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Genome-wide analysis of cyclins in maize (*Zea mays*)

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ABSTRACT. Cyclins are primary regulators of the activity of cyclin-dependent kinases and play crucial roles in cell cycle progression in eukaryotes. Although extensive studies have revealed the roles of some cyclins and underlying mechanisms in plants, relatively few cyclins have been functionally analyzed in maize. We identified 59 cyclins in the maize genome, distributed on 10 chromosomes; these were grouped into six types by phylogenetic analysis. The cyclin genes in the maize genome went through numerous tandem gene duplications on five chromosomes. However, no segmental duplications, which occur in rice, were found on maize chromosomes. This information allows us to assess the position of plant cyclin genes in terms of evolution and classification, which will be useful for functional studies of maize cyclins.

Key words: Cyclin; Gene duplication; Phylogenetic analysis; *Zea mays*

