVKLIIF VIIRCDSAFIGGVTIMLERCVVWLKLVSYAHTNYDWRALIKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLFRQLVKLIIF	8904 ZYD4617 ZYD3708
197 198 198 197	VIIRCDSAFIGGVTIMLERCVVWLKIJSYAHTNYDMRALTKSVEKGEALERTIAMDYPYNVSFKSLAYFIVAPTLCYQPSYPRTPYIRKGWLERQLVKLIIF VIIRCDSAFIGGVTIMLERCVVWLKIJSYAHTNYDMRALTKSVEKGEALER VIIRCDSAFIGGVTIMLERCVVWLKIJSYAHTNYDMRALTKSVEKGEALERTIAMDYPYNVSFKSLAYFIVAPTLCYQPSYPRTPYIRKGWLERQLVKLIIF	8904 ZYD4617 ZYD3708 ZYD4174
197 198 198 197 198	VIIRCDSAFIGGVTIMLERCVWILKIJSYAHTINYDMRALIKSVEKGEALE TIAMDYPYNVSFKSLAYFIVAPTLCYQPSYPRTPYIRKGMLERQUVKLIIF VIIRCDSAFISGVTIMLERCVWILKIJSYAHTINYDMRALIKSVEKGEALE TIAMDYPYNVSFKSLAYFIVAPTLCYQPSYPRTPYIRKGMLERQUVKLIIF VIIRCDSAFISGVTIMLERCVWILKIJSYAHTINYDMRALIKSVEKGEALE TIAMDYPYNVSFKSLAYFIVAPTLCYQPSYPRTPYIRKGMLERQUVKLIIF VIIRCDSAFISGVTIMLERCVWILKIJSYAHTINYDMRALIKSVEKGEALE TIAMDYPYNVSFKSLAYFIVAPTLCYQPSYPRTPYIRKGMLERQUVKLIIF	8904 ZYD4617 ZYD3708 ZYD4174 ZYD4433
197 198 198 197 198 197	VIIRCDSAFIGGVTIMLECVVWLKUSYAHTNYDWRALTKSVEKGEALE TILMDYPYNVSFKSLAYFUVAPTLCYQPSYPRTPYIRKGWLFRQLVKLIIF VIIRCDSAFIGGVTIMLECVVWLKUSYAHTNYDWRALTKSVEKGEALE TILMDYPYNVSFKSLAYFUVAPTLCYQPSYPRTPYIRKGWLFRQLVKLIIF VIIRCDSAFIGGVTIMLECVVWLKUSYAHTNYDWRALTKSVEKGEALE TILMDYPYNVSFKSLAYFUVAPTLCYQPSYPRTPYIRKGWLFRQLVKLIIF VIIRCDSAFIGGVTIMLECVVWLKUSYAHTNYDWRALTKSVEKGEALE TILMDYPYNVSFKSLAYFUVAPTLCYQPSYPRTPYIRKGWLFRQLVKLIIF	8904 ZYD4617 ZYD3708 ZYD4174 ZYD4433 ZYD3235
197 198 198 197 198 197 203	VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQLVKLIIF VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQLVKLIIF VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQLVKLIIF VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQLVKLIIF VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQLVKLIIF VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQLVKLIIF	8904 2YD4617 2YD3708 2YD4174 2YD4433 2YD3235 PW0063
197 198 198 197 198 197 203	VIIRCDSABIGSVTIMLERCVVWLKUSYAHTINYDWRALITKSVEKGEALEFTINMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSABIGSVTIMLERCVVWLKUSYAHTINYDWRALITKSVEKGEALEFTINMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSABIGSVTIMLERCVVWLKUSYAHTINYDWRALITKSVEKGEALEFTINMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSABIGSVTIMLERCVVWLKUSYAHTINYDWRALITKSVEKGEALEFTINMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSABIGSVTIMLERCVVWLKUSYAHTINYDWRALITKSVEKGEALEFTINMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSABIGSVTIMLESCVVWLKUSYAHTINYDWRALITKSVEKGEALEFTINMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSABIGSVTIMLESCVVWLKUSYAHTINYDWRALITKSVEKGEALEFTINMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSABIGSVTIMLESCVVWLKUSYAHTINYDWRALITKSVEKGEALEFTINMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLFRQUVKLIIF	2YD4617 2YD3708 2YD4174 2YD4433 2YD3235 PW0063
197 198 198 197 198 197 203 204	VIIRCDSAFIGGVTIMLER CVWLKLIVSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKLIVSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUVKLIIF VIIRCDSAFIGSVTIMLEGVWLKUVSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKUVSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUVKLIIF VIIRCDSAFIGGVTIMLEGVWLKUVSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUVKLIIF VIIRCDSAFIGGVTIMLEGVWLKUVSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUVKLIIF VIIRCDSAFIGGVTIMLEGVWLKUVSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUVKLIIF VIIRCDSAFIGGVTIMLEGVWLKUVSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUVKLIIF	2YD4617 2YD3708 2YD4174 2YD4174 2YD4433 2YD3235 PW0063 PW0031
197 198 198 197 198 197 203 204	VIIRCDSAFISGVTIMLERCVVWLKIJSYAHTNYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQLVKLIIF VIIRCDSAFISGVTIMLERCVVWLKIJSYAHTNYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQLVKLIIF VIIRCDSAFISGVTIMLERCVVWLKIJSYAHTNYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQLVKLIIF VIIRCDSAFISGVTIMLERCVVWLKIJSYAHTNYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQLVKLIIF VIIRCDSAFISGVTIMLERCVVWLKIJSYAHTNYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQLVKLIIF VIIRCDSAFISGVTIMLERCVVWLKIJSYAHTNYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQLVKLIIF VIIRCDSAFISGVTIMLERCVVWLKIJSYAHTNYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQLVKLIIF	2YD4617 2YD3708 2YD4174 2YD4433 2YD2235 PW0063 PW0031
197 198 198 197 198 197 203 204 299	VIIRCDSAFIGGVTIMLER CVWLIKLISYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLE CVWLIKLISYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGSVTIMLE CVWLIKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLE CVWLIKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLE CVWLIKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTYIRKGWLFRQUVKLIFF	2YD4617 2YD3708 2YD3708 2YD4174 2YD4433 2YD3235 PW0063 PW0031 Xiangchundou15
197 198 198 197 198 197 203 204 299 301	VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF TGVMCFTIEDVINNGWELKGUVIXLIVSYLHTYUDKAFULTYNVFYNWHINTMARALITKSVEKGEALE TILNMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF	8904 2YD4617 2YD3708 2YD4174 2YD4433 2YD4235 PW0063 PW0063 PW0031 Xiangchundou15 DiarYD028
197 198 197 198 197 203 204 299 301	VIIRCDSAFIGGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGSVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF TGYMGFIIEQVINPIVONSOHPLKGNLLYAIFTVLKUSYPNUYGCMFYCFFHLWINILAELLRFGDREFY DWWNAKTVEDYWRWMWPHKMMIRHLYF TGYMGFIIEQVINPIVONSOHPLKGNLLYAIFTVLKUSVPNUYGUCMFYCFFHLWINILAELLRFGDREFY DWWNAKTVEDYWRWMWPHKMMIRHLYF	8904 2YD4617 2YD3708 2YD4174 2YD4433 2YD3225 PW0063 PW0031 Xiangchundou15 DianYD028
197 198 197 198 197 203 204 299 301 300	VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILMIDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILMIDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILMIDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILMIDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILMIDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILMIDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILMIDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF TIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILMIDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF TIRCDSAFISGVTIMLERCVVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILMIDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF TGVMGFIIEQVINPIVONSOHPLKGNLLYALERVLKLISVPNLVVULCMFYCFFHLWLNILAELLERGBREFYDDWWNAKTVEDVYMMMMPHKMWLERLYF TGVMGFIIEQVINPIVONSOHPLKGNLLYALERVLKLISVPNLVWLCMFYCFFHLWLNILAELLERGBREFYDDWWNAKTVEDVYMMMMPHKMWLERLYF TGVMGFIIEQVINPIVONSOHPLKGNLLYALERVLKLSVPNLVWLCMFYCFFHLWLNILAELLERGBREFYDDWWNAKTVEDVWMAMMPHKMWLERLYF	2504 27074617 2703708 2704174 2704433 2703235 PW0063 PW0063 PW0063 Viangchundou15 DianYD028 Heilong38
197 198 197 198 197 203 204 299 301 300 299	VIIRCDSAFIGGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGSVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF TGVMGFIIGQYINPIVONSQHFLKGNLLYAIFEVLKLSVPNLYWLCMFYCFFHLWLNILAELLRFGDREFY DWWNAKTVEDYWMNNMPVHKMMIRHLYF TGVMGFIIGQYINPIVONSQHFLKGNLLYAIFEVLKLSVPNLYWLCMFYCFFHLWLNILAELLRFGDREFY DWWNAKTVEDYWRMMNMPVHKMIRHLYF TGVMGFIIGQYINPIVONSQHFLKGNLLYAIFEVLKLSVPNLYWLCMFYCFFHLWLNILAELLRFGDREFY DWWNAKTVEDYWRMMNMPVHKMIRHLYF	2504 2704617 2703708 2704174 2703423 2703235 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12
197 198 197 198 197 203 204 299 301 300 299 300	VIIRCDSAFISGVTIMLERCVWLKLIVSYAHTINYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVWLKLVSYAHTINYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVWLKLVSYAHTINYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVWLKLVSYAHTINYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVWLKLVSYAHTINYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVWLKLVSYAHTINYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF VIIRCDSAFISGVTIMLERCVWLKLVSYAHTINYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF TIRCDSAFISGVTIMLERCVWLKLVSYAHTINYDMRALITKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQPSYPRTPYIRKGWLERQUVKLIIF TGVGFTIEQVINFIVONSQHFLKGNLLVALERVLKLSVPNUTYWLCMFYCFFHLWLNILAELLRFGDREFYDOWNAKTVEDYWMMMPHKMMIRHLYF TGVGFTIEQVINFIVONSQHFLKGNLLVAIERVLKLSVPNUTYWLCMFYCFFHLWLNILAELLRFGDREFYDOWNAKTVEDYWRMMPHKMMIRHLYF TGVGFTIEQVINFIVONSQHFLKGNLLVAIERVLKLSVPNUTYWLCMFYCFFHLWLNILAELLRFGDREFYDOWNAKTVEDYWRMMPHKMMIRHLYF TGVGFTIEQVINFIVONSQHFLKGNLLVAIERVLKLSVPNUTVWLCMFYCFFHLWLNILAELLRFGDREFYDOWNAKTVEDYWRMMPHKMMIRHLYF	2504 2703708 2703708 2704174 2703423 2703235 PW0033 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidoul2 Jilin30
197 198 197 198 197 203 204 299 301 300 299 300 301	VIIRCDSAFIGGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGSVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGSVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGSVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGSVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGSVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGSVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIF VIIRCDSAFIGSVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNUYWLCMEYCFFHLWINILAELLRFGDREFY ODWINAKTVEDYWMNMPVHKMMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY ODWINAKTVEDYWMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY ODWINAKTVEDYWMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY ODWINAKTVEDYWMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY ODWINAKTVEDYWMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY ODWINAKTVEDYWMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY ODWINAKTVEDYWMMMPVHKMIRHLYF	2504 2704617 2703708 2704174 2704433 2703225 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilion3 Mandou16
197 198 198 197 203 204 299 300 299 300 300 299	VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLERCVWLKLISYAHTINYDMRALIKSVEKGEALE TILMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF TGVMSFIIEQYINPIVONSQHPLKGNLLYAIERVLKLSYPNIVWLCMFYCFFHLMINILAELLRFGDREFY GWMNAKTVEDYMRMMMPHKMMIRHLYF TGVMSFIIEQYINPIVONSQHPLKGNLLYAIERVLKLSVPNLVWLCMFYCFFHLMINILAELLRFGDREFY GWMNAKTVEDYMRMMMPHKMMIRHLYF TGVMSFIIEQYINPIVONSQHPLKGNLLYAIERVLKLSVPNLVWLCMFYCFFHLMINILAELLRFGDREFY GWMNAKTVEDYMRMMMPHKMMIRHLYF TGVMSFIIEQYINPIVONSQHPLKGNLLYAIERVLKLSVPNLVWUCMFYCFFHLMINILAELLRFGDREFY GWMNAKTVEDYMRMMMPHKMMIRHLYF TGVMSFIIEQYINPIVONSQHPLKGNLLYAIERVLKLSVPNLVWUCMFYCFFHLMINILAELLRFGDREFY GWMNAKTVEDYMRMMMPHKMMIRHLYF TGVMSFIIEQYINPIVONSQHPLKGNLLYAIERVLKLSVPNLVWUCMFYCFFHLMINILAELLRFGDREFY GWMNAKTVEDYMRMMMPHKMMIRHLYF TGVMSFIIEQYINPIVONSQHPLKGNLLYAIERVLKLSVPNLVWUCMFYCFFHLMINILAELLRFGDREFY GWMNAKTVEDYMRMMMPHKMMIRHLYF TGVMSFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLVWUCMFYCFFHLMINILAELLRFGDREFY GWMNAKTVEDYMRMMMPHKMMIRHLYF TGVMSFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLVWUCMFYCFFHLMINILAELLRFGDREFY GWMNAKTVEDYMRMMMPHKMMIRHLYF TGVMSFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLVWUCMFYCFFHLMINILAELLRFGDREFY GWMNAKTVEDYMRMMMPHKMMIRHLYF	2504 27034617 2703708 2704174 2703433 2703235 PW0031 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8004
197 198 198 197 198 197 203 204 299 301 300 299 300 301 2299	VIIRCDSAFIGGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDYMMMMPYHKMMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDYMMMMPYHKMMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDYMMMMPYHKMMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDWMMMMPYHKMMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDWMMMMPYHKMMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDWMMMMPYHKMMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDWMMMMPYHKMMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDWMMMMPYHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSVPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDWMMMMPYHKMIRHLF TGVMCFIIEQYINPIVONSQHPLKGNLLXAIERVLKUSVPNLYWLKWFYFFFHHWINILAELLRFGDREFY COMMAKTVEDWMMMMPYHKMIRHLF	2504 2704617 27047708 2704174 2704433 2703225 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilia0 Jidou12 Jilia30 Wandou16 8904
197 198 198 197 198 197 203 204 299 301 300 299 300 301 299 300	VIIRCDSAFISGVTIMLE CVWLKLIVSYAHTINYDMRALIKSVEKGEALE TINMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLE CVWLKLIVSYAHTINYDMRALIKSVEKGEALE TINMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLE CVWLKLIVSYAHTINYDMRALIKSVEKGEALE TINMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLE CVWLKLIVSYAHTINYDMRALIKSVEKGEALE TINMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLE CVWLKLIVSYAHTINYDMRALIKSVEKGEALE TINMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLE CVWLKLIVSYAHTINYDMRALIKSVEKGEALE TINMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF VIIRCDSAFISGVTIMLE CVWLKLIVSYAHTINYDMRALIKSVEKGEALE TINMDYPYNVSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQLVKLIIF TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKLISYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMIRHLFT TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKLSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMMIRHLFT TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKLSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMMIRHLFT TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKLSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMMIRHLFT TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKLSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMMIRHLFT TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKLSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMMIRHLFT TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKLSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMMIRHLFT TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKLSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMMIRHLFT TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKLSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMMIRHLFT TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKLSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMMIRHLFT TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKLSVPNLYWUCMFYCFFHLWINILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMMIRHLFT TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKUSVPNLWWRCMHTWEYFFHLWINILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMMIRHLFT TGVMGFIIEQYINPIVONSOHFLKGNLLYAIETVLKUSVPNLWWRCMHTWEYFFHLWMILAELLRFGDREFY CDWINAKTVEDYWRMMMPHKMMIRHLFT	2504 27034617 2703708 2704174 2703433 2703235 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617
197 198 198 197 198 197 203 204 299 301 300 299 300 300 300 300 300	VIIRCDSAFIGGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDYMRMMMPVHKMMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDYMRMMMPVHKMMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDYMRMMMPVHKMMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDWRMMMPVHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDWRMMMPVHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDWRMMMPVHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMAKTVEDWRMMMPVHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHHUINILAELLRFGDREFY COMMAKTVEDWRMMMPVHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHHUNILLAELLRFGDREFY COMMAKTVEDWRMMMPVHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHHUMINILAELLRFGDREFY COMMAKTVEDWRMMMPVHKMIRHLYF	2504 2704617 2703708 2704174 2704433 2703225 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617 2705708
197 198 198 197 198 197 203 204 299 301 300 299 300 300 300 300 299	VIIRCDSAFISGVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUKLLIF VIIRCDSAFISGVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUKLLIF VIIRCDSAFISGVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUKLLIF VIIRCDSAFISGVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUKLLIF VIIRCDSAFISGVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUKLLIF VIIRCDSAFISGVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUKLLIF VIIRCDSAFISGVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUKLLIF TGVGSFIIBQVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUKLLIF TGVGSFIIBQVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLFRQUKLLIF TGVGSFIIBQVINFIVONSOFELKGNLLYAIERVLKLSVPNLYWLCMFYCFFHLUNILAELLRFGDREFY DWNNAKTVEDYWRMMMPVHKMIRHLYF TGVGSFIIBQVINFIVONSOFELKGNLLYAIERVLKLSVPNLYWLCMFYCFFHLUNILAELLRFGDREFY DWNNAKTVEDYWRMMMPVHKMIRHLYF TGVGSFIIBQVINFIVONSOFELKGNLLYAIERVLKLSVPNLYWLCMFYCFFHLUNILAELLRFGDREFY DWNNAKTVEDYWRMMMPVHKMIRHLYF TGVGSFIIBQVINFIVONSOFELKGNLLYAIERVLKLSVPNLYWLCMFYCFFHLUNILAELLRFGDREFY DWNNAKTVEDYWRMMMPVHKMIRHLYF TGVGSFIIBQVINFIVONSOFELKGNLLYAIERVLKLSVPNLYWLCMFYCFFHLUNILAELLRFGDREFY DWNNAKTVEDYWRMMMPVHKMIRHLYF TGVGSFIIBQVINFIVONSOFELKGNLLYAIERVLKLSVPNLYWLCMFYCFFHLUNILAELLRFGDREFY DWNNAKTVEDYWRMMMPVHKMIRHLYF TGVGSFIIBQVINFIVONSOFELKGNLLYAIERVLKLSVPNLYWLCMFYCFFHLUNILAELLRFGDREFY DWNNAKTVEDYWRMMMPVHKMIRHLYF TGVGSFIIBQVINFIVONSOFELKGNLLYAIERVLKLSVPNLYWLCMFYCFFHLUNILAELLRFGDREFY DWNNAKTVEDYWRMMMPVHKMIRHLYF TGVGSFIIBQVINFIVONSOFELKGNLLYAIERVLKLSVPNLYWLCMFYCFFHLUNILAELLRFGDREFY DWNNAKTVEDYWRMMMPVHKMIRHLYF TGVGSFIIBQVINFIVONSOFELKGNLLYAIERVLKLSVPNLWWLCMFYCFFHLUNILAELLRFGDREFY DWNNAKTVEDYWRMMMPVHKMIRHLYF TGVGSFIIBQVINFIVONSOFELKGNLLYAIERVLKLSVPNLWWLCMFYCFFHLUNILAELLRFGDREFY DWNNAKTVEDYWRMMMPVHKMIRHLYF TGVMSFIIBQVINSOFELKGNLLYAIERVLKLSVPNLWWLGMFYCFFHHUNI	2504 27054617 2705708 2704174 2705423 2705423 2705225 PW0033 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617 2705708 2704174
197 198 198 197 198 197 203 204 299 300 300 299 300 300 299 300 300 299	VIIRCDSAFIGGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLLIF VIIRCDSAFIGGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFIGGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFIGGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFIGGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFIGGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFIGGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFIGGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKKLIF VIIRCDSAFIGGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKKLIF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPYHKMMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPYHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPYHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPYHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPYHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPYHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPYHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPYHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPYHKMIRHLF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPYHKMIRHLF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPYHKMIRHLF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHWINNILLAELLRFGDREFY C	2504 27D4617 27D3708 27D4174 27D433 27D3235 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 27D4617 27D4708 27D4174 27D708
197 198 198 197 198 197 203 204 299 301 300 299 300 300 299 300 300 299 300	VIIRCDSAFISGVTIMLERCVWLKLUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQUKLLIF VIIRCDSAFISGVTIMLERCVWLKLUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQUKLLIF VIIRCDSAFISGVTIMLERCVWLKLUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQUKLLIF VIIRCDSAFISGVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQUKLLIF VIIRCDSAFISGVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQUKLLIF VIIRCDSAFISGVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQUKLLIF VIIRCDSAFISGVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQUKLLIF TGVGSFIIBQVTIMLERCVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQUKLLIF TGVGSFIIBQVINERCVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQUKLLIF TGVGSFIIBQVINERCVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQUKLLIF TGVGSFIIBQVINERCVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLERQUKLLIF TGVGSFIIBQVINEFUNSOFFLKGNLLYAIERVLKLSVPNLYWLCMEYCFFHLUNILAELLRFGBREFY DMWNAKTVEDYWRMMMPVHKMIRHLF TGVGSFIIBQVINFIVONSOFFLKGNLLYAIERVLKLSVPNLYWLCMEYCFFHLUNILAELLRFGBREFY DMWNAKTVEDYWRMMMPVHKMIRHLF TGVGSFIIBQVINFIVONSOFFLKGNLLYAIERVLKLSVPNLYWLCMEYCFFHLUNILAELLRFGBREFY DMWNAKTVEDYWRMMMPVHKMIRHLF TGVGSFIIBQVINFIVONSOFFLKGNLLYAIERVLKLSVPNLYWLCMEYCFFHLUNILAELLRFGBREFY DMWNAKTVEDYWRMMMPVHKMIRHLF TGVGSFIIBQVINFIVONSOFFLKGNLLYAIERVLKLSVPNLYWLCMEYCFFHLUNILAELLRFGBREFY DMWNAKTVEDYWRMMMPVHKMIRHLF TGVGSFIIBQVINFIVONSOFFLKGNLLYAIERVLKLSVPNLYWLCMEYCFFHLUNILAELLRFGBREFY DMWNAKTVEDYWRMMMPVHKMIRHLF TGVGSFIIBQVINFIVONSOFFLKGNLLYAIERVLKLSVPNLYWLCMEYCFFHLUNILAELLRFGBREFY DMWNAKTVEDYWRMMMPVHKMIRHLF TGVGSFIIBQVINFIVONSOFFLKGNLLYAIERVLKLSVPNLYWLCMEYCFFHLUNILAELLRFGBREFY DMWNAKTVEDYWRMMMPVHKMIRHLF TGVMSFIIBQVINFIVONSOFFLKGNLLYAIERVLKLSVPNLVWLCMEYCFFHLUNILAELLRFGBREFY DMWNAKTVEDYWRMMMPVHKMIRHLF TGVMSFIIBQVINFIVNONSOFFLKGNLLYAIERVLKLSVPNLVWLCMEYCFFHLUNILAELLRF	2504 27054617 2705708 2704174 2705423 2705423 2705225 PW0063 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 27054617 2705708 27054174 27054433
197 198 198 197 198 197 203 204 299 301 300 299 300 300 299 300 299 300 299 300	VIIRCDSAFIGGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIGGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWLNILAELLRFGDREFY CDWNAKTVEDYWRMMPVHKMMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWLNILAELLRFGDREFY CDWNAKTVEDYWRMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWLNILAELLRFGDREFY CDWNAKTVEDYWRMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWLNILAELLRFGDREFY CDWNAKTVEDYWRMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWLNILAELLRFGDREFY CDWNAKTVEDYWRMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWLNILAELLRFGDREFY CDWNAKTVEDYWRMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWLNILAELLRFGDREFY CDWNAKTVEDYWRMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWLNILAELLRFGDREFY CDWNAKTVEDYWRMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWLNILAELLRFGDREFY CDWNAKTVEDYWRMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWLNILAELLRFGDREFY CDWNAKTVEDYWRMMMPVHKMIRHLYF TGVMGFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHHWLNILAELLRFGDREFY CDWNAKTVEDYWRMMMPHKMKMIRHLYF TGVMGFI	2504 27D4617 27D3708 27D4174 27D4133 27D3235 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 27D4617 27D3708 27D4174 27D4433 27D4255
1997 1988 1978 1978 1977 2033 204 2999 3001 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2	VIIRCDSAFISGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLLIF VIIRCDSAFISGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKULIF VIIRCDSAFISGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKULIF VIIRCDSAFISGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKULIF VIIRCDSAFISGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKULIF VIIRCDSAFISGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKULIF VIIRCDSAFISGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKULIF VIIRCDSAFISGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKULIF TGVMSFIIBQVINFLVONSOFFLKGNLLYAIFRVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWWNAKTVEDYWRWMMPVHKWMIRHLYF TGVMSFIIBQVINFIVONSOFFLKGNLLYAIFRVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWWNAKTVEDYWRWMMPVHKWMIRHLYF TGVMSFIIBQVINFIVONSOFFLKGNLLYAIFRVLKUSVPNLYWLCMFYCFFHHUNILAELLRFGDREFY DWWNAKTVEDYWRWMMPVHKWMIRHLYF TGVMSFIIBQVINFIVONSOFFLKGNLLYAIFRVLKUSVPNLYWLCMFYCFFHHUNILAELLRFGDREFY DWWNAKTVEDYWRWMMPVHKWMIRHLYF TGVMSFIIBQVINFIVONSOFFLKGNLLYAIFRVLKUSVPNLYWLCMFYCFFHHUNILAELLRFGDREFY DWWNAKTVEDYWRWMMPVHKWMIRHLYF TGVMSFIIBQVINFIVONSOFFLKGNLLYAIFRVLKUSVPNLYWLCMFYCFFHHUNILAELLRFGDREFY DWWNAKTVEDYWRWMMPVHKWMIRHLYF TGVMSFIIBQVINFIVONSOFFLKGNLLYAIFRVLKUSVPNLYWLCMFYCFFHHUNILAELLRFGDREFY DWWNAKTVEDYWRMMMPVHKWMIRHLYF TGVMSFIIBQVINFIVONSOFFLKGNLLYAIFRVLKUSVPNLYWLCMFYCFFHHUNILAELLRFGDREFY DWWNAKTVEDYWRMMMPVHKWMIRHLYF TGVMSFIIBQVINFIVONSOFFLKGNLLYAIFRVLKUSVPNLYWLCMFYCFFHHUNILAELLRFGDREFY DWWNAKTVEDYWRMMMPVHKWMIRHLYF TGVMSFIIBQVINPIVONSOFFLKGNLLYAIFRVLKUSVPNLYWLCMFYCFFHHUNILAELLRFGDREFY DWWNAKTVEDYWRMMMPVHKWMIRHLYF TGVMSFIIBQVINPIVONSOFFLKGNLLYAIFRVLKUSVPNLYWLCMFYCFFHHUNILAELLRFGDREFY DWWNAKTVEDYWRMMMPVHKWMIRHLYF TGVMSFIIBQVINPIVNONSOFFLKGNLLYAIFRVLKUSVPNLYWLCMFYCFFHHUNILAELLRFGDREFY DWWNAKTVEDYWRMMMPVHKWMIRHLYF TGVMSFIIBQVINPIVNONSOFFLKGNLLAIFLYR	2504 27D4617 27D3708 27D4174 27D423 27D3235 PW0063 PW0063 Viangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 27D4617 27D3708 27D4174 27D4433 27D4235
1997 1988 1978 1979 203 204 2999 3001 2999 3000 2000 20	VIIRCDSAFIBGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLLIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKKLIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKKLIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKKLIF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPYHKMIRHLYF TGVMCFIIEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMNAKTVEDYMMMMPHKMIRHLYF TGVMCFIIEQYINPIVNSQHPLKGNLLYAIERVLKUSYPNLYWLCMEYCF	2504 27D4617 27D3708 27D4174 27D4137 27D3225 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 27D4617 27D4174 27D4433 27D3255 PW0063 PW0063
197 198 198 197 203 204 299 301 300 299 300 300 299 300 300 299 300 209 300 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 300 209 300 300 300 300 209 300 300 300 300 300 300 300 300 300 3	VIIRCDSAFI GGVTIMLE CVWLKLUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLLIF VIIRCDSAFI GGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFI GGVTIMLE CVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKULIF TGWGFI IEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKWMIRHLYF TGWGFI IEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKWMIRHLYF TGWGFI IEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKWMIRHLYF TGWGFI IEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKWIRHLYF TGWGFI IEQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHHWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKWIRHILYF TGWGFI IEQYINPIVONSQHPLKGNLLYAIERVLKUSYPN	2504 2704617 2703708 2704174 2704433 2703235 PW0063 PW0063 VianyD028 Heilong38 Jidoul2 Jilin30 Wandoul6 8904 2704617 2703708 2704433 2704433 2704433 2704433 PW0063 PW0031
1997 1988 197 198 197 203 204 2999 3001 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2000 2	VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF TGVMCFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNAKTVEDYWRMMPYHKWMIRHLYF TGVMCFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNAKTVEDYWRMMPYHKWMIRHLYF TGVMCFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNAKTVEDYWRMMPYHKWMIRHLYF TGVMCFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNAKTVEDYWRMMPYHKWMIRHLYF TGVMCFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNAKTVEDYWRMMPYHKWMIRHLYF TGVMCFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNAKTVEDYWRMMPYHKWMIRHLYF TGVMCFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNAKTVEDYWRMMPYHKWMIRHLYF TGVMCFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNAKTVEDYWRMMPHKWMIRHLYF TGVMCFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNAKTVEDYWRMMPHKWMRHHHKMIRHLYF TGVMCFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNAKTVEDYWRMMPHKWMIRHLYF TGVMCFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNAKTVEDYWRMMPHKWMIRHLYF TGVMCFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPN	2504 2704617 2703708 2704174 2704433 2703225 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617 27054708 2704473 2705425 PW0063 PW0063
197 198 198 197 198 197 203 204 299 301 300 299 300 300 299 300 299 300 299 300 299 300 299 300 299 300 204	VIIRCDSAFI GGVTIMLE CVWLKLUSYAHTNYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIT VIIRCDSAFI GGVTIMLE CVWLKUSYAHTNYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKULIT TGWGFTI EQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMMPYHKMIRHLYF TGWGFTI EQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFTI EQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMMPYHKMIRHLYF TGWGFTI EQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMMPYHKMIRHLYF TGWGFTI EQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMMPYHKMIRHLYF TGWGFTI EQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMMPYHKMIRHLYF TGWGFTI EQYINPIVONSQHPLKGNLLYAIERVLKUSYPNLYWLCMFYCF	2504 2704617 2703708 2704174 2704433 2703235 PW0063 PW0063 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617 2704433 2704174 2704433 270474 2704433 270474 2704433 270474 2704433 270474 2704433 270443 270443 270443 270443 270443 270443 270443 270443 270443 270443 270443 270443 270443 270443 270443 2704433 27044 270443 27045 270577 270577 27057777777777
197, 1988 197 1988 197 203 204 299 301 300 299 300 203 203 203 203 203 203 203 203 203	VIIRCDSAFIBGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TIAMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMEVCNSQHFLKGNLLYAIERVLKLSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNARTVEDVYRMMMPYHKMMIRHLYF TGVMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNARTVEDVYRMMMPYHKMIRHLYF TGVMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNARTVEDVYRMMMPYHKMIRHLYF TGVMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNARTVEDVYRMMMPYHKMIRHLYF TGVMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNARTVEDVYRMMMPYHKMIRHLYF TGVMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNARTVEDVYRMMMPYHKMIRHLYF TGVMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNARTVEDVYRMMMPYHKMIRHLYF TGVMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNARTVEDVWRMMPYHKMIRHLYF	2504 2704617 2703708 2704174 2704433 2703225 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617 27054708 2704433 27054174 2705403 PW0063 PW0063 PW0063 PW0063 PW0063
198, 1988 1988 1977 2033 204 2999 3001 2999 3000 2000 2	VIIRCDSAFISGVTIMLERCVWLKUSYAHTNYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIT VIIRCDSAFISGVTIMLE CVWLKUSYAHTNYDMRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKULIT TGWGFTIEQYINFIVONSOHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWMNAKTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINFIVONSOHPLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWMNA	2504 2704617 2703708 2704174 2704433 2703235 PW0063 PW0063 Xiangchundou15 DianYD028 Heilong38 Jidoul2 Jilin30 Wandoul6 8904 2704617 2704774 2704433 27043255 PW0063 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38
1997 1998 1997 1998 1997 2003 204 2999 3001 2999 3000 2999 3000 2999 3000 2999 3000 2999 3000 2999 3005 3006 4001 4003 4002	VIIRCDSAFIBGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF TGWGFIIEQYINPIVONSQHFLKGNLLYAIERVLKLSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIEQYINPIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIEQYINPIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIEQYINPIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIEQYINPIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIEQYINPIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIEQYINPIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIEQYINPIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIEQYINPIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIEQYIN	2504 2704617 2703708 2704174 2704433 2703225 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617 2703708 2704433 27074 270325 PW0063 PW0063 PW0063 PW0063 PW0063 PW0063 IianYD028 Heilong38
197 198 198 197 203 204 299 301 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 209 300 209 209 300 209 209 300 209 300 209 209 300 209 209 300 209 209 300 209 209 300 200 209 200 209 200 200 200 200 200 2	VIIRCDSAFIGGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFIGGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKULIF TGWGFIIGQYINFIVONSQHLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMMAKTVEDYRMMMPYHKMMIRHLYF TGWGFIIGQYINFIVONSQHLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMMAKTVEDYRMMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMMAKTVEDYRMMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMMAKTVEDYRMMMPYHKMIRHLYF TGWGFIIEQYINFIVONSQHLKGNLLYAIERVLKUSYNLYWLCMFYCFFHLWINILAELLRFGDREFY COMMAKTVEDYRMMMPYHKMIRHLYF TGWGFIIEQYINFIVONSQHLKGNLLYAIERVLKUSYNLYWLCMFYCFFHLWINILAELLRFGDREFY COMMAKTVEDYRMMMPYHKMIRHLYF TGWGFIIEQYINFIVONSQHLKGNLLYAIERVLKUSYNLYWLCMFYCFFHLWINILAELLRFGDREFY COMMAKTVEDYRMMMPYHKMIRHLYF TGWGFIIEQYINFIVONSQHLKGNLLYAIERVLKUSYNLYWLCMFYCFFHLWINILAELLRFGDREFY COMMAKTVEDYRMMMPYHKMIRHLYF TGWGFIIEQYINFIVONSQHLKGNLLYAIERVLKUSYNLYWLCMFYCFFHLWINILAELLRFGDREFY COMMAKTVEDYRMMMPYHKMIRHLYF TGWGFIIEQYINFIVONSQHLKGNLLYAIERVLKUSYNLYWLCMFYCFFHLWINILAELLRFGDREFY COMMAKTVEDYRMMMPYHKMIRHLYF TGWGFIIEQYINFIVONSQHLKGNLLYAIERVLKUSYNLYWLCMFYCFFHLWINILAELLRFGDREFY COMMAKTVEDYRMMMPYHKMIRHLYF TGWG	2504 27D34617 27D3708 27D4174 27D3235 PW0063 PW0063 Xiangchundou15 DianYD028 Heilong38 Jidoul2 Jilin30 Wandoul6 8904 27D4617 27D4708 27D4708 27D4774 27D433 27D3708 27D4774 27D433 PW0065 PW0065 PW005 PW05 PW
197, 1988 197 1988 197 203 204 299 301 2099 300 2999 300 2099 200 2099 300 2099 200 2099 200 2099 200 2099 200 200	VIIRCDSAFIBGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TINMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNARTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNARTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNARTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNARTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNARTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNARTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNARTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNARTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY CDWNNARTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYIN	2504 2704617 2703708 2704174 2704433 2703225 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jiling38 2704433 2704433 27078 2704433 27078 2704433 2704433 27078 2704433 270325 PW0063 PW0063 PW0063 PW0063 PW0063 JianYD028 Heilong38 Jidou12 Jiling38
197, 198, 198, 197, 203, 204, 299, 300, 300, 299, 300, 300, 299, 300, 300, 299, 300, 300, 299, 300, 300, 299, 300, 300, 299, 300, 300, 299, 300, 300, 299, 300, 300, 299, 300, 300, 299, 300, 300, 209, 300, 209, 300, 209, 300, 209, 300, 209, 300, 209, 300, 209, 300, 209, 300, 209, 300, 209, 300, 209, 300, 209, 300, 209, 200, 209, 200, 200, 200, 200, 2	VIIRCDSAFISGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIIF VIIRCDSAFISGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIIF TGWGFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DOWNAKTVEDYRMMMPYHKMMIRLYF TGWGFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DOWNAKTVEDYRMMMPYHKMIRLIYF TGWGFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DOWNAKTVEDYRMMMPYHKMIRLIYF TGWGFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DOWNAKTVEDYRMMMPYHKMIRLIYF TGWGFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DOWNAKTVEDYRMMMPYHKMIRLIYF TGWGFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DOWNAKTVEDYRMMMPYHKMIRLIYF TGWGFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNLYWLCMFYCFFHLWINILAELLRFGDREFY DOWNAKTVEDYRMMMPYHKMIRLIYF TGWGFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNLYWLCMFYCFFHLWINILAELLRFGDREFY DOWNAKTVEDYRMMMPYHKMIRLIYF TGWGFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNLYWLCMFYCFFHLWINILAELLRFGDREFY DOWNAKTVEDYRMMMPYHKMIRLIYF TGWGFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNLYWLCMFYCFFHLWINILAELLRFGDREFY DOWNAKTVEDYRMMMPYHKMIRLIYF TGWGFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNLYWLCMFYCFFHLWINILAELLRFGDREFY DOWNAKTVEDYRMMMPYHKMIRLIYF TGWGFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNLYWUCMFYCFFHLWINILAELLRFGDREFY DOWNAKTVEDYR	2504 2704617 2703708 2704174 2704433 2703235 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidoul2 Jilin30 Wandou16 8904 2704617 2704617 2704708 2704174 2704433 2703235 PW0063 PW0065 PW0065 PW0065 PW0065 PW0065 PW05 PW05 PW05 PW05 PW05 PW05 PW05 PW0
197, 198 197 198 197 203 204 299 301 300 299 300 299 300 299 300 299 300 299 300 299 300 299 300 299 300 401 402 401 402 401 402 403 401 402 401 402 403 401 402 403 401 402 403 401 402 403 401 402 403 401 402 403 401 402 403 403 403 405 405 405 405 405 405 405 405	VIIRCDSAFIBGVTIMLER CVWLKLUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNYSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLER CVWLKUSYAHTINYDMRALITKSVEKGEALE TILMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFTIEQYINPIVONSQHFLKGN	2504 2704617 2703708 2704174 2704174 2703225 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidoul2 Jilin30 Wandoul6 2704617 2703708 2704433 270708 2704433 2703235 PW0063 PW0063 PW0063 PW0063 PW0063 PW0063 Jidoul2 Jilin30 Wandoul6 8904
197, 198 197 198 197 203 204 299 301 300 299 300 299 300 299 300 299 300 209 300 299 300 209 200 209 300 200 209 200 200 200 200 200 2	VIIRCDSAFISGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKLIF VIIRCDSAFISGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUKKLIFF VIIRCDSAFISGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPYNSFKSLAYFUAPTLCYQFSYRUWNAKTVEDYWRMMPYHKMMIRLYF TGWGFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNAKTVEDYWRMMPYHKMIRLYF TGWGFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNAKTVEDYWRMMPYHKMIRLIYF TGWGFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNAKTVEDYWRMMPYHKMIRLIYF TGWGFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNAKTVEDYWRMMPYHKMIRLIYF TGWGFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNAKTVEDYWRMMPYHKMIRLIYF TGWGFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNAKTVEDYWRMMPYHKMIRLIYF TGWGFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIBQYINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY COMNAKTV	2504 27D34617 27D3708 27D4174 27D3478 27D4133 27D3235 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidoul2 Jilin30 Wandou16 8904 27D4617 27D3708 27D3708 27D47433 27D3708 27D370708 27D370708 27D370708 27D3707070707070000000000000000000000000
197, 1988 1977 1988 1977 2033 204 2999 301 3000 2999 3000 3000 2999 3000 3000 2999 3000 3000	VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF TGWGFIIGQYINFICNONSOFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFICNONSOFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUNNSOFFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUNNSOFFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGYINFIVONSOFFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGYINFIVONSOFFLKGNLLYAIERVLKUSYPNLYWLCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGYINFIVONSOFFLKGNLLYAIERVLKUSYNLWYUCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGYINFIVONSOFFLKGNLLYAIERVLKUSYNLWYUCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGYINFIVONSOFFLKGNLLYAIERVLKUSYNLWYUCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGYINFIVONSOFFLKGNLLYAIERVLKUSYNLWYUCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGYNNFIYDVNSOHFLKGNLLYAIERVLKUSYNLWYUCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGYNNFIYDVNSOHFLKGNLLYAIERVLKUSYNLWYUCMFYCFFHLWINILAELLRFGDREFY DWNNAKTVEDY	2504 2704617 2703708 2704174 2704433 2703225 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617 2703708 2704433 2703235 PW0063 PW0063 PW0063 PW0063 PW0063 PW0063 Jidou12 Jilin30 Wandou15 DianYD028 Heilong38 Jidou23 Jilin30 Wandou16
197, 198, 197, 198, 197, 203, 204, 299, 301, 209, 300, 200, 209, 200,	VIIRCDSAFISGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPINSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLPRQUKLIIF VIIRCDSAFISGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPINSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLPRQUKKLIIF VIIRCDSAFISGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPINSFKSLAYFUAPTLCYQFSYPRTPYIRKGMLPRQUKKLIIF VIIRCDSAFISGVTIMLE CVNNSQHFLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMARTVEDYMRMMMPHKMMIRHLYF TGMGFIIEQVINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMARTVEDYMRMMMPHKMMIRHLYF TGMGFIIEQVINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMARTVEDYMRMMMPHKMMIRHLYF TGMGFIIEQVINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMARTVEDYMRMMMPHKMMIRHLYF TGMGFIIEQVINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMARTVEDYMRMMMPHKMMIRHLYF TGMGFIIEQVINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMARTVEDYMRMMMPHKMMIRHLYF TGMGFIIEQVINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMARTVEDYMRMMMPHKMMIRHLYF TGMGFIIEQVINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILAELLRFGDREFY COMMARTVEDYMRMMMPHKMMIRHLYF TGMGFIIEQVINFIVONSQHFLKGNLLYAIERVLKUSYPNLYWLCMEYCFFHLWINILA	2504 2704617 2703708 2704174 270433 270433 270433 270433 270433 270433 270405 100028 Heilong38 Jidoul2 Jilin30 Wandoul6 8904 2704617 2703708 27047433 2704743 2704235 PW0063 PW0063 PW0031 Xiangchundoul5 DianYD028 Heilong38 Jidoul2 Jilin30 Wandoul6 8904 2704617 2703708
197, 198, 197, 198, 197, 203, 204, 299, 301, 300, 299, 300, 300, 300, 300, 300, 300, 300, 3	VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF TGWGFIIGQYINFUCNSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUCNSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUCNSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUCNSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUNSSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUNSSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWUCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWUCMFYCFFHLWINILAELLRFGDREFY G	2504 2704617 2703708 2704174 2704433 2703225 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617 2703708 2704174 2703235 PW0063 PW0063 PW0063 PW0063 PW0063 PW0063 Jidou12 Jilin30 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617 2703708 2704174
197, 1988 197 198 197 203 204 299 301 299 300 299 300 299 300 299 300 299 300 299 300 299 300 204 401 402 402 402 402 402 402 402 402	VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLPRQUKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDMRALTKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLPRQUKLIIF VIIRCDSAFIBGVTIMLF CVWLKUSYAHTNYDMRALTKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLPRQUKKLIIF VIIRCDSAFIBGVTIMLF CVNNSQHFLKGNLLYAIERVLKUSYNLYWLCMEYCFFHLWINILAELLRFGDREFY CDMNAKTVEDYMRMMMPYHKMMIRHLYF TGMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNLYWLCMEYCFFHLWINILAELLRFGDREFY CDMNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNLYWLCMEYCFFHLWINILAELLRFGDREFY CDMNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNLYWLCMEYCFFHLWINILAELLRFGDREFY CDMNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNLYWLCMEYCFFHLWINILAELLRFGDREFY CDMNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNNLYWLCMEYCFFHLWINILAELLRFGDREFY CDMNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNNLYWLCMEYCFFHLWINILAELLRFGDREFY CDMNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNNLYWLCMEYCFFHLWINILAELLRFGDREFY CDMNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNNLYWLCMEYCFFHLWINILAELLRFGDREFY CDMNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSQHFLKGNLLYAIERVLKUSYNNLYWLCMEYCFFHLWINILAELLR	2504 27D4617 27D3708 27D4174 27D4174 27D433 27D4235 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidoul2 Jilin30 Wandou16 8904 27D4617 27D3708 27D4174 27D4235 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidoul2 Jilin30 Wandou16 8904 27D4617 27D3708 27D4174 27D433
197, 198, 197, 198, 197, 198, 197, 198, 203, 204, 203, 204, 209, 300, 209, 401, 402,	VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF TGWGFIIGQYINFUCNSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUCNSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUCNSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUCNSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUNSSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUNSSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWUCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWUCMFYCFFHLWINILAELLRFGDREFY G	2504 2704617 2703708 2704174 2704433 2703225 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617 2703708 2704174 2703235 PW0063 PW0063 PW0063 PW0063 PW0063 Jidou12 Jilin30 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617 2704617 2703708 2704174 2704433
197, 198, 197, 198, 197, 203, 204, 299, 300, 300, 299, 300, 300, 299, 300, 209, 401, 402, 401, 402, 402, 402, 401, 402, 402, 402, 401, 401, 402, 401,	VIIRCDSAFINGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLPRQUKLIIF VIIRCDSAFINGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLPRQUKKLIIF VIIRCDSAFINGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGMLPRQUKKLIIF VIIRCDSAFINGVTIMLE CVWLKUSYAHTNYDMRALIKSVEKGEALE TINMDYPYNSFKSLAYFUAPTLCYQFSYPRTYN IKKGMLPRQUKKLIIF TGMSFIIEQYINFIVONSOHFLKGNLLYAIERVLKUSYNLYWLCMEYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSOHFLKGNLLYAIERVLKUSYNLYWLCMEYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSOHFLKGNLLYAIERVLKUSYNLYWLCMEYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSOHFLKGNLLYAIERVLKUSYNLYWLCMEYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSOHFLKGNLLYAIERVLKUSYNNLYWLCMEYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSOHFLKGNLLYAIERVLKUSYNNLYWLCMEYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSOHFLKGNLLYAIERVLKUSYNNLYWLCMEYCFFHLWINILAELLRFGDREFY CDWNNAKTVEDYMRMMMPYHKMIRHLYF TGMSFIIEQYINFIVONSOHFLKGNLLYAIERVLKUSYNNYMUCMEYCFFHLWINILAEL	8504 27D4617 27D3708 27D4174 27D3708 27D4174 27D433 27D3235 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidoul2 Jilin30 Wandou16 8904 27D4617 27D3708 27D3708 27D3708 27D3708 27D3708 27D3708 27D3708 27D4174 27D3708 27D4174 27D433 Jilin30 Wandou16 8904 27D4617 27D3708 27D4174 27D3708 27D4174 27D3708 27D4174 27D3708 27D4174 27D3708
19,6 198 197 198 197 198 197 203 203 203 209 300 299 300 300 299 300 300 299 300 300 299 300 300 299 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 300 209 209 300 209 200 209 300 209 200 209 300 209 200 200 209 200 200 200 2	VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYPRTPYIRKGWLFRQUVKLIIF VIIRCDSAFIBGVTIMLE CVWLKUSYAHTNYDRALITKSVEKGEALE TINMDYPYNSFKSLAYFLVAPTLCYQFSYRWMMPYHKMURHKUSY TGWGFIIGQYINFUVONSQHFLKGNLLYAIERVLKLSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFUVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDREFY GWNNAKTVEDYWRMMPYHKMIRHLYF TGWGFIIGQYINFIVONSQHFLKGNLLYAIERVLKUSVPNLYWLCMFYCFFHLWINILAELLRFGDR	2504 2704617 2703708 2704174 2704433 2703225 PW0063 PW0063 PW0031 Xiangchundou15 DianYD028 Heilong38 Jidou12 Jilin30 Wandou16 8904 2704617 2703708 2704473 270325 PW0063 PW0063 PW0063 Jilin30 Wandou16 8904 2704617 2704617 2703708 2704174 2704617 2703708 2704174 2704617 2703708 2704174 2704235 PW0063 PW0063

B

Percent Similarity

		1	2	3	4	5	6	7	8	9	10	11	12	13	14			
	1	-	99.4	99.0	99.8	99.2	99.2	100.0	98.8	99.2	100.0	99.2	100.0	95.4	96.6	1	Xiangchundou15	
	2	0.0	_	98.2	99.2	98.4	99.8	99.4	98.0	98.4	99.4	98.4	99.4	94.4	97.2	2	DianYD028	
	3	0.4	0.4	-	98.8	99.8	98.0	99.0	99.0	99.4	99.0	99.6	99.0	95.0	96.2	3	Heilong38	
e	4	0.2	0.2	0.6	—	99.0	99.0	99.8	98.6	99.0	99.8	99.0	99.8	95.2	96.4	4	Jidou12	G.max
ŭ	5	0.2	0.2	0.2	0.4	_	98.2	99.2	99.2	99.6	99.2	99.8	99.2	95.2	96.4	5	Jilin30	
136	6	0.2	0.2	0.6	0.4	0.4	—	99.2	97.8	98.2	99.2	98.2	99.2	94.2	97.0	6	Wandou16	
ive	7	0.0	0.0	0.4	0.2	0.2	0.2	—	98.8	99.2	100.0	99.2	100.0	95.4	96.6	7	8904	
9	8	0.6	0.6	1.0	0.8	0.8	0.8	0.6	—	99.6	98.8	99.0	98.8	95.2	96.0	8	ZYD4617	
ent	9	0.2	0.2	0.6	0.4	0.4	0.4	0.2	0.4	_	99.2	99.4	99.2	95.2	96.4	9	ZYD3708	
2C	10	0.0	0.0	0.4	0.2	0.2	0.2	0.0	0.6	0.2	—	99.2	100.0	95.4	96.6	10	ZYD4174	G. soja
Pa	11	0.2	0.2	0.4	0.4	0.2	0.4	0.2	1.0	0.6	0.2	—	99.2	95.0	96.2	11	ZYD4433	
	12	0.0	0.0	0.4	0.2	0.2	0.2	0.0	0.6	0.2	0.0	0.2	—	95.4	96.6	12	ZYD3235	
	13	2.9	2.9	3.3	3.1	3.1	3.1	2.9	3.1	3.1	2.9	3.3	2.9	—	95.0	13	PW0063	G. tomentella
	14	1.6	1.6	2.0	1.8	1.8	1.8	1.6	2.2	1.8	1.6	2.0	1.6	3.7	_	14	PW0031	G. latifolia
		1	2	3	4	5	6	7	8	9	10	11	12	13	14			

Fig. 4 Southern analysis of the *GmDGAT* gene in the different accessions of soybean. The genomic DNA was digested with *TaqI* and then subjected to Southern analysis. Names of accessions are listed on the top of the figure and subgenera classifications are marked above the names



A pair of specific primers was then designed from the 0.8 kbp cDNA fragment and partial genomic sequences of the DGAT were amplified from six accessions, which belong to G. max, G. gracilis, G. tomentella and G. latifolia, respectively (Fig. 5a). Comparative and cluster analysis indicated that the two genomic sequences from G. max were the same and very similar to that from the two accessions of G. gracilis (Fig. 5a). This relationship is consistent with the fact that G. gracilis is classified in the subgenus Soja. However, the sequences from G. tomentella and G. latifolia were more diverged (Fig. 5a, b). Differences in the intron between cultivated accessions and wild-type accessions were found (Fig. 5b). The largest difference was an insertion of 130 bp at the 1,833th position of G. tomentella (PW0063) compared to others. Moreover, there were 17 small differences among the three sequences. These differences were insertions/deletions from 3 to 14 bp in length. In addition, there were many minor differences of 1 or 2 bp among these sequences. We did not find major differences between the exons of six accessions. Therefore, the introns are the most variable part of the DGAT genomic sequences. Through comparison of the partial genomic sequences from the subgenus Soja and Glycine accessions, we found that the differences in genomic architecture were mainly due to the difference in intron sequence and/or size, which was possibly affected by the deletion or insertion event.

Based on the cDNA sequences, the full-length of the DGAT genomic sequences from the cultivated accession 8904 (GmDGAT) and the wild-type accession PW0031 (GlDGAT) were cloned by PCR. Their intron/exon structures were analyzed and compared with those from other plants (Fig. 6). The full-length genomic sequences of AtDGAT from Arabidopsis, OsDGAT from rice and

LcDGAT from Lotus were obtained from Genebank, and the sizes of AtDGAT, OsDGAT, LcDGAT, GmD-GAT and GlDGAT were 3,020, 6,220, 5,762, 7,575 and 6,614 bp, respectively. Although there were major differences in length among them, they shared high similarity in the deduced amino acid sequences (Figs. 2, 3). Both the genomic DNAs of AtDGAT and OsDGAT had 16 exons and most exon lengths were very similar (Fig. 6), while most of the introns (11 out of 15) were longer in OsDGAT than those in AtDGAT. Unlike the DGAT genes in rice and Arabidopsis, all three genes from legume had 15 exons, 12 of these were exactly the same among the three genes. The only difference in length lies in the first, second and the last exon (Fig. 6). The difference in the exon number between AtDGAT and OsDGAT and three legume genes may be due to the combination of the last two exons in the legume genes. The lengths of the last two exons in AtDGAT and OsDGAT showed much similarity with the last exon in the three legume genes. The introns of five genomic DNAs showed great variation in length, ranging from 75 to 141 bp in AtDGAT and 98 to 1,299 bp in GmDGAT. The introns of the three legume genes also showed much difference in length. The intron size may determine the gene size and the genome size of each plant. However, the biological significance of the variation of the intron size remains to be further studied.

Expression of the soybean DGAT gene

Transcript abundance of the *DGAT* was examined in different organs from the cultivar 8904 and wild-type *G. latifolia* PW0031 by RT-PCR. The same cDNAs were also used to amplify the β -Tubulin gene as an internal

Fig. 5 Comparison of the partial genomic sequences of the DGATs from six soybean accessions. a The phylogenetic tree of the DGATs from six accessions of soybean. The length of each pair branches represents the distance between sequence pairs. The units at the **B** bottom of the tree indicate the number of substitution events. **b** Alignment of the *DGAT* partial genomic sequences. The names of accessions are shown on the right and nucleotide sequence numbers were shown on the left. Conserved sequences are shown on a white background and the differences are shaded in black. The bold lines under the sequence indicate the positions of the exons. Because the sequences from G. max Heihuangdou, G. gracilis y43 and G. gracilis y74 are highly homologous to the sequence from G. max PI547844, only the sequences from G. max PI547844, G. latifolia PW0031 and G. tomentella PW0063 were compared



Fig. 6 Genomic DNA structure of the *DGATs* from soybean and other plants. The *filled boxes* indicate exons and the *lines* indicate introns

Arabidopsis thaliana



control. The results showed that the DGAT expression was relatively higher in flower and pods at 30 DAF, but lower in mature leaves and the pods at 20 DAF in both cultivar 8904 and PW0031 (Fig. 7). However, almost no expression was detected in young leaves and in pods at 10 DAF (Fig. 7). This pattern resembled the RNA expression pattern in Arabidopsis (Kaup et al. 2002). These results suggest that the DGAT gene is expressed at the later stage of the pod development, and that the DGAT expression patterns have not significantly changed during the evolution of legume plants.

Although the soybean DGAT gene has been cloned from a number of accessions, it seems that this gene is not closely related to the oil content based on the structural and expression analysis (Table 1; Figs. 3a, 7, and data not shown). This is due to the fact that many steps are involved in the lipid biosynthesis and many oil QTLs have been detected. Currently, more than 60 oil QTLs have been detected (http://www.soybase.ncgr.org; Zhang et al. 2004) and it is not known if the soybean DGAT gene is linked to or belongs to any oil QTL. Because no polymorphism was detected between the two parents from which a mapping population has been derived, the soybean DGAT gene cannot be mapped onto the linkage map available (Zhang et al. 2004; data



Fig. 7 RT-PCR analysis of the *DGAT* gene expression in different organs of soybean plants. Total RNA from cultivated soybean 8904 and wild-type soybean PW0031 were extracted from young leaves, mature leaves, flowers, and pods at 10 DAF, 20 DAF and 30 DAF. The first-strand cDNA was used as template to amplify the *GmDGAT*. β -Tubulin gene was amplified as an internal control

not shown). Further detection of the soybean *DGAT* gene polymorphism in other parents and its mapping in the corresponding population may facilitate our understanding of the relationship between the *DGAT* gene and oil QTLs in soybean.

In conclusion, we cloned *DGAT* genes from different accessions of soybean plants and compared the difference at both the amino acid level and the nucleotide level. We find that the difference at the amino acid level is relatively small whereas the difference at the genomic sequence level is large. These results may have significance in elucidation of the gene evolution between wild-type soybean plants and the cultivated ones.

Acknowledgements This work was supported by the Major Basic Research Program of China (2002CB111303), National Nature Science Foundation (30392100) and National 863 Program (2002AA211051), and CAS Project (KSCX2-SW-328)

References

- Aravind L (2001) The WWE domain: a common interaction module in protein ubiquitination and ADP ribosylation. Trends Biochem Sci 26:273–275
- Cao YZ, Huang AHC (1986) Diacylglycerol acyltransferase in maturing oil seeds of maize and other species. Plant Physiol 82:813–820
- Cases S, Smith SJ, Zheng YW, Myers HM, Lear SR, Sande E, Novak S, Collins C, Welch CB, Lusis AJ, Erickson SK, Farese RV (1998) Identification of a gene encoding an acyl CoA:diacylglycerol acyltransferase, a key enzyme in triacylglycerol synthesis. Proc Natl Acad Sci USA 95:13018–13023
- Chen SY, Zhu LH, Hong J, Chen SL (1991) Molecular biological identification of a salt-tolerant rice line. Acta Bot Sin 33:569–573
- Doyle JJ (1988) 5S ribosomal gene variation in the soybean and its progenitor. Theor Appl Genet 75:621–624
- Doyle JJ, Beachy RN (1985) Ribosomal gene variation in soybean (*Glycine*) and its wild relatives. Theor Appl Genet 70:369–376
- Frohman MA (1993) Rapid amplification of complementary DNA ends for generation of full-length complementary DNAs: thermal RACE. Methods Enzymol 218:340–358
- He CY, Zhang JS, Chen SY (2002) A soybean gene encoding a proline-rich protein is regulated by salicylic acid, an endogenous circadian rhythm and by various stresses. Theor Appl Genet 104:1125–1131
- He CY, Tian AG, Zhang JS, Zhang ZY, Chen SY (2003) Isolation and characterization of a full-length resistance gene homolog from soybean. Theor Appl Genet 106:786–793
- He X, Turner C, Chen GQ, Lin JT, McKeon TA (2004) Cloning and characterization of a cDNA encoding diacylglycerol acyltransferase from castor bean. Lipids 39:311–318
- Hobbs DH, Hills MJ (2000) Expression and characterization of diacylglycerol acyltransferase from *Arabidopsis thaliana* in insect cell cultures. Biochem Soc Trans 28:687–689
- Hobbs DH, Lu C, Hills MJ (1999) Cloning of a cDNA encoding diacylglycerol acyltransferase from *Arabidopsis thaliana* and its functional expression. FEBS Lett 452:145–149
- Hofmann K (2000) A superfamily of membrane-bound O-acyltransferases with implications for wnt signaling. Trends Biochem Sci 25:111–112
- Hymowitz T (1970) On the domestication of the soybean. Econ Bot 24:408–421
- Jako C, Kumar A, Wei Y, Zou J, Barton DL, Giblin EM, Covello PS, Taylor DC (2001) Seed-specific over-expression of an arabidopsis cDNA encoding a diacylglycerol acyltransferase enhances seed oil content and seed weight. Plant Physiol 126:861–874

- Kaup MT, Froese CD, Thompson JE (2002) A role for triacylglycerol acyltransferase during leaf senescence. Plant Physiol 129:1616–1626
- Kennedy EP (1961) Biosynthesis of complex lipids. Fed Proc 20:934–940
- Lacey DJ, Hill MJ (1996) Heterogeneity of the endoplasmic reticulum with respect to lipid synthesis in developing seeds of *Brassica napus* L. Planta 199:545–551
- Liu F, Zhuang BC, Zhang JS, Chen SY (2000) Construction and analysis of soybean genetic map. Acta Bot Sin 27:1018–1026
- Lu C, Hills MJ (2002) Arabidopsis mutants deficient in diacylglycerol acyltransferase display increased sensitivity to abscisic acid, sugars, and osmotic stress during germination and seedling development. Plant Physiol 129:1352–1358
- Lu C, de Noyer SB, Hobbs DH, Kang J, Wen Y, Krachtus D, Hills MJ (2003) Expression pattern of diacylglycerol acyltransferase-1, an enzyme involved in triacylglycerol biosynthesis, in Arabidopsis thaliana. Plant Mol Biol 52:31–41
- Luo GZ, Wang HW, Huang J, Tian AG, Wang YJ, Zhang JS, Chen SY (2005) A putative plasma membrane cation/proton antiporter from soybean confers salt tolerance in Arabidopsis. Plant Mol Biol 59:809–820
- Nykiforuk CL, Laroche A, Weselake RJ (1999) Isolation and sequence analysis of a novel cDNA encoding a putative diacylglycerol acyltransferase from a microspore-derived cell suspension culture of *Brassica napus* L. cv Jet Neuf. Plant Physiol 120:99–123
- Perry HJ, Harwood JL (1993) Changes in the lipid content of developing seeds of *Brassica napus*. Phytochemistry 32:1411– 1415
- Settlage SB, Kwanyuen P, Wilson RF (1998) Relation between diacylglycerol acyltransferase activity and oil concentration in soybean. JAOCS 75:775–781
- Settlage SB, Wilson RF, Kwanyien P (1995) Localization of diacylglycerol acyltransferase to oil body associated endoplasmic reticulum. Plant Physiol Biochem 33:399–407
- Shoemaker RC, Hatfield PM, Palmer RG, Atherly AA (1986) Chloroplast DNA variation and evolution in the genus *Glycine* subgenus *soja*. J Hered 77:26–30
- Singh RJ, Hymowitz T (1999) Soybean genetic resources and crop improvement. Genome 42:605–616
- Tian AG, Zhao JY, Zhang JS, Gai JY, Chen SY (2004a) Genomic characterization of the S-adenosylmethionine decarboxylase genes from soybean. Theor Appl Genet 108:842–850
- Tian AG, Wang J, Cui P, Yu J, Xu HH, Cong LJ, Huang XG, Wang XL, Jiao YZ, Wang BJ, Wang YJ, Zhang JS, Chen SY (2004b) Characterization of soybean genomic features by analysis of its expressed sequence tags. Theor Appl Genet 108:903–913
- Triki S, Ben Hamida J, Mazliak P. (2000) Diacylglycerol acyltransferase in maturing sunflower seeds. Biochem Soc Trans 28:689–692
- Wang YJ, Li YD, Luo GZ, Tian AG, Wang HW, Zhang JS, Chen SY (2005) Cloning and characterization of an HDZip I gene GmHZ1 from soybean. Planta 221:831–843
- Wu XL, He CY, Wang YJ, Zhang ZY, Dongfang Y, Zhang JS, Chen SY, Gai JY (2001) Construction and analysis of a genetic linkage map of soybean. Acta Genet Sin 28:1051–1061
- Zhang DS, Dong W, Hui DW, Chen SY, Zhuang BC (1997) Construction of a soybean linkage map using an F2 hybrid population from a cultivated variety and a semi-wild soybean. Chin Sci Bull 42:1326–1330
- Zhang WK, Wang YJ, Luo GZ, Zhang JS, He CY, Wu XL, Gai JY, Chen SY (2004) QTL mapping of ten agronomic traits on the soybean (*Glycine max* L. Merr.) genetic map and their association with EST markers. Theor Appl Genet 108:1131–1139
- Zhang JS, Zhou JM, Zhang C, Chen SY (1996) Differential gene expression in a salt-tolerance rice mutant and its parental variety. Sci China (Series C) 39:310–319
- Zou J, Wei Y, Jako C, Kumar A, Selvaraj G, Taylor DC (1999) The Arabidopsis thaliana TAG1 mutant has a mutation in a diacylglycerol acyltransferase gene. Plant J 19:645–653