

Update section

Sequence

Nucleotide sequence of a wheat (*Triticum aestivum* L.) cDNA clone encoding the *waxy* protein

Joanna R. Clark, Morag Robertson¹ and Charles C. Ainsworth*

Department of Biochemistry and Biological Sciences, Wye College (University of London), Wye, Kent TN25 5AH, UK (* author for correspondence); ¹ present address: Now at Centre for Genome Research, University of Edinburgh, Kings Buildings, West Mains Road, Edinburgh EH9 3JQ, UK

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The *waxy* mutation in maize is characterised by the complete loss of amylase in the starch fraction of the kernel [1, 2, 3]. In addition, there is a significant reduction in the amount of granule-bound starch synthase activity in the mutant [2] which correlates with the absence of a protein of 60 kDa, which in wild-type kernels is the most abundant protein associated with starch granules [4, 5]. For this reason, it has been assumed that the 60 kDa *waxy* protein is the granule-bound starch synthase. Unequivocal evidence for this is lacking and in pea, evidence suggests that another protein, only distantly related to the *waxy* protein, is the granule-bound starch synthase [6]. It remains to be seen whether this is the case in cereals. The *waxy* locus has been cloned from a number of plants including maize [3], rice [7], barley [8] and potato [9]. We report here the isolation of a full-length cDNA clone for the *waxy* protein of hexaploid wheat and present the complete nucleotide sequence.

A cDNA library of was constructed in λ gt10 from poly(A)⁺ RNA isolated from wheat grains harvested at 20 days post anthesis from the hexaploid variety Chinese Spring. Isolation of

RNA, selection of poly(A)⁺ RNA and cDNA synthesis were carried out according to manufacturer's protocols (Amersham). After addition of linkers the cDNAs were ligated into the *Eco* RI site of λ gt10 and packaged to produce 1.5×10^5 recombinants per μ g poly(A)⁺ RNA. The library was screened for *waxy* protein clones by hybridising plaque lifts with a barley *waxy* protein cDNA (pcwx27 [4]) and 9 clones with inserts that ranged in size from 0.5 to 4.4 kb were isolated and plaque-purified. The insert from a single cDNA clone of 2.2 kb was subcloned into pUC18 for further analysis since northern blots of wheat RNA hybridised with pcwx27 allowed the *waxy* protein mRNA size to be estimated at 2.2–2.3 kb (data not shown). The plasmid clone containing the 2.2 kb insert was designated pcSS22.

The complete nucleotide sequence of the cDNA insert of pcSS22 was determined by dideoxy chain termination sequencing [10] of *Bal* 31 deletions and restriction fragments cloned into pUC18. Synthetic oligonucleotide primers to the *waxy* cDNA were also used. Staden programs were used for sequence assembly [11] and the UWGCG programs for sequence analysis. The

1 CCGAGTTCGGAAGAGATCAGACCAGTCGTCTCTTGCTGCAGGTAGCCACACCCCTGCGCGC 60
 61 GCCATGGCGGCTCTGGTCACGTCCCAGCTCGCCACCTCCGGCACCGTCCTCAGCGTCACC 120
 M A A L V T S Q L A T S G T V L S V T
 121 GACAGATTCGGCGTCCAGTTTTTCAGGGCCTGAGGCCCGGAACCCGGCGGATGCGGCG 180
 D R F R R P G F Q G L R P R N P A D A A
 181 CTCGGCATGAGGACTGTCCGAGCGAGCGCCGCCAAAGCAAAGCAGGAAACCGCACCGA 240
 L G M R T V G A S A A P K Q S R K P H R
 241 TTCGACCGGCGGTGCCTCTCCATGGTGGTGC GCGCCACGGGCAGCGGCGGCATGAACCTC 300
 F D R R C L S M V V R A T G S G G M N L
 301 GTGTTCTGTCGGCGCGAGATGGCCCCCTGGAGCAAGACTGGCGGCCCTCGGCGACGTCCCTC 360
 V F V G A E M A P W S K T G G L G D V L
 361 GGGGGCTCCCCGCCCATGGCCGCCAACGGTCACCGGGTCATGGTCATCTCCCCGCGC 420
 G G L P A A M A A N G H R V M V I S P R
 421 TACGACCAGTACAAGGACGCCTGGGACACCAGCGTCATCTCCGAGATCAAGGTCGTTGAC 480
 Y D Q Y K D A W D T S V I S E I K V V D
 481 AGGTACGAGAGGGTGAGTACTTCCACTGCTACAAGCGGGGGTGGACCGGTGTTTCGTC 540
 R Y E R V R Y F H C Y K R G V D R V F V
 541 GACCACCGTGCTTCTGGAGAAGGTCGGGGCAAGACCAAGGAGAAGATCTATGGACCC 600
 D H P C F L E K V R G K T K E K I Y G P
 601 GACGCCGACCGACTACGAGGACAACCAGCAGCGCTTACGCCTTCTCTGCCAGGCAGCA 660
 D A G T D Y E D N Q Q R F S L L C Q A A
 661 CTTGAGGTGCCAGGATCCTCGACCTCAACAACAACCCACACTTTTCTGGACCCTACGCC 720
 L E V P R I L D L N N N P H F S G P Y A
 721 ATGCTATGCCGTGCCGTGCCGCGCGCAGGGGAAGACGTGGTGTGTTGTGTGCAACGAC 780
 M L C R A V P R R A G E D V V F V C N D
 781 TGGCACACGGCCCTTCTGGCCTGCTACTCAAGAGCAACTACCAGTCCAATGGCATCTAT 840
 W H T G L L A C Y L K S N Y Q S N G I Y
 841 AGGACGGCCAAGGTGGCATTCTGCATCCACAACATCTCGTACCAGGGCCGCTTCTCCTTC 900
 R T A K V A F C I H N I S Y Q G R F S F
 901 GACGACTTCGCGCAGCTCAACCTGCCTGACAGGTTCAAGTCGTCTTCGACTTCATCGAC 960
 D D T A Q L N L P D R F K S S F D F I D
 941 GGCTACGACAAGCCGGTGGAGGGGGCGCAAGATCAACTGGATGAAGCCGGGGCTCCTGCG 1020
 G Y D K P V E G R K I N W M K A G I L Q
 1021 GCCGACAAGGTGCTGACTGTGAGCCCCTACTATGCTGAGGAGCTAATCTCTGGCGAAGCC 1080
 A D K V L T V S P Y Y A E E L I S G E A
 1081 AGGGCTGCGAGCTCGACAACATCATGCGCCCTCACTGGGATCACCGGCATCGTCAACGGC 1140
 R G C E L D N I M R L T G I T G I V N G
 1141 ATGGACGTCAGCGAGTGGGACCCCATCAAGGACAAGTTCTCTCACCGTCAACTACGACGTC 1200
 M D V S E W D P I K D K F L T V N Y D V
 1201 ACCACCGCTTGGAGGGGAAGGCGCTGAACAAGGAGGCGCTGCAGGCCGAGGTGGGGCTG 1260
 T T A L E G K A L N K E A L Q A E V G L
 1261 CCGGTGGACCGGAAGGTGCCCTGGTGGCGTTCATCGGCAGGCTGGAGGAGCAGAAGGC 1320
 P V D R K V P L V A F I G R L E E Q K G
 1321 CCGACGTGATGATCGCCGCATCCCGGAGATCGTGAAGGAGGAGGACGTCCAGATCGTT 1380
 P D V M I A A I P E I V K E E D V Q I V
 1381 CTCCTGGGCACCGGGAAGAAGAAGTTTGAGCGGCTGCTCAAGAGCGTGGAGGAGAAGTTC 1440
 L L G T G K K K F E R L L K S V E E K F
 1441 CCGACCAAGTGAGGGCCGTGGTCAGGTTCAACGCGCCGCTGGCTCACCAGATGATGGCC 1500
 P T K V R A V V R F N A P L A H Q M M A
 1501 GCGCCGACGTGCTGGCGGTCAACAGCCGCTTCGAGCCCTGCGCCTCATCCAGCTCCAG 1560
 G A D V L A V T S R F E P C G L I Q L Q
 1561 GGAATGCGCTACGGAACCGGTGCGCCTGCGCGTTCGACAGGCGGGCTCGTCCGACTATC 1620
 G M R Y G T P C A C A S T G G L V D T I
 1621 GTGGAAGGCAAGACCGGTTCCACATGGGCCCGCTCAGCGTTGACTGCAACGTGGTGGAG 1680
 V E G K T G F H M G R L S V D C N V V E
 1681 CCGGCCGACGTGAAGAAGGTGGTCACCACCTGAAGCGCGCCGTCAGGTCGTCGGCACG 1740
 P A D V K V V T T L K R A V K V G G T
 1741 CCGCGTACCATGAGATGGTCAAGAAGTCAAGATACAGGATCTCTCCTGGAAGGGCCT 1800
 P A Y H E M V K N C M I Q D L S W K G P
 1801 GCCAAGAAGTGGGAGGACGTGCTTCTGGAACTGGGGGTGGAGGGGAGCGAGCCGGGCATC 1860

A K N W E D V L L E L G V E G S E P G I
 1861 GTCGGCGAGGAGATCGCGCCGCTCGCCCTGGAGAACGTCGCCGCTCCCTGAAGAGAGAAA 1920
 V G E E I A P L A L E N V A A P
 1921 GAAGAGGAGCTTCTGGTGCATGGAGCATCCATCCAATCTGCAGGGTTCTCGTATGGGGAG 1980
 1981 ATAGCCGCTTGTGTAGTGAAGAAGGGCCGATATATATATATAATATAGACTAATAAGTA 2040
 2041 CTTTAACTTTTGTGTGCCGCTTGCCCTCTTTTACAAACAAAAAAGGAGTTAGGGGTTGTG 2100
 2101 CCTATGATAGTGTGCTGAATTGTGCTTGCATTTTGGTGTGGTATATTGCAATAAAACAAAG 2160
 2161 GATTTGTTAAAAAATAAAAAAAAAA 2186

Fig. 1. Complete nucleotide sequence of the wheat *waxy* protein cDNA insert of pcSS22. The derived amino acid sequence is shown underneath the nucleotide sequence. The translation initiation and termination codons and the putative polyadenylation signal are underlined.

cDNA insert in pcSS22 is 2186 nucleotides and includes an open reading frame of 1845 nucleotides from the initiating ATG at position 64 to the termination codon, TGA, at position 1909 (Fig. 1). The cDNA includes a 5' untranslated region of 63 nucleotides and a 3' untranslated region of 278 nucleotides. A putative polyadenylation signal at position 2150 precedes a poly(A) tail of 18 residues. The deduced protein contains 615 amino acids with a calculated molecular weight of 67.7 kDa. The mature *waxy* proteins of all species investigated to date are 58–60 kDa as is the case in wheat (data not shown) which suggests the existence of a 7 kDa transit peptide. A 7 kDa transit peptide which targets the maize *waxy* protein to the amyloplast is also 7 kDa [3, 12]. The cDNA sequence of pcSS22 exhibits a high degree of homology with the sequence of the genes encoding the *waxy* proteins of barley, maize and rice.

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