

Characterization of transposable elements and other repeat sequences in the genome of *Epimedium* L. using FISH

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Introduction

The *Epimedium* genus comprises about 50 species including five species taken in Chinese Pharmacopoeia. Approximately 80% of the total species are found in central-southeastern China (Ying, 2001). This herb has been praised as 'Chinese Viagra', which was used to treat a many of diseases such as impotence, spermatorrhea, infertility in women and so on.

The aim of this study is the characterization of distribution patterns of transposable elements and other repetitive sequences in the *Epimedium* chromosomes. This is the base for the later research like genome evolution, population genetics, construction of EST library, even improved breeding.

Results I

Flow cytometry was used to measure genome size of 6 species. Genome sizes in this plant were large, varying 1.19-fold from 4.21 to 5.03 pg/C (Table 1). Comparative to large genome of model plants, this is nearly twice than maize genome (2400-2700 Mbp, Rabinowicz *et al.*, 2006), even if its chromosome number is only 12, small than maize (2n=20).

Results II

It is well known that retrotransposable elements account for the majority component in the large plant genomes (SanMiguel *et al.*, 1996). Referring to other large plant genome, we investigated the distribution of the repetitive sequences on the *Epimedium* chromosomes using Fluorescence *in situ* hybridization (FISH). These repetitive sequences include 5S and 45S rDNA, simple repetitive sequences, and retrotransposable elements. The 5S and 45S rDNA sequences were amplified by PCR according to Sun *et al.* (2005). Retrotransposable elements sequences of Ty1-*copia* and Ty3-*gypsy* were amplified and cloned using degenerate primers (Flavell *et al.*, 1992; Hill *et al.*, 2005). The signals of the 5S and 45S rDNA probes were located almost identically on the one chromosome among 3 species (Fig. 1). SSR signals of bio-(CA)₈, bio-(GAA)₇ probes were distributed ubiquitously in all chromosomes of *E. sagittatum* (Fig. 2) This indicates that SSR was one of the main components in the *Epimedium* genome.

Up to now, we already acquired the sequences of the retrotransposon of Ty1-*copia* and Ty3-*gypsy* from 3 species genome. The FISH work was going on schedule.

Conclusion

The genome size of *Epimedium* was large relative to its chromosome number, range from 4.21 to 5.03 pg/C in this study. According to the results of SSR distribution, it was suggested that SSR ubiquity is one of causes lead to the large genome size. So maybe retrotransposable elements acquired, which was undetermined by present results.

References

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Table 1. Genome size of *Epimedium* species, measurement by flow cytometry (*Lycopersicon esculentum* var. *cerasiforme* as a internal standard, 1C=980 Mbp).

Species	DNA content (pg/C)	Genome size (Mbp/C)
<i>E. koreanum</i>	4.21±0.30	4125.8±294
<i>E. sagittatum</i> (HN)	4.91±0.21	4811.8±205.8
<i>E. sagittatum</i> (GD)	4.96±0.25	4860.8±245
<i>E. sagittatum</i> (GX)	4.91±0.26	4811.8±254.8
<i>E. franchetii</i>	4.27±0.16	4184.6±156.8
<i>E. pubesens</i>	4.79±0.11	4694.2±107.8
<i>E. wushanense</i>	5.03±0.11	4929.4±107.8
LTttz (non-identified)	4.42±0.13	4331.6±127.4

Fig. 1 5S and 45S rDNA located on the *Epimedium* genome using FISH. (a) 5S rDNA on *E. sagittatum* chromosomes; (b) 5S rDNA on *E. wushanense* chromosomes; (c) 5S rDNA on *E. pubesens* chromosomes; (d) 45S rDNA on *E. sagittatum* chromosomes; (e) 45S rDNA on *E. wushanense* chromosomes; (f) 45S rDNA on *E. pubesens* chromosomes.

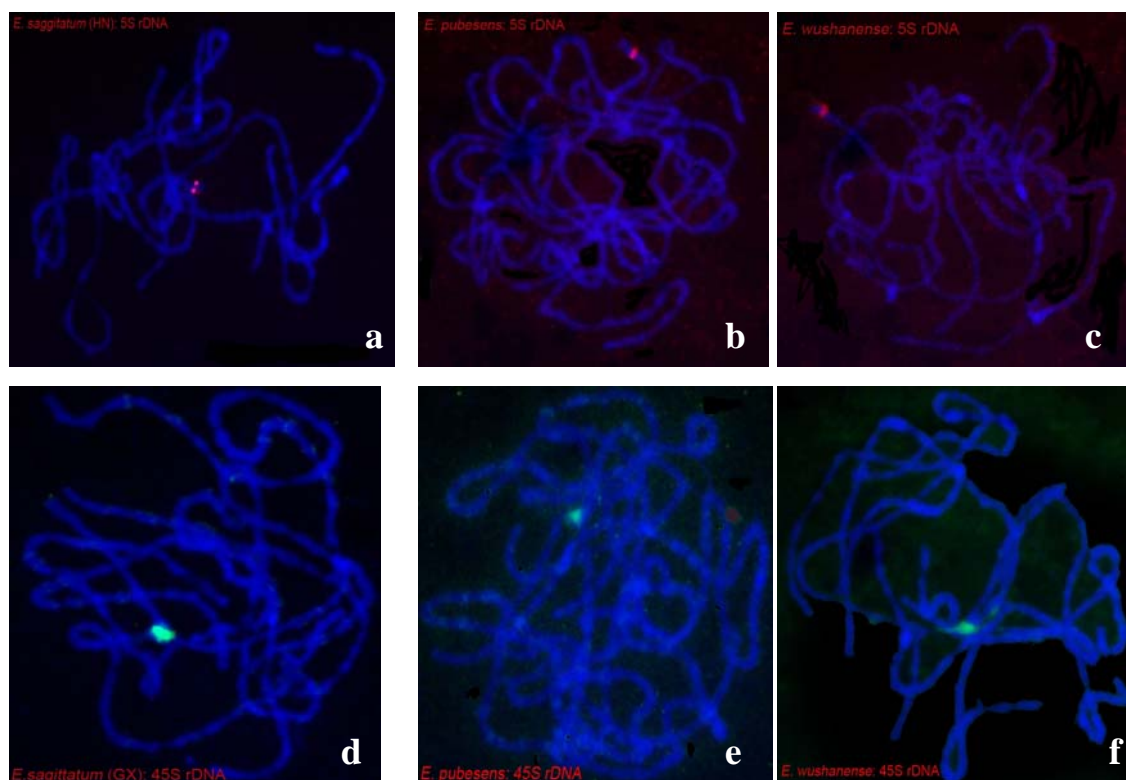


Fig. 2 SSR distributed on *E. sagittatum* (GX) chromosomes. (g) (CA)₈ probes; (h) (GAA)₇ probes.

