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## Grapevine identification in “Abandonado” vineyard using SSR-Multiplex PCR, SNP genotyping and HRM assays

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Accurate identification of older grapevine varieties can be difficult considering the existence of many synonyms, homonyms, and misidentifications. In this work, SSR-Multiplex PCR and SNP genotyping were performed in combination with HRM assays, to determine the identity of nineteen grapevine varieties present in “Abandonado”, an old portuguese vineyard at Quinta da Gaivosa. The combination of the three approaches allowed the identification of eighteen out of the nineteen grapevines from the vineyard, where ten grapevines were correctly identified by ampelography and the remaining eight were misidentified. SSR and SNP data retrieved for one sample did not match any profile present in the VIVC database, but pedigree analyses suggested it may be a new variety. We obtained new information regarding three SSR *loci* for one sample identified as Cerceal Branco, that interestingly presented a red colour berry which was not expected. One other sample identified as Malvasia Preta/Preta Roxa also presented a berry colour non-coincident with its molecular identification. Both these samples might represent new somatic variants of the identified varieties by SSR/SNP profiles, but further studies are required to confirm these situations. Three HRM assays were performed to validate SSR/SNP analysis, using available reference material, representing a useful tool for varietal identification through melting curve profile comparison.

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