BIOINFORMATION

Supplementary material:

Table 1: Performance comparison of microsatellite mining software GMATo, SSR Locator and MISA in *Setaria Italica* whole genome

Soft	*Setaria Italica* whole genome			SSR Loci
	Time			
	Windows*	Linux#	Mac&	
GMATo	10m0s	8m40s	8m6s	46,739
SSR Locator	>12h+	Not executable	Not executable	46,625
MISA	16m11s	12m14s	15m13s	46,782

SSR motif length ranging from 2 to 10 bp, minimum repeated times at least 5. SSR locator V1.1 and MISA was downloaded from official site http://www.ufpel.tche.br/ and http://pgrc.ipk-gatersleben.de/misa/ respectively.

Foxtail millet (*Setaria Italica*) whole genome sequence (~515Mb) file Sitalica_164.fa was downloaded from phytozome http://www.phytozome.net/.

*environment: HP 8000 Elite 32 byte Windows 7, Inter core2 CPU 2.83 GHz, 4G RAM, disk space 500 G ; # environment: Linux gridview 2.6.18, 64 byte, AMD Opteron Processor 612 CPU 2.0 GHz, 66G RAM, disk space 500G; & environment: Mac Pro OS 10.7.5, Intel Xeon CPU 2.66 GHZ, 12G RAM, disk space 1T; + Summary of SSR loci was produced at 29m49s but it took more than 12 hours to export mined SSR data.