

Complete chloroplast genomes of *Erianthus* and *Miscanthus*, and phylogenetic relationships within the *Saccharum* complex

The genera *Erianthus* and *Miscanthus*, both members of the *Saccharum* complex, are of interest as potential resources for sugarcane improvement and as bioenergy crops. Ongoing studies focus on the conservation and use of wild *Erianthus* and *Miscanthus* accessions as breeding materials. However, despite current interest, the taxonomy and phylogenetic relatedness of *Saccharum* and these related genera have been controversial. Because the chloroplast (cp) genome has conserved gene content and uniparental inheritance, polymorphism within the chloroplast genome is a valuable tool for phylogenetic and evolutionary studies. In this study, we determined the complete cp genome sequence of *Erianthus arundinaceus* and *Miscanthus sinensis*. Our analysis of these cp genomes provides insight into the phylogeny and the evolution of the *Saccharum* complex based on the sequence variations of these cp genomes.

The complete cp genomes of *E. arundinaceus* (Accession No.: LC160130) and *M. sinensis* (LC160131) had typical circular structures with 141,210 bp and 141,416 bp in length, respectively (Fig. 1). The number of genes was 143 in *E. arundinaceus* and 141 in *M. sinensis*, including 79 and 78 protein-coding genes, respectively. Alignment of the *E. arundinaceus* and *M. sinensis* chloroplast genome sequences with the known sequence of *S. officinarum* demonstrated a high degree of conservation in gene content and order. Using the data sets of 76 chloroplast protein-coding genes, we performed phylogenetic analysis in the *Saccharum* complex. Our results show that *S. officinarum* is more closely related to *M. sinensis* than to *E. arundinaceus*. We estimated that *E. arundinaceus* diverged from the subtribe Sorghinae before the divergence of *Sorghum bicolor* and the common ancestor of *S. officinarum* and *M. sinensis* (Fig. 2).

This is the first report of the phylogenetic and evolutionary relationships inferred from maternally inherited variation in the *Saccharum* complex. Our study provides an important framework for understanding the phylogenetic relatedness of the economically important genera *Erianthus*, *Miscanthus*, and *Saccharum*.

(S. Tsuruta, M. Ebina [NARO-ILGS], M. Kobayashi [NARO-ILGS], W. Takahashi [NARO-ILGS])

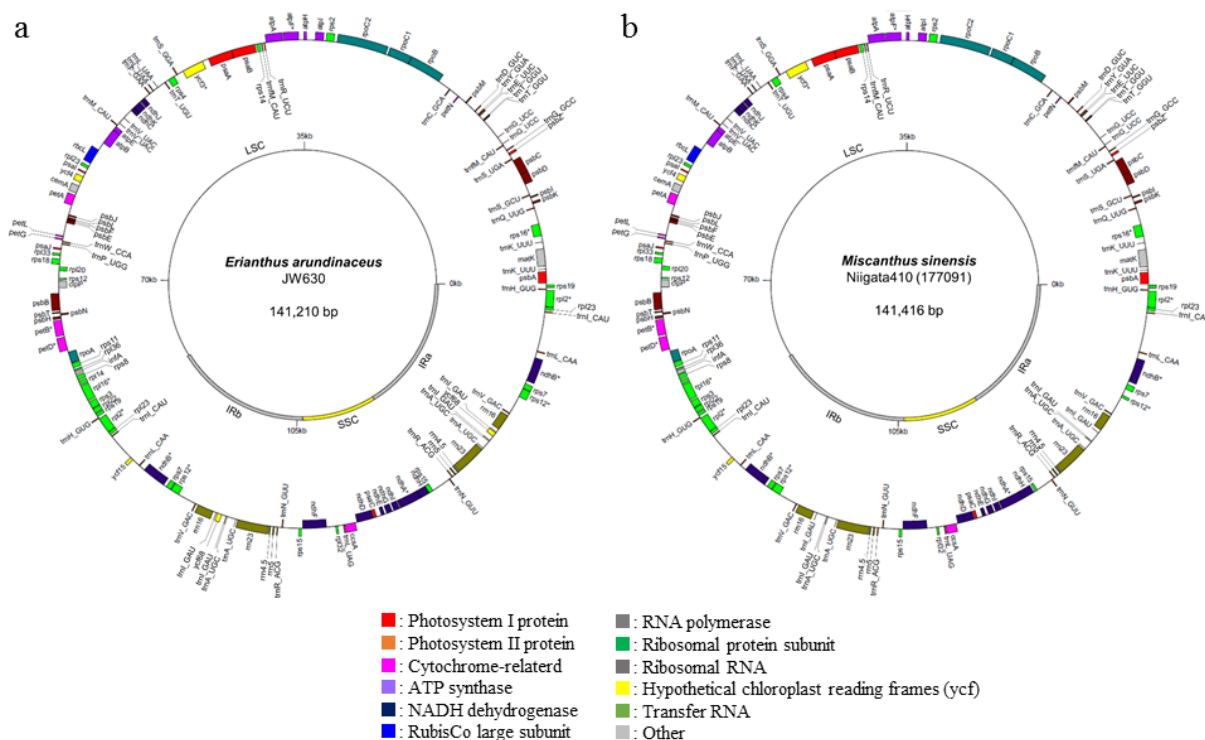


Fig. 1. Chloroplast genome maps of *Erianthus arundinaceus* (a) and *Miscanthus sinensis* (b). LSC: large single-copy, SSC: small single-copy, IRa and IRb: inverted repeat a and b

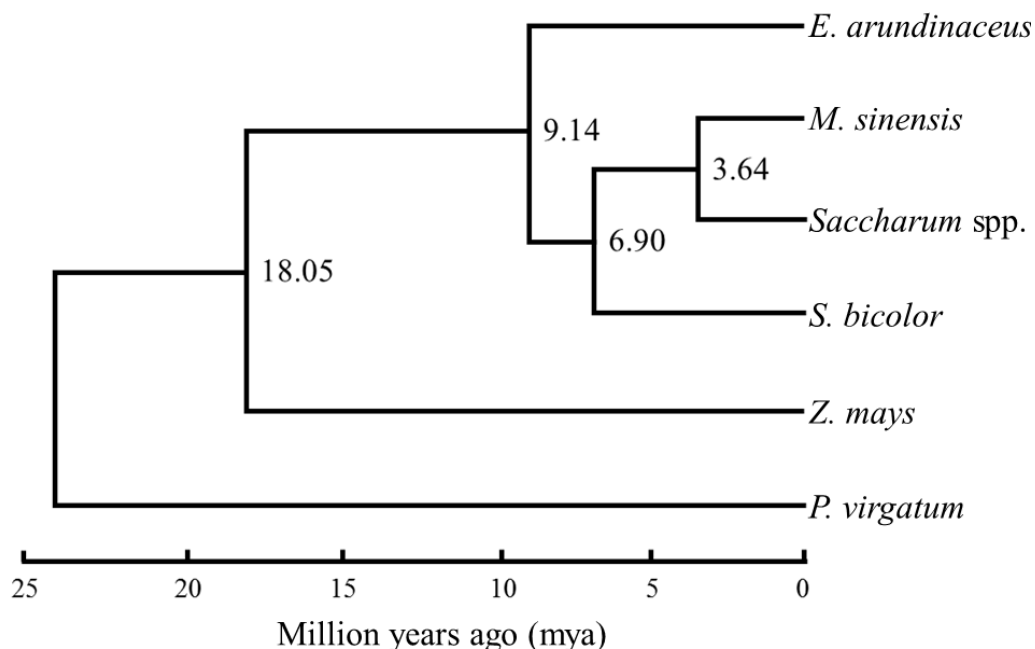


Fig. 2. Divergence times of the *Saccharum* complex estimated based on variation of 76 concatenated protein-coding chloroplast genes