Cite this as: Hui-min JIA, Yu-tong SHEN, Yun JIAO, Guo-yun WANG, Xiao DONG, Hui-juan JIA, Fang DU, Sen-miao LIANG, Chao-chao ZHOU, Wei-hua MAO, Zhong-shan GAO, 2014. Development of 107 SSR markers from whole genome shotgun sequences of Chinese bayberry (*Myrica rubra*) and their application in seedling identification. *Journal of Zhejiang University-SCIENCE B (Biomedicine & Biotechnology)*, **15**(11):997-1005.

Development of 107 SSR markers from whole genome shotgun sequences of Chinese bayberry (*Myrica rubra*) and their application in seedling identification

Key words: Chinese bayberry, Simple Sequence Repeat,
SSR, Genetic diversity

Research design and methods

WGSs database of Chinese bayberry

Identification of di-nucleotide SSRs

Primer design and polymorphism testing

New SSR markers in analyzing *M. rubra* genetic relationships.

Identification of three new varieties of Chinese bayberry

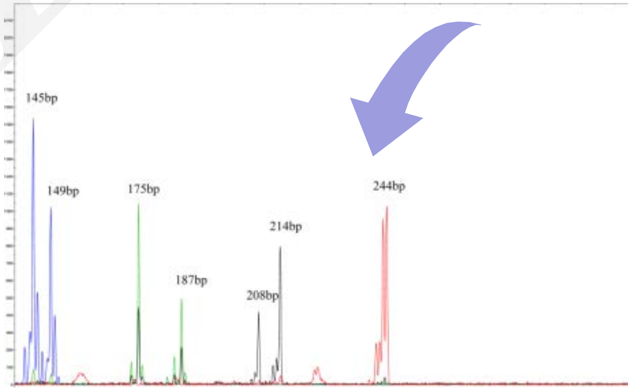
M13

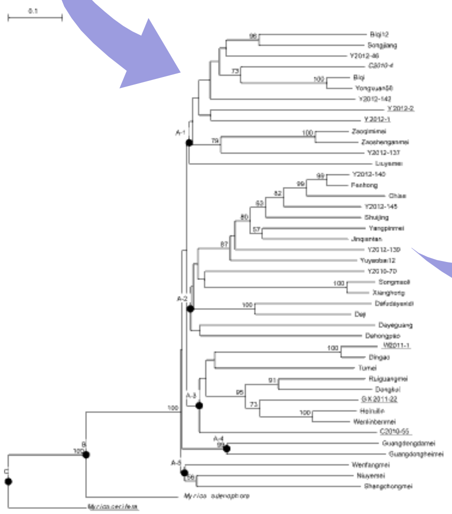
M13

M13

M13

Added to the 5’ end of each forward primer respectively





Innovation points

A series of comprehensive Tables and Figures were generated to summarize the new SSR markers and their application in genetic study and breeding practice

Table 2│Detaied characteristics of the 107 SSR markers .

Table 3│ Main fruit characters of the identified *Myrica rubra* accessions.

Figure 1│Dendrogram for 45 *M. rubra* accessions derived from Neighbor-Joining cluster analysis based on 107 SSR markers .

Figure 2 │ Fruit size and color of three new selections and reference cultivars.