

P77. Variation of chromosome 1 DNA contents in maize (*Zea mays* L.) inbred and hybrid lines

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Abstract. Analyses of flow karyotypes using different maize inbred and hybrid lines have been performed. The accumulation and isolation of high quality and quantity metaphase chromosomes from root tips can be achieved from many kinds of maize lines. The chromosome suspensions were prepared by a simple slicing method from synchronized maize root tips and analyzed with a flow cytometry. The variations of experimental flow karyotypes were detected among inbred and hybrid lines in terms of the positions and/or the numbers of chromosome peaks. The 2C DNA amount among 8 inbred lines ranged from 5.09 to 5.52 pg. The selection of appropriate maize lines is critical for sorting specific single chromosome types. At least five different chromosome types can be discriminated and sorted from five maize lines. The variability of DNA content in maize chromosome 1 was 9.1 % ranging from 0.685 to 0.747 pg. The differences of DNA content in homologous chromosome 1 of hybrid lines were detected.

Plant Materials

Eight maize inbred lines: A188, A619, B73, B79, KYS, N28, Oh43, and W23

eight hybrid lines : A188/B73, B73/W23, B73/A619, A619/B73, A619/A188, A619/Oh43, A188/Oh43, and Oh43/A188

Results and Discussion

The accumulation and isolation of high quality and quantity of metaphase chromosomes from maize root tips can be performed from many kinds of maize lines.

The knowledge of the experimental flow karyotype of maize lines is useful for sorting specific chromosomes. For example, all of maize lines are suitable sources for sorting chromosome 1; B79 and KYS inbred lines are good for sorting at least 3 single chromosome types; Oh43 inbred line is a better choice for sorting chromosome 1 and 10.

The variability of DNA content between homologous chromosomes can be useful information for study of maize genome analysis, genetic variation, or hybrid vigor among their offsprings.

Variations in flow karyotyping suggested that the fingerprint patterns of the flow karyotype may be used for pedigree analysis, or chromosomal analysis.

Table 1. DNA content and base composition (%GC) of 2C nuclear DNA from 8 different maize inbred lines.

Maize line	Pedigree/origin	2C DNA content (pg) \pm SD	Base composition (% GC) \pm SD
A188	4-29 (Silver King)/46 (N.W.Dent)4 ⁴	5.09 \pm 0.10	45.16 \pm 0.24
A619	(A171/Oh43)Oh43	5.25 \pm 0.11	45.22 \pm 0.21
B73	Iowa stiff stalk synthetic C5	5.16 \pm 0.13	45.49 \pm 0.18
B79	BS10 (Iowa 2-ear synthetic)	5.36 \pm 0.15	45.74 \pm 0.19
KYS	Yellow selection, pride of Saline	5.52 \pm 0.13	45.78 \pm 0.17
N28	Stiff stalk synthetic	5.20 \pm 0.11	45.58 \pm 0.15
Oh43	Oh40B/W8	5.29 \pm 0.13	45.32 \pm 0.16
W23	Golden Glow	5.23 \pm 0.18	45.72 \pm 0.19

Note: The DNA content of chicken red blood cells (CRBC) was used as internal standards (2C=2.33 pg, 42.7 % GC base composition). Propidium iodide (PI) was used for 2C DNA content, and bisbenzimidazole Hoechst 33342 and mithramycin for base composition. Four nucleus isolations were performed for each line. Analyses were repeated twice for four nucleus suspensions per line.

Fig. 1. Flow karyotypes of maize hybrid lines. A. A188/B73; B. B73/W23; C. B73/A619; D. A619/B73; E. A619/A188; F. A619/Oh43; G. A188/Oh43; H. Oh43/A188. The instrument settings were the same as Fig. 2. The same instrument settings were used for analyses of chromosomes isolated from other hybrid lines. The chromosome 1 indicated as 1 in all flow karyotypes. The flow karyotypes generated from reciprocal crosses were closely matched to each other; Fig. 3, C vs. D, and Fig. 3, G vs. H. Homologous chromosome 1 of hybrid lines (B73/A619, A619/A188, A619/Oh43, A188/Oh43) revealed different chromosome peaks.

