表 2 全基因组和转录区域内毛白杨及毛新杨遗传杂合水平分析比较

Table 2 Comparison of the results of heterozygosity analysis between whole genome and transcribed regions

	全基因组 Whole genome		转录区域 Transcribed region	
可检测标记均数 Average number of detectable markers	65.73		33.28	
多态性标记均数 Average number of polymorphic markers	17.87		6.53	
扩增条带数最多引物 PCs with max detectable bands	E_{AAT}/M_{ATC} (110)		E_{AAA}/M_{AC} (51)	
扩增条带数最少引物 PCs with min detectable bands	E_{AAG}/M_{AAC} (50) E_{AAG}/M_{TCT} (50)		E_{AAT}/M_{GT} (22)	
检测多态性片段最多引物 PCs with max polymorphic bands	E_{AAT}/M_{ATC} (26) E_{ATC}/M_{ATT} (26) E_{GAA}/M_{CTG} (26)		E_{ATC}/M_{CA} (15)	
检测多态性片段最少引物 PCs with min polymorphic bands	E_{AAG}/M_{TCT} (8)		E_{GAA}/M_{TA} (3)	
平均多态性水平(%) Average level of polymorphism	27.41		19.60	
	毛新杨 *P. tomentosa* × *P. bolleana*	毛白杨 *P. tomentosa*	毛新杨 *P. tomentosa* × *P. bolleana*	毛白杨 *P. tomentosa*
平均多态性标记 Average Number of loci	5.57	12.30	2.40	4.10
平均杂合水平(%) Average heterozygosity (%)	8.47	18.71	7.16	12.47

注: 表中全基因组部分数据引自张德强等(2003)

Note: Data of whole genome in the table were cited from Zhang D.Q., et al. (2003)