**Plant Gene Register**

**Complete cDNA and Genomic Sequence Encoding a Flooding-Responsive Gene from Maize (Zea mays L.) Homologous to Xyloglucan Endotransglycosylase**

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The vast majority of identified flooding-responsive genes encode enzymes of Glc-P metabolism, which function to allow limited energy production in the face of limited oxygen supply (Sachs, 1994). However, in addition to the induction of these genes, flooded plants also undergo structural changes, such as formation of intercellular air spaces, which may help in survival by facilitating gas exchange between submerged and aerated plant parts (Drew et al., 1979). These structural modifications have not been addressed at the molecular level.

Here we report the isolation of a complete cDNA (MZEXETHOM) and genomic sequence (g1005) encoding a flooding-responsive gene that is homologous to XET and related glucanases (Table I). XET is a recently discovered enzyme that is proposed to play a role in wall loosening during cell expansion and fruit softening (e.g. Nishitani and Tominaga, 1992; Redgwell and Fry, 1993). The activity of XET is that of transglycosylation: the enzyme catalyzes cutting and rejoining of xyloglucans, and thus allows molecular grafting between polysaccharide chains that cross-link cellulose microfibrils (Fry et al., 1992; Nishitani and Tominaga, 1992). In accordance with its proposed role, increased XET activity was correlated with growth of cells in culture (Hetherington and Fry, 1993) and with altered wall rheology during water deficit (Spollen et al., 1993). In addition, increased XET activity was also correlated with fruit ripening, which results from enzymatic degradation of the cell wall, leading to loss of structural integrity. In this case, XET is proposed to loosen the cell wall prior to degradation by other enzymes (Redgwell and Fry, 1993). Thus, g1005 is likely to encode a flooding-responsive form of XET or a related glucanase, which may be involved in cell wall metabolism during processes leading to structural modifications.

The deduced amino acid sequence of MZEXETHOM exhibits homology to XET sequences from a range of species.

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**Table I. Characteristics of cDNA and genomic sequences encoding a xyloglucan endotransglycosylase homolog from maize**

<table>
<thead>
<tr>
<th>Organism: Zea mays B73Ht.</th>
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</thead>
<tbody>
<tr>
<td>Gene: wus(1005fgu) (Peschke and Sachs, 1994).</td>
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<tr>
<td>Gene Product: Homologous to XET; actual function unknown.</td>
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<tr>
<td>Method of Identification: Comparison with XET sequences in GenBank.</td>
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<tr>
<td>Source: cDNA library in AZAPII (Stratagene) constructed from mRNA isolated from roots of preemergent seedlings (2 d old) that were treated anaerobically for 6 h; genomic library in AGERM11 (Promega).</td>
</tr>
<tr>
<td>Cloning Techniques: For cDNA cloning, cDNA library was screened with a partial clone of MZEXETHOM (Peschke and Sachs, 1994) and six clones were selected for sequence analysis. For genomic cloning, genomic library was screened with the partial clone and then with a gene-specific 3'-end fragment. Two genomic clones were selected for restriction mapping, Southern analysis, subcloning, and sequencing.</td>
</tr>
<tr>
<td>Features of cDNA Sequence: 1240 bp long, containing a complete open reading frame of 843 nucleotides. The first ATG is 120 nucleotides downstream from the 5' end. Contains 257 nucleotides in the 3' untranslated region.</td>
</tr>
<tr>
<td>Features of Genomic Sequence: Sequence is 1827 bp long covering the complete cDNA open reading frame. Gene contains one intron, 125 nucleotides long, starting 261 nucleotides downstream of the initiation codon.</td>
</tr>
<tr>
<td>Features of Deduced Protein: The open reading frame encodes 280 amino acids with a predicted mass of 30.77 kD and a pI of 6.23.</td>
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</tbody>
</table>

including soybean (Glycine max L.), wheat (Triticum aestivum L.), Vigna (Vigna angularis), tomato (Lycopersicon esculentum L.), and Arabidopsis thaliana (Okazawa et al., 1993). Stretches of homology are present along the entire length of the sequence, and the homology is particularly high in the middle and carboxy-terminal regions. For example, the

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Abbreviation: XET, xyloglucan endotransglycosylase.
deduced sequence shares 67% identity and 81% positives with the wheat sequence over a 90-amino acid stretch. g1005 is also homologous to an Arabidopsis gene specific to meristems (meri-5; Medford et al., 1991) and to a brassinosteroid-regulated gene from soybean (Zurek and Clouse, 1994). Furthermore, MZEXETHOM and all homologous sequences contain several identical stretches, including a nine-amino acid stretch proposed to be the catalytic domain of Bacillus subtilis lichenases (a related set of glucanases; Borriss et al., 1990). Thus, analysis of MZEXETHOM and the encoding gene will likely offer molecular insights into flooding-induced structural modifications. Current and future studies will address the function of the protein and characterize the regulatory elements required for gene induction.

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The GenBank accession numbers for the sequences reported in this article are U15781 (MZEXETHOM) and U15964 (g1005).

LITERATURE CITED

Borriss R, Buettner K, Maentsaelae P (1990) Structure of the beta-1,3-1,4-glucanase gene of Bacillus macerans: homologies to other beta-glucanases. Mol Gen Genet 222: 278-283


