Figure S3  Phylogenetic relationship of MoDMT1 with other eukaryotic DNA methyltransferases
(A) A phylogenetic tree of eukaryotic DNA methyltransferases (DMT). The unrooted phylogenetic tree was constructed by neighbor-joining method after alignment of deduced amino acid sequences of DMT protein. Values at the interior nodes are bootstrap percentages derived from 1000 replications. The scale bar indicates an evolutionary distance of 0.1 amino acid substitution per position in the sequence. (B) Multiple alignment of the amino acid sequences of the Dnmt1 methyltransferase family proteins. Eight conserved domains were indicated as I, IV, V, VI, VII, VIII, IX, and X.