https://doi.org/10.17221/35/2020-PPS

Genotypic differentiation of *Monilinia* spp. populations in Serbia using a High-Resolution Melting (HRM) analysis

Antonios Zambounis[1], Eleni Stefanidou[2], Panagiotis Madesis[2,3], Jovana Hrustić[4], Milica Mihajlović[4], Brankica Tanović[4]*

[1]*Institute of Plant Breeding and Genetic Resources, Department of Deciduous Fruit Trees, ELGO-DEMETER, Naoussa, Greece*

[2]*Institute of Applied Biosciences, CERTH, Thermi, Thessaloniki, Greece*

[3]*Laboratory of Molecular Biology of Plants, School of Agricultural Sciences, University of Thessaly, Thessaly, Greece*

[4]*Laboratory of Phytopathology, Institute of Pesticides and Environmental Protection, Belgrade, Serbia*

**Corresponding authors: antonios.zamb@gmail.com*

ELECTRONIC SUPPLEMENTARY MATERIAL (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

Table S1. Sequences and amplicon lengths of the *Monilinia* species-specific primers used in this study

Monilinia spp.	Primer name	Primer sequence	Amplicon length
Monilinia laxa	ILaxaS	TGAGCACGAGTGAATGTATAG	226 bp
	ILaxaAS	TGAGCACGAGGGCATATC	
Monilinia fructicola	IColaS	GAGACGCACACAGAGTCAG	336 bp
	IColaAS	GAGACGCACATAGCATTGG	
Monilinia fructigena	IGenaS	TGCTCTGCCCGTACCCAG	734 bp
	IGenaAS	GGATTTATTGTGATGTAGTTTCG	

Table S2. Analysis of molecular variance for the three *Monilinia* spp. populations based on the HRM analysis

Monilinia spp.	Source	SS	MSS	Variance component	variation (%)
Monilinia laxa	among populations	2.604	1.302	0.06	7
Monilinia fructicola		6.000	3.000	0.423	44
Monilinia fructigena		4.418	2.209	0.425	44
Monilinia laxa	within populations	18.473	0.803	0.803	93
Monilinia fructicola		8.000	0.533	0.533	56
Monilinia fructigena		5.429	0.543	0.543	56
Monilinia laxa	total	21.077		0.863	
Monilinia fructicola		14.000		0.956	100
Monilinia fructigena		9.846		0.968	

SS –sum of squares; MSS – mean sum of squares

https://doi.org/10.17221/35/2020-PPS

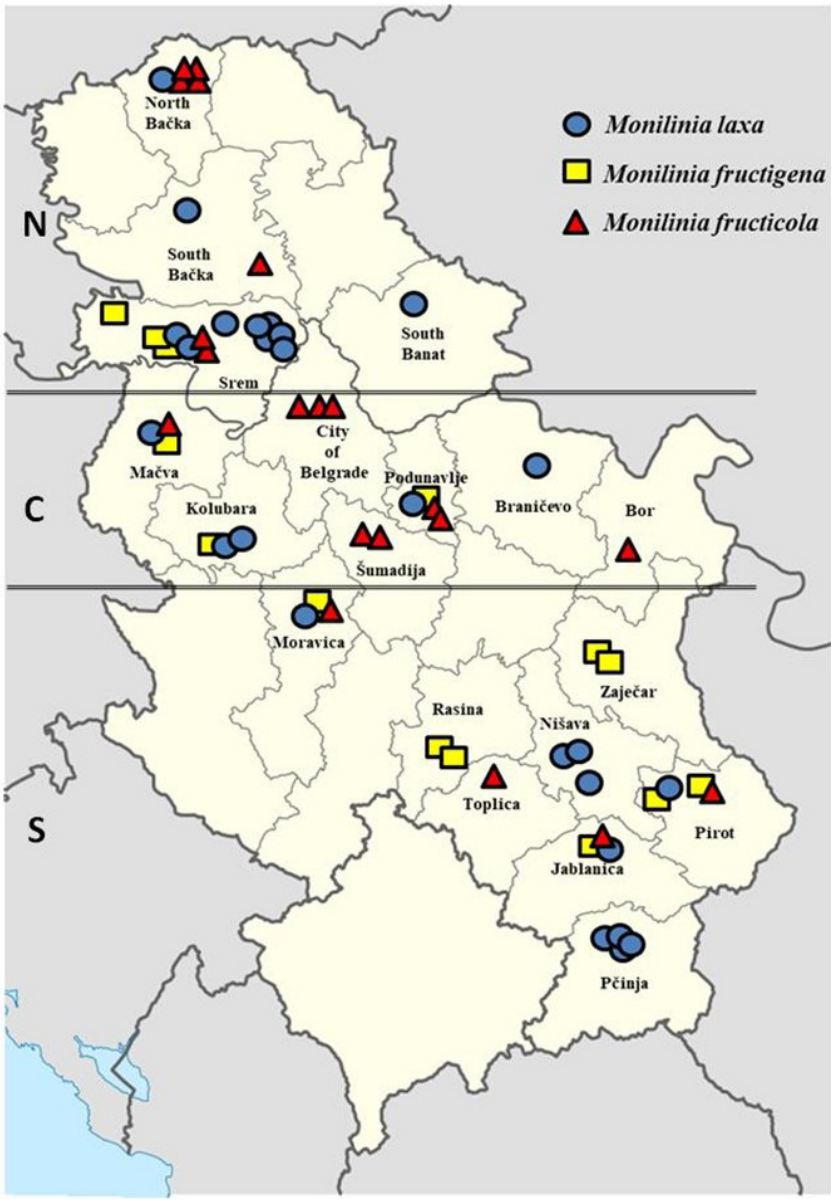

Figure S1. Geographical map indicating the sampling locations across the three geographical regions of Serbia

N – north; C – central; S – south

https://doi.org/10.17221/35/2020-PPS

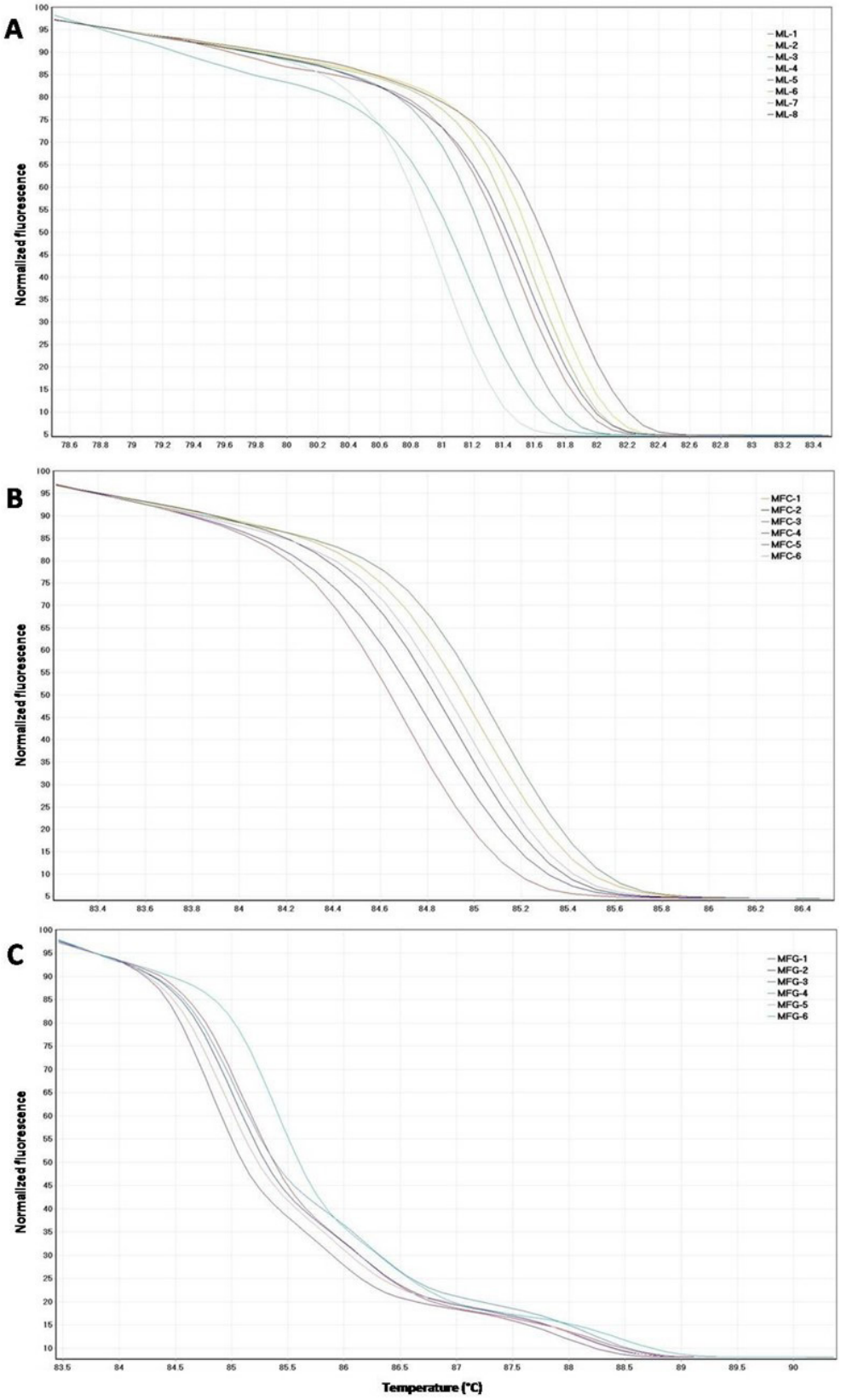

Figure S2. Discrimination of *Monilinia* spp. genotypes upon their normalized melting curves profiles generated by the HRM analysis of (A) *M. laxa*, (B) *M. fructicola* and (C) *M. fructigena*

https://doi.org/10.17221/35/2020-PPS

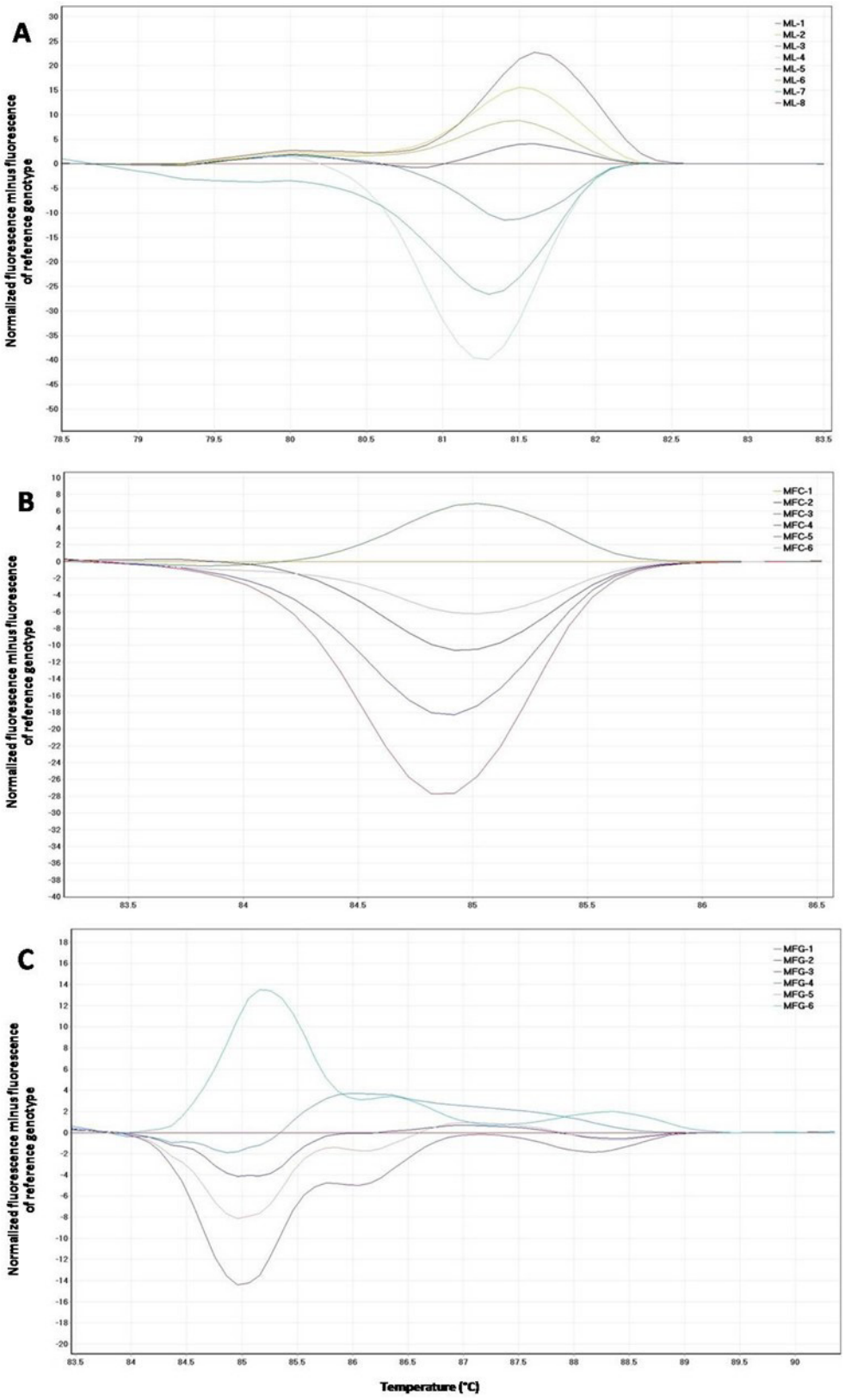

Figure S3. Difference graphs of the *Monilinia* spp. genotypes using reference genotypes converted to a horizontal lines upon the HRM analysis of (A) *M. laxa*, (B) *M. fructicola* and (C) *M. fructigena*

https://doi.org/10.17221/35/2020-PPS

Figure S4. Nucleotide alignments of the HRM genotypes for each *Monilinia* spp. *M. laxa* (ML^{-1} up to ML^{-8})

The SNPs positions among the HRM genotypes are indicating with colored annotations

https://doi.org/10.17221/35/2020-PPS

Figure S4: Nucleotide alignments of the HRM genotypes for each *Monilinia* spp. *M. fructicola* (MFC^{-1} up to MFC-$^{6)}$
The SNPs positions among the HRM genotypes are indicating with colored annotations

https://doi.org/10.17221/35/2020-PPS

Figure S4. Nucleotide alignments of the HRM genotypes for each *Monilinia* spp. *M. fructigena* (MFG^{-1} up to MFG^{-6})
The SNPs positions among the HRM genotypes are indicating with colored annotations