

Figure S1. Evolution of amino nitrogen (a), ammonium nitrogen (b) and yeast assimilable nitrogen (YAN) (c) in control musts and in musts obtained from vines with foliar urea fertilization.

Table S1. Coefficients of linear discriminants

|  |  |  |
| --- | --- | --- |
|  | **LD1** | **LD2** |
| Phosphoserine | 0.28464574 | 0.3245030 |
| Asparticacid | -0.01790553 | 0.9881373 |
| Glutamicacid | -0.65060752 | -0.8319516 |
| Phosphoethanolamine | 0.63473990 | 0.7165766 |
| Serine | 7.32226330 | 0.7204632 |
| Asparagine | -1.38756771 | -1.7972411 |
| Glycine | -1.03962549 | 0.7149691 |
| Taurine | -2.34919046 | -3.5123645 |
| Histidine | 1.54048708 | -0.7730192 |
| γ-Aminobutyricacid | -2.37237401 | -3.5123645 |
| Threonine | 1.54048708 | -0.7730192 |
| Alanine | -3.18694773 | 4.2276188 |
| Arginine | -3.19467867 | 1.4473360 |
| Proline | 0.36940133 | -2.7614262 |
| Tyrosine | -0.48640132 | 2.0283725 |
| Valine | -0.15894999 | 0.8370905 |
| Methionine | 0.23685137 | 1.4286660 |
| Isoleucine | 0.90830376 | 0.6929498 |
| Leucine | -0.06664520 | -0.5849377 |
| Phenylalanine | 0.17927391 | -1.1772778 |
| Tryptophan | -1.78851229 | 2.1467836 |
| Lysine | 1.45308646 | 0.3409647 |

Table S2. Repeated measures ANOVA.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **Effect** | **DFn** | **DFd** | **F** | **p-value** |
| **Glutamic acid** | TreatmentTimeTreatment\*Time | 236 | 92727 | 534.2924.623.88 | 4.4\*10-106.9\*10-80.0063 |
| **Arginine** | TreatmentTimeTreatment\*Time | 23\*0.44a6\*0.44a | 927\*0.44a27\*0.44a | 489.0310.016.67 | 6.6\*10-100.00540.0078 |
| **Aspartic acid** | TreatmentTimeTreatment\*Time | 23\*0.22a6\*0.22a | 927\*0.22a27\*0.22a | 333.0131.606.57 | 3.7\*10-91.2\*10-50.0047 |
| **Asparagine** | TreatmentTimeTreatment\*Time | 23\*0.03a6\*0.03a | 927\*0.03a27\*0.03a | 2340.419.4819.23 | 3.7\*10-90.00850.0002 |
| **Alanine** | TreatmentTimeTreatment\*Time | 23\*0.37a6\*0.37a | 927\*0.37a27\*0.37a | 188.3619.9418.87 | 4.5\*10-80.0010.0004 |
| **Serine** | TreatmentTimeTreatment\*Time | 23\*0.39a6\*0.39a | 927\*0.39a27\*0.39a | 588.925.877.12 | 2.9\*10-70.03070.0091 |
| **Threonine** | TreatmentTimeTreatment\*Time | 23\*0.04a6\*0.04a | 927\*0.04a27\*0.04a | 150.0510.9616.78 | 1.2\*10-70.00076.3\*10-6 |
| **γ-Aminobutyric acid** | TreatmentTimeTreatment\*Time | 23\*0.01a6\*0.01a | 927\*0.01a27\*0.01a | 386.422.863.72 | 1.9\*10-90.11610.0534 |

aAs the Mauchly sphericity condition was rejected the degrees of freedom (DF) of the F-distribution were multiplied by the Greenhouse-Geisser correction.

If dv is the dependent variable in the regression model, a classical ANOVA study would consider the model:

dv = β0 + β1\*Time + β2\*Treatment + β3\*Time\*Treatment + ε (M1)

This is a fixed effect model, because the β values are considered fixed. As in this work, we repeated measures in individuals throughout the time, we can consider that β0 randomly changes from individual to individual, this would be model M2, or β1 is random, model M3, or both are random, model M4. These models are known in the statistical literature as mixed models because some β values remain fixed and the rest of β values are random.

In any case, model M1 is a basic model, which is improved with models M2, M3 and M4 since the variability of the error ε decreases significantly. In Table S2 a summary of that study is shown. In this Table, the chosen model for each amino acid is indicated and the significant β values (p-value<0.05) are reported along with their variability in case of random effects (an empty cell means that there are no significant effects throughout the time).

Table S3

|  |  |  |
| --- | --- | --- |
| **Amino acid** | **Model(s) chosen** | **Time effect** |
| C | T1 | T2 |
| Glutamic acid | M1, M3 | - | 4.9 (0.37) | 5.3 (0.93) |
| Arginine | M1, M3 | - | - | 36.6 (6.2) |
| Aspartic acid | M1, M2 | - | 7.18 | 9 |
| Asparagine | M1(=M3) | - | - | - |
| Alanine | M1(=M3) | 4.32 | 11.6 | -3.2 |
| Serine | M1, M3 | - | - | 3.4 (0.2) |
| Threonine | M1(=M3) | - | - | - |
| γ-Aminobutyric acid | M1, M3 | - | 4 (0.93) | - |

Observe that M1 model is chosen in all the cases, although sometimes models M3 and M2 are also appropriate. Choosing M1 means that the evolution throughout the time, if significant, is quite stable and the inclusion of random β values hardly diminishes the error variability.

In order to select one model vs another one we have used the ratio likelihood test along with the Akaike criterion for model selection. In terms of ratio likelihood test, the inclusion of random slopes or intercepts does not significantly reduces the variance error, however, the Akaike Criterion provide similar values to the M1 model and the M3 model (M2 model for aspartic acid) except for alanine, threonine and asparagine where any advantage is found including random slopes. In those cases, M1 model and M3 model provide the same estimates for the slopes.