

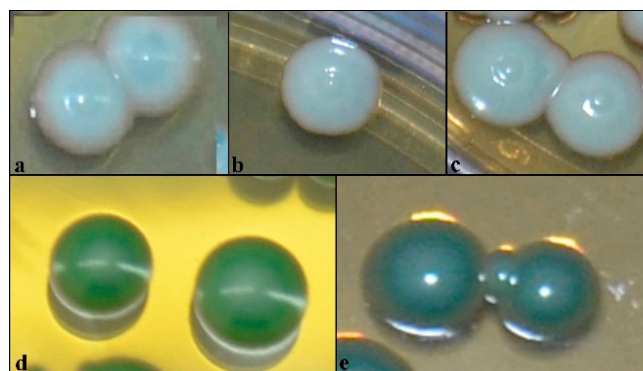


Figure S1. Yeast morphology. Color and morphology of each isolate on WL semisolid plates are reported accordingly to Cavazza et al., 1992 and Pallmann et al., 2001. **a** *M. pulcherrima* N20/006; **b** *M. pulcherrima* Ale4; **c** *M. pulcherrima* Pr7; **d** *L. thermotolerans* N10; **e** *H. uvarum* Ale5.

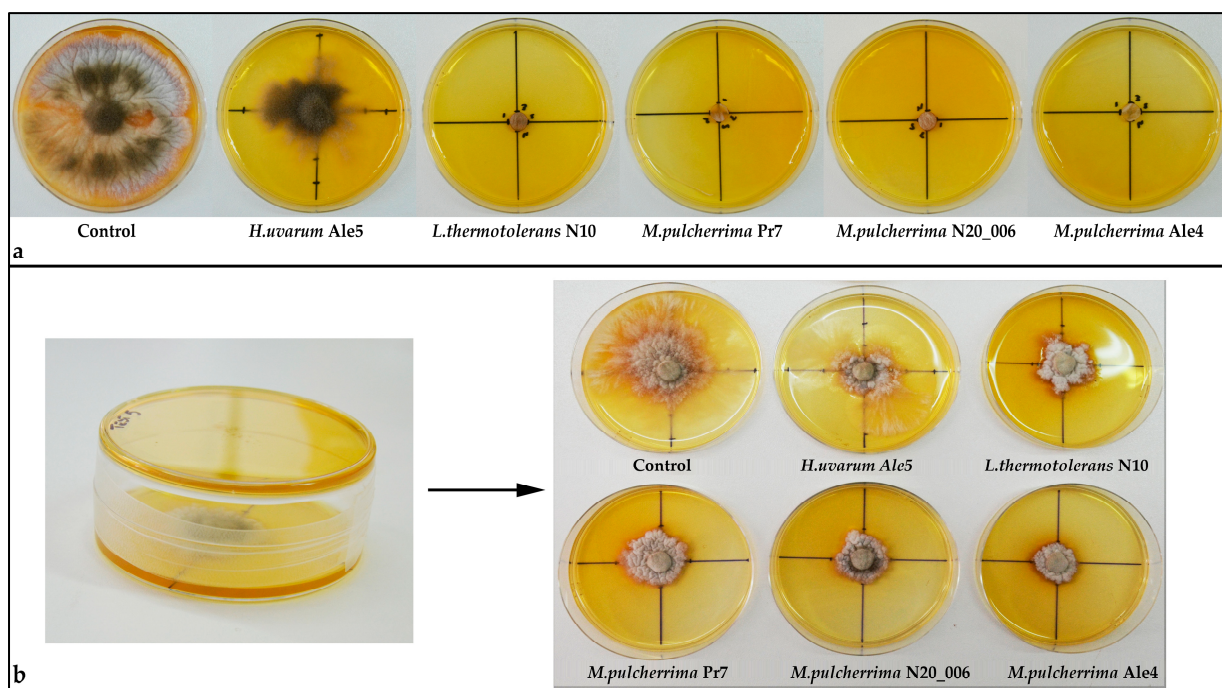


Figure S2. In vitro antagonistic tests. **a.** Cellophane agar *in vitro* antagonistic test. Growth of *B. cinerea* in YPDA previously covered with cellophane discs containing the different yeasts strain. **b.** *in vitro* antagonistic test to assess the production of VOCs. Growth of *B. cinerea* in YPDA covered with plates of YPDA with the different yeast strains.

Table S1. Agronomic characteristics of the new table grape genotypes.¹Mean value of 30 typical berries of 5 bunches; ²Mean value of 30 non deformed berries taken from the middle part of 10 bunches; ³Examination of seeds formation in 30 berries taken from the middle part of 10 bunches. 1=no formation of seeds; 2=seeds with soft seed coat; 3=seeds fully developed; ⁴Mean value of the largest bunch of 10 shoots; ⁵Mean value of the largest bunches of 10 shoot.

Genotype code	Berry				Bunch	
	Weight (g) ¹	Length (mm) ²	Color	Formation of seeds ³	Weight (g) ⁴	Length (mm) ⁵
N20/006	4.9	17.4	Red	1	669.0	430.0
N10	4.2	21.1	Blu-black	1	322.5	245.0

Table S2. Yeast characterization. Code and source of each isolate are indicated, column C and D refer to the description of different yeast isolates on WL medium basing on the descriptors proposed by Pullmann et al., 2001.; columns E-H report BLAST main results. Sequence analysis have been reported accordingly GenBank output.

Isolate code	Source (<i>V.vinifera</i> L.)	Colony Morphology		18S sequencing match			5.8S sequencing match		
		Color (front view)	Topography	Closest related type strain (GenBank)	E-value	Identity%	Closest related type strain (GenBank)	E-value	Identity%
Strain Ale 4	Aleativo cv.	Slightly blue, a hint of red-brown in the center	Convex, surface: glossy, radial pattern streak	Uncertain	/	/	M.Pulcherrima (NR_164379.1)	4e-165	97.63
Strain Ale 5	Aleatico cv.	Intensive green in the center	Flat, surface: smooth, opaque. Consistency of butter.	<i>H.uvarum</i> (NG_063250.1)	0	97	Uncertain	/	/
Strain N10	New table grape crossing	Dark green, cream at the periphery	Convex, surface: smooth, glossy, opaque	L.thermotolerans (NG_061071.1)	0	99.63	L.thermotolerans (NR_11334.1)	0	98.89
Strain N20/006	New table grape crossing	Blue green, transparency at the periphery	Convex, surface: smooth, glossy	Uncertain	/	/	M.Pulcherrima (NR_164379.1)	2e-162	97.87
Strain Pr7	Primitivo cv.	Blue green, transparency at the periphery	Convex, surface: smooth, glossy	M.pulcherrima (NG_065490.1)	0	99.81	M.Pulcherrima (NG_065490.1)	2e-172	97.8

Table S3. Incidence and McKinney's Index of grey mold in wounded berries artificial inoculated with two different concentration of yeasts. Data are presented as mean of three replicates with standard deviation Values within columns followed by the same letters are not significantly different (Dunn's test; P<0.05)

Yeast strain.	yeasts at 1.5 x 10 ⁷ CFU mL ⁻¹		yeasts at 1.5 x 10 ⁴ CFU mL ⁻¹	
	Incidence (%)	McKinney's Index (%)	Incidence (%)	McKinney's Index (%)
Control	100±0a	12.75±1.50a	100±0a	11.57±1.58a
<i>H. uvarum</i> Ale5	100±0a	6.12±0.83ab	100±0a	7.25±0.84ab
<i>M. pulcherrima</i> Ale4	9.52±13.47b	0.34±0.48b	14.29±16.66ab	0.51±0.42ab
<i>M. pulcherrima</i> Pr7	4.76±6.73b	0.34±0.24b	23.80±6.73ab	1.19±1.34ab

<i>L. thermotolerans</i> N10	4.76±6.73b	0.17±0.24b	0.00±0b	0.00±0b
<i>M. pulcherrima</i> N20/066	4.76 ±6.73b	0.17±0.24b	4.73±6.73b	0.17±0.24b

Table S4. Percentage of reduction in fresh weight of 'Red globe' berries treated with different yeast strains and SO₂ generator pads and stored at 0°C. Data are presented as mean of three replicates with standard deviation.

Yeast strain	Reduction in fresh weight (%)
Control	0.70±0.58
<i>M. pulcherrima</i> N20/006	1.78±0.17
<i>M. pulcherrima</i> Pr7	1.68±0.73
<i>H. uvarum</i> Ale5	1.11±0.80
<i>L. thermotolerans</i> N10	0.67±0.33
<i>M. pulcherrima</i> Ale4	1.61±0.11
SO ₂	0.84±0.44

Table S5. Incidence and McKinney's Index of sporulation of *B. cinerea* on pedicel of 'Red globe' berries treated with different yeast strains and SO₂ generator pads and stored at 0°C. Data are presented as mean of three replicates with standard deviation. Values within columns followed by the same letters are not significantly different (Turkey's test; P<0.05)

Yeast strain	SPI (%)	McKinney's Index (%)
Control	90.0±4.08 a	2.52±0.37 a
<i>M. pulcherrima</i> N20/006	90.0±7.07 a	1.54±0.29 b
<i>M. pulcherrima</i> Pr7	90.0±4.08 a	1.29±0.03 b

<i>H. uvarum</i> Ale5	81.67±6.23 a	1.27±0.21 b
<i>L. thermotolerans</i> N10	71.67±6.24 a	1.06±0.41 b
<i>M. pulcherrima</i> Ale4	66.67 ±6.24 a	0.11±0.11 b
SO ₂	0.00±0 b	0.00±0 c

Supplementary sequencing Data

1. Sequencing of 18S rDNA

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>Strain_N10

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>Strain_Pr7

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3. *M.pulcherrima* sequence analysis

3.1 Blast2 alignment

M.Pulcherrima_N20.006

Summary alignment IS1_vs_ITS4

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Sbjct 244	AAACTTTCAACAACGGATCTCTTGTTCTCGCATCGATGAAGAACGCAGCGAATTGCGAT	185		
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Summary Alignment.SAM

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M.Pulcherrima_Ale4

Summary alignment IS1_vs_ITS4

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Summary Alignment.SAM

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>lcl|consensus
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M.Pulcherrima_Pr7

Summary alignment IS1_vs_ITS4

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Summary Alignemtn.SAM

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>ld|consensus

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>Idl|Query_27305

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AATTAAAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGA
A

TTGCGATACGTAATATGACTTGCAGACGTGAATCATTGAATCTTTGAACGCACATTGCGC
CCCGGGGTATTCCCCAGGGCATGCGTGGGTGAGCGATATTTACTCTCAAACCTCCGGTTT
GGTCCTGCTTCGGCATAATATCAACGGCGCTAGAATAAGTTTTAGCCCCATTCTTTTCC
TCACCCTCGTAAGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAA

4. Multi-alignment *M.pulcherrima*_ClustalW (<https://www.genome.jp/tools-bin/clustalw>)

CLUSTAL 2.1 multiple sequence alignment

```
N20.006_consensus -----TACGAGGGTGAGGAAAAAGAATGG
Ale4_consensus -----TCTTACGAGGGTGAGGAAAAAGAATGG
Pr7_consensus  GGGTTCATACGCTTGACCTTCCTATAGCACGAACTCTAAATACTTAACCGTCAATAACAC
                  **  *  *  *
```

```
N20.006_consensus  GGCTAAAACCTTATTC--TAGCG---CCGTTGATATTATGCCGAAGCAGGACCAAACCGG
Ale4_consensus     GGCTAAAACCTTATTC--TAGCG---CCGTTGATATTATGCCGAAGCAGGACCAAACCGG
Pr7_consensus      AATTAAAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGC--G
                *****  ***  *  *  *  *  *  *  *  *  *  *  *
```

```
N20.006_consensus
AGGTTTGAGAGTAAATATCGCTCACCCACGCATGCCCTGGGGAATACCCCGGGGCGCAAT
Ale4_consensus     AGGTTTGAGAGTAAATATCGCTCACCCACGCATGCCCTGGGGAATACCCCGGGGCGCAAT
Pr7_consensus      AATTGCGATACGTAATATGACTTGCAGACGTGAATCATTG--AATCTTTGAACGCACATT
                *  *  *  *  *****  *  *  *  *  *  *  *  *  *  *  *
```

```
N20.006_consensus  GTGCGTTCAAAGATTCA--ATGATTACGTCTGCAAGTCATATTACGTATCGCAATTC--
Ale4_consensus     GTGCGTTCAAAGATTCA--ATGATTACGTCTGCAAGTCATATTACGTATCGCAATTC--
Pr7_consensus      GCGCCCCGGGGTATTCCCCAGGGCATGCGTGGGTGAGCGATATTTACTCTCAAACCTCCG
                *  *  *****  *  *  *  *  *  *  *  *  *  *  *
```

```
N20.006_consensus  GCTGCGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTT----TTAAT
Ale4_consensus     GCTGCGTTCTTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTT----TTAAT
Pr7_consensus      GTTTGGTCTGCTTCGGCATAATATCAACGG----CGCTAGAATAAGTTTTAGCCCCATT
                *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
```

N20.006_consensus TGTGTTATTGACGGTTAAGATTATAGAGTTTGTGCCTAAAAGTGTATCAAGT-GT-----
Ale4_consensus TGTGTTATTGACGGTTAAGATATTAGAGTTTGTGCCTAAAAGTGTACTAAGTTGKTTKT
Pr7_consensus CTTTTTCCTCACCTCGTAAGACTACCCGCTGAACTTAA--GCATATCAATAAGCGGAGG
 *

N20.006_consensus ----
Ale4_consensus TAAT
Pr7_consensus AAA-

