



# Reply to Blanco-Pastor: Introgression and heterozygosity complicated grapevine domestication

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We thank Blanco-Pastor for comments on our recent publication, which focused principally on a maximum-likelihood (ML) phylogenetic tree and argued that admixed individuals affected ML inference, the subsequent definition of groups, and downstream population genetic analyses (1).

Blanco-Pastor failed to note that we defined groups not only by the ML tree but also by integrating information about their genetic structure, usage, and geographic distribution. For example, the clades from the phylogenetic tree were quite consistent with Admixture analyses using *K* values from 2 to 4 (2). Of course, that larger numbers of *K* lead to more apparent histories of admixture and this may be especially true when considering a highly heterozygous taxon like grapevines (3, 4). We contend that using multiple sources of evidence is a better practice than determining genetic groups by structure results only, such as applied in the paper referenced consistently by Blanco-Pastor as contradicting our results (5). Based on phylogenetic analyses and population structure, we removed 17 individuals (5%) that did not cluster with their reported group for population genetic analyses, which included apparent histories of recent admixture (2).

Blanco-Pastor also suggested that the individuals (ME2) were not a natural grouping, perhaps an “artificial clade formed by recently admixed individuals” and likely closely related to table grapes. First, these individuals were all sampled from Israel and can also be reliably distinguished by SSR analyses (6); it is completely reasonable to consider them a group on that evidence alone. Second, we believe that Blanco-Pastor may misunderstand the meaning of the Admixture result, because mixed ancestral components do not necessarily represent hybridization events (7). Using this same logic, the group “Syl-E2” in ref. 5 also represents a set of recently admixed individuals; this is important because this group was crucial to concluding that there may have been two domestication events. Does, then, the same criticism apply to that conclusion?

His principal complaint seems to be that our estimates differ from those reported in ref. 5. For example, we estimated that there has been continuous gene flow between wine grapes and European *Vitis sylvestris* over the last 1,800 y, whereas ref. 5 estimated that gene flow commenced 7,000 y ago. Our estimate was based on the analysis of 40 different demographic population models. However ref. 5, employed MSMC2 for evaluation using only two individuals from each group for demographic inference. Based on this fact alone, we believe our result is likely to provide a more nuanced and accurate evaluation of divergence and introgression times. Our result is also more consistent with the ~3,000-y history of grape cultivation in Europe (8).

Many of Blanco-Pastor’s arguments are based on contrasting our findings to those of ref. 5, subtly assuming that their conclusions are correct and that ours, by necessity, must be wrong. We recognize that science advances because ideas and conclusions are challenged, and we welcome it here. Further examination of various genetic factors surrounding the history of grapevine will continue to modify our understanding of this fascinating crop.

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The authors declare no competing interest.

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