We report the nucleotide sequence of a cDNA clone encoding the complete amino acid sequence of the glyoxysomal enzyme malate synthase (EC 4.1.3.2) in cotton seeds. A cDNA library was constructed in UNI-ZAP (Stratagene) from poly(A)+ RNA extracted from cotyledons of 48-h-grown seedlings and screened with the MS clone pGMS1 (1). The insert is 2024 base pairs (bp) in length and contains a 5' (57 bp) and 3' (266 bp) noncoding region with a 1701 bp open reading frame. The deduced amino acid sequence is 567 residues with a molecular weight of 64,677 daltons. This predicted molecular weight is similar to the experimentally obtained value (SDS-PAGE) of 63,000 daltons reported for cotton MS (2). The amino acid sequence is 86.3, 80.7 and 46.9% identical to MS from cucumber (3), rapeseed (4) and E. coli (5), respectively, and contains a carboxy-terminal tripeptide of S-K-L. The tripeptide contains a carboxy-terminal tripeptide of S-K-L. The tripeptide contains a carboxy-terminal tripeptide of S-K-L.

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S-K-L has been reported to be a peroxisomal trafficking signal in mammals (6).