

IRAP-analysis of genetic diversity in Chinese plum (*Prunus salicina*) varieties distributed in southern regions of Siberia

Denis Garapov ¹, Ilya Stepanov ²

¹ Federal Altai Scientific Center For Agrobiotechnology, Barnaul, Russia

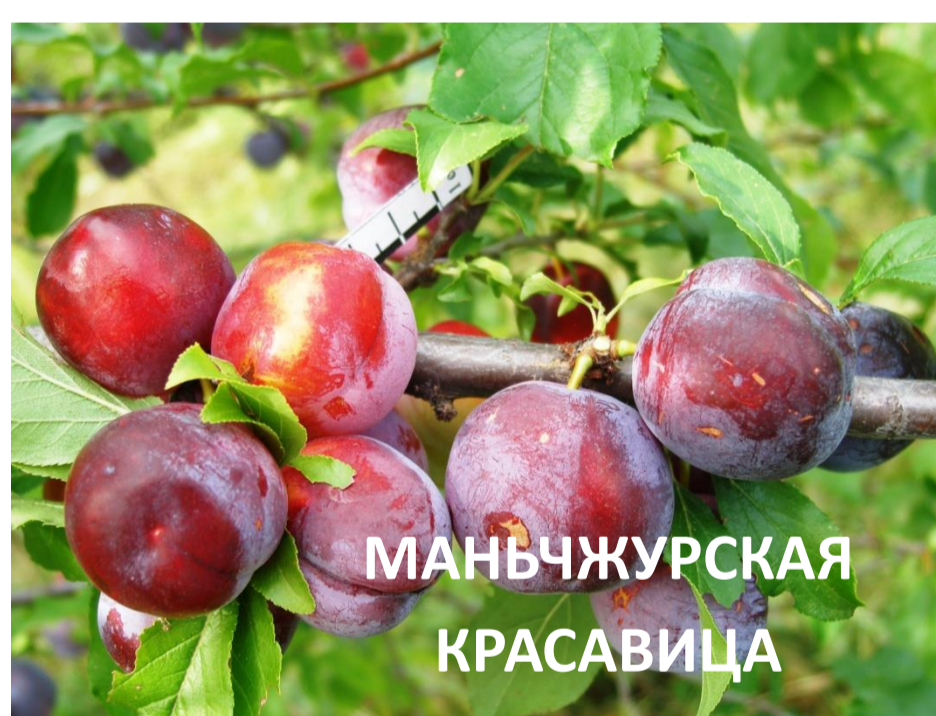
² North Caucasian Federal Scientific Center For Horticulture, Viticulture, Wine-Making, Krasnodar, Russia

IRAP (inter-retrotransposon amplified polymorphism) primers were designed in Slovak University of Agriculture, Nitra (Senkova et al., 2012) and derived from European plum (*Prunus domestica*) retrotransposon *Cassandra* (NCBI accession number AY860314)

Primer	Sequence	Thermal profile of PCR
PrunCassLTR1	ACGGCGGAGCCGATCCCGGGATGTGACA	94°C – 1 min; 32 cycles of 94°C 1 min, 54°C 1 min, 72°C 3 min; final 72°C 10 min
PrunCassLTR2	TCTCCGTTGGTCGATGTGGGATGTTACA	94°C – 3 min; 32 cycles of 94°C 40 s, 61°C 40 s, 72°C 2 min; final 72°C 5 min

Genetic diversity of 2 IRAP-markers tested within 12 Chinese plum varieties

Primer	Observed number of alleles (Na)	Effective number of alleles (Ne)	Shannon's information index (I)	Nei's gene diversity (h)
PrunCassLTR1	11	1.563	0.511	0.341
PrunCassLTR2	16	1.535	0.494	0.324



Principal coordinate analysis of 12 plum varieties by IRAP

