



# Analysis of genetic and epigenetic variability of grapevine cultivar Shiraz in Barossa Valley

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## **Abstract**

The wine industry in Australia has rapidly increased in past decades and wine quality is the key factor to settle an appropriate price for wine. The wine quality mostly relies on the quality of grape in different environmental condition, whereas this specific environmental conditions are described as Terroir. In this study, we applied both Methylation Sensitive Amplification Polymorphism (MSAP) and methylation sensitive Genotyping by Sequencing to investigating the variation of DNA methylation between plants of Shiraz variety collected from 22 vineyards of six regions in the Barossa Valley. Results shows that different DNA methylation patterns of regions were obtained due to their various environmental conditions. However, two vineyards show a significant difference compared to other vineyards which may due to accumulated somatic mutation. To reduce genetic effect, we selected samples which were the same clones with the same pruning method. The result suggests that different farm managements can induce variability in DNA methylation. Since both environmental conditions and farming systems define a terroir, we infer that DNA methylation may play an important role in this concept.