transcripts of altered size suggests that Bt2 is most probably the structural gene for this transcript.

4.2 The Structure of the Bt2 cDNA Clone

The cloned 1.7kb Bt2 cDNA was sequenced. To confirm that the cDNA sequence contains the 5' end of the transcript, it was necessary to perform primer extension and mRNA sequencing directly from primer extension. A synthetic 34 base oligonucleotides, complementary to nucleotides #58-#91 (Figure 5) of the mRNA transcript, was prepared, annealed to poly(A)⁺RNA and subjected to chain termination reactions using reverse transcriptase. An additional 26 nucleotides at the 5' end was obtained by this method (Figure 4). The 5' to 3' sense strand nucleotide sequence of Bt2 cDNA and amino acid sequence deduced from the Bt2 cDNA are presented in Figure 5. The 5'-3' direction of the sequence was verified by the sequence obtained by mRNA sequencing from primer extension. An open reading frame (ORF) of 475 residues was found which begins with the first ATG at base pair position 25 and ends at the termination codon TGA at bp-position 1450. This ORF of 475 amino acids predicts a protein with a molecular weight of approximately 52,000 consistent with the size of the polypeptide of 51,000 estimated by Western blotting of maize endosperm protein [Giroux, 1992]. This result suggests that the obtained ORF is representative of the complete ADPglucose pyrophosphorylase coding sequence. The translation initiation