

Phenotypic and molecular analysis of scab in autochthonous apple germplasm from Northeastern Spain



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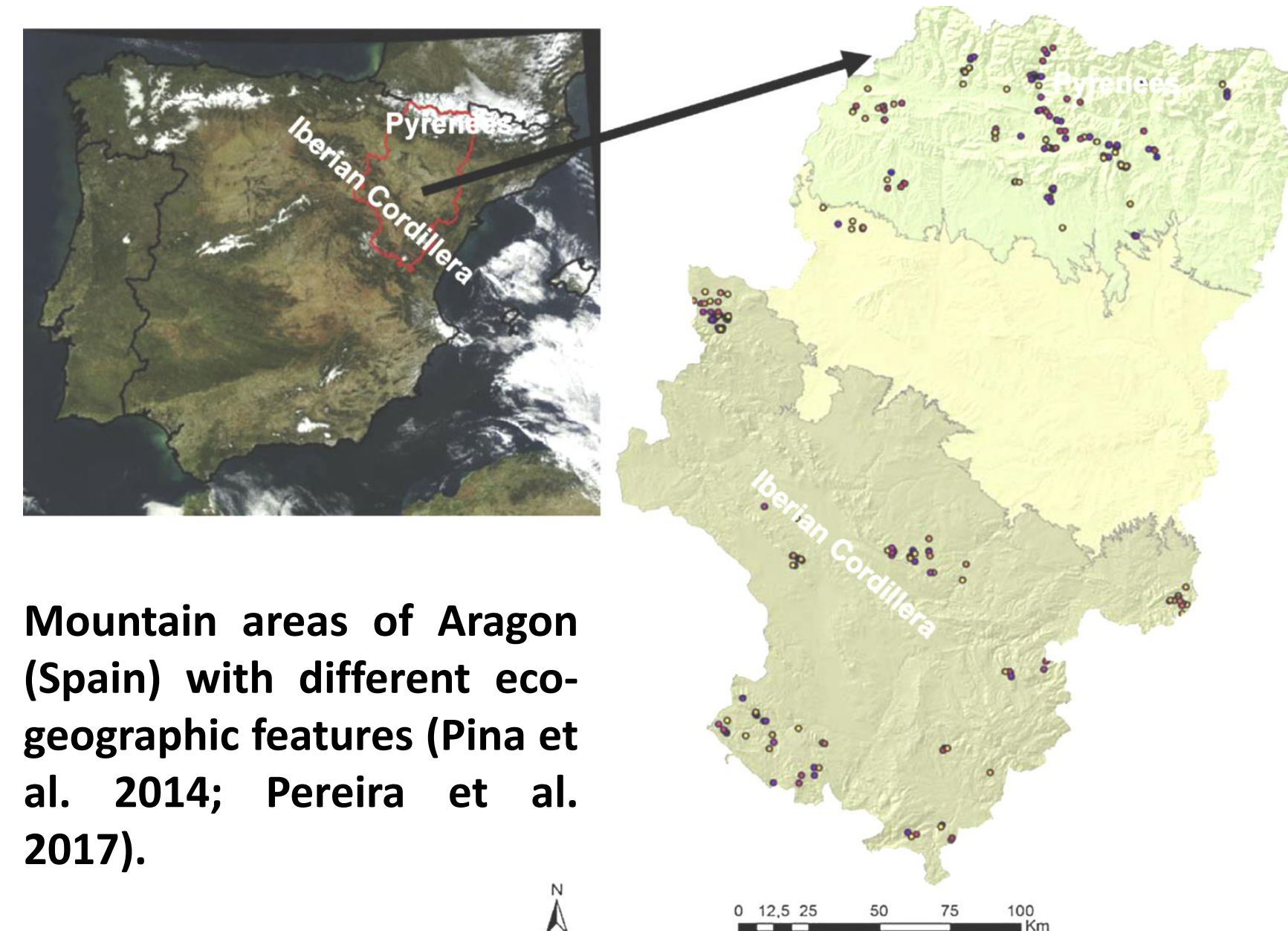
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Apple scab caused by the pathogenic fungus *Venturia inaequalis* is one of the most important disease of apple worldwide and orchards affected by scab infection require integrated plant protection management (Höfer et al. 2022). Management of scab through **resistant cultivars** with sufficient fruit quality represents a cost effective and eco-friendly alternative to chemical control. In this study, we evaluated the scab resistance/susceptibility of **autochthonous apple cultivars** prospected in mountainous areas from **Northeastern Spain** (Pyrenees and Iberian Cordillera), both at phenotypic as well as genotypic levels. Since this local material are very old traditional cultivars maintained in their environment for decades, a good adaptation to the environment is assumed. Hence, these genotypes could be of great interest, as they could represent new potential sources for scab resistance.



Mountain areas of Aragon (Spain) with different eco-geographic features (Pina et al. 2014; Pereira et al. 2017).

86 genotypes
68 apple local accessions
+
18 commercial cultivars



Phenotyping



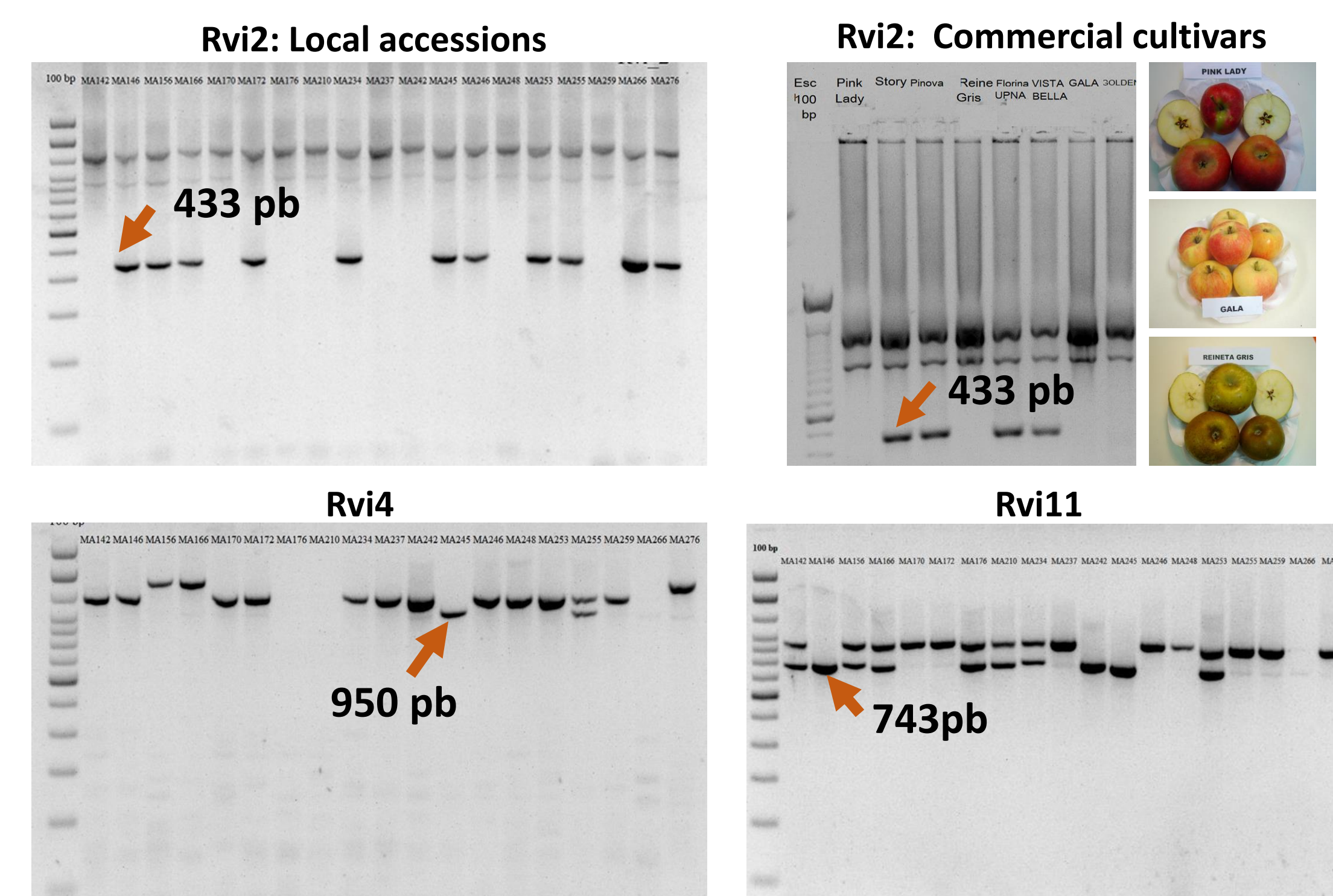
The **field evaluation** was carried out in 2020 and 2021 and the accessions were classified into four classes of susceptibility based on a visual assessment of the scab response type on **visible leaves** throughout the tree canopy and **fruits** (presence/absence).

Scale	Susceptibility	Symptoms	% of local accessions infected		
			2021	2022	Mean
0	No infection	No visible macroscopic symptoms	7,7	4,4	6,0
1	Low	Few visible lesions, with low symptoms	35,9	30,9	33,4
2	Medium	Numerous lesions widespread over a large part of the tree	43,6	38,2	40,9
3	High	Severe infection with half of the leaves infected by multiple lesions	12,8	26,5	19,65

Molecular Analysis

DNA extraction → PCR amplification of resistance marker → Gel Electrophoresis → Data analysis

Detected gene	Marker primers	PCR type	Size (bp)	Reference
Rvi2	OPL 19	SCAR	433	Bus at al. 2005
Rvi4	AD13	SCAR	950	Boudichevskaia et al. 2006
Rvi11	SCAR a+b	SCAR a+b	743	Gygax et al. 2004
Rvi6	VfT F+R	SCAR	466	Tartarini et al. 1999



3 local accessions amplified 3 resistance genes Rvi2, Rvi4 and Rvi11
22 amplified the Rvi2 and Rvi11 genes
4 accessions combined the Rvi4 and Rv11 genes.
Scab resistance gene Rvi6 (Vf) amplified only in the reference cultivars 'Story', 'Prima' and 'Florina'.

Until now, there are more than 150 scab resistant or tolerant apple cultivars on the market, but these cultivars have been obtained in northern Europe or America (Belete and Boryaz, 2017), areas where climatic conditions are very different from those of the **Mediterranean regions** (Iglesias et al. 2014). Therefore, it is important to evaluate and characterize **apple genetic resources** available in our growing areas against resistance to scab, since it represents a great opportunity to identify **resistant genotypes adapted to our conditions**.

The apple germplasm collection prospected in mountain areas from Aragon (Spain) show a wide phenotypic variability of resistance genes to scab disease. These results will serve as a basis for the selection of local cultivars that present resistance to scab, and these mountain areas (Pyrenees and Iberian Cordillera) can therefore be viewed as an untapped source of genes for future apple breeding program.

References

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