

Intra-varietal Agronomical Variability in *Vitis vinifera* L. cv. Cannonau Investigated by Fluorescence, Texture and Colorimetric Analysis

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To date, innovative, rapid and non-invasive techniques have been used to assess variations in morphological and technological characteristics between grape cultivars. In order to improve knowledge of the qualitative expression of the genetic traits of cv. Cannonau (syn. Grenache), fluorescence, texture and colorimetric analyses were performed on 85 biotypes attributable to this variety. Eighty-five Cannonau biotypes cultivated in the same vineyard were analysed in order to evaluate their morphological and agronomical characteristics. As regards the morphological traits, of the six descriptors observed, five were able to discriminate the Cannonau population according to different expression levels. Must composition, berry colour (using the Minolta tristimulus colorimeter), texture (assessed using the TaxT2i plus texturimeter) and fluorescence (using the Multiplex III detector) were determined on clusters harvested at the same time. Cluster analysis was able to separate the Cannonau population into five groups, characterised by differences in the following criteria: L*, a* and b*, berry skin thickness, FERARI, TSS, pH and titratable acidity, total polyphenols and total anthocyanins. The FERARI index was highly and positively correlated with total anthocyanins and negatively correlated with grape colour, while berry weight and berry skin thickness were not correlated with any variable assessed. The remarkable intra-variability encountered for the qualitative and quantitative characters in the Cannonau variety suggests that new biotypes could be selected for different oenological purposes, using techniques such as the measure of fluorescence and colorimetry. This is the first study carried out within the cv. Cannonau using innovative and classical techniques suitable to investigate intra-varietal variability.

INTRODUCTION

Natural biodiversity has played a leading role in the evolution of agriculture over the centuries, in terms of which crops were selected according to the identification, manipulation and domestication of wild species (Chessa & Nieddu, 2005). Although a cultivar consists of vines presenting the same basic characteristics, there is remarkable genetic variability within each cultivar, resulting from the occurrence of spontaneous genetic mutations and their transmission to subsequent progeny (Mannini *et al.*, 2011). Vegetative propagation helped to multiply and spread cultivars and clones around the world, further expanding intra-varietal variability. Numerous studies investigating the impact of clonal variability on the yield component and fruit composition of different grapevine varieties have been carried out since the late 1980s. Knowledge about intra-varietal variability is widely recognised in the wine industries. Indeed, understanding the agronomic and technological characteristics of the different clones and their wines has led to an increase in oenological

products and improvements in wine quality. Differences among clones may relate to ampelographic characteristics and phenological phases (Nieddu *et al.*, 2006), disease resistance (Van Leeuwen *et al.*, 2012), yield and berry composition (Fidelibus *et al.*, 2006; Anderson *et al.*, 2008; Mercenaro *et al.*, 2009), as well as secondary metabolite concentrations (Belancic & Agosin, 2007; Mulas *et al.*, 2011). However, the level of intra-varietal variability is also cultivar dependent. Some cultivars, such as Pinot noir and Chenin, show great variability, whereas others, such as Cabernet Sauvignon and Garnacha Tintorea, are more homogeneous (Boso *et al.*, 2004). Another approach to studying the intra-varietal variability in *Vitis vinifera* L. involves molecular techniques (Carimi *et al.*, 2011). Meneghetti *et al.* (2011) studied 53 Garnacha (syn. Grenache) accessions coming from France, Spain and Italy using a PCR-derived marker system to characterise the clones. They confirmed that all accessions belonged to the same cultivar, yet the molecular marker system was clearly able to distinguish the Garnacha

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