Biogeography of *Oenococcus oeni* reveals distinctive but non-specific populations in wine-producing regions

Mariette El Khoury, Hugo Campbell-Sills, Franck Salin, Erwan Guichoux, Olivier Claisse, Patrick M. Lucas

Supplemental material

FIG. S1. Phylogenomic tree based on 50 O. oeni genome sequences used to define groups of genetically related strains. The tree was obtained with ANIm using publicly available genome sequences as described in (1). Groups indicated in red were delineated on the basis of genetic distances between strains and named A1 to A6 and B1 to B3 to conform to group designations employed in (2).

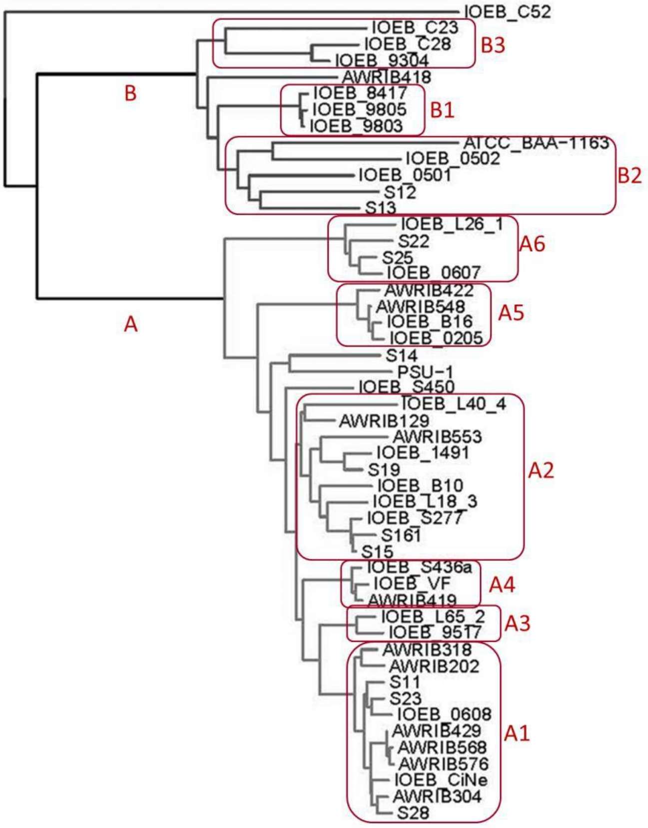

TABLE S1. SNPs used for Sequenom genotyping

Group	Number of SNPs per genetic group		
	Total	Manual preselection	Used for genotyping
A	1626	10	4
A1	198	10	5
A2	11	7	4
A3	164	9	5
A4	207	9	3
A5	808	10	2
A6	1181	7	2
B	1695	9	6
B1	130	10	5
B2	12	0	0
B3	70	13	4
Total	6120	94	40

TABLE S2. Primers used for SNP genotyping.

TERM	SNP_ID	2nd-PCRP	1st-PCRP	AMP_LEN	UP_CONF	MP_CONF	Tm	PcGC	PWARN	UEP_DIR	UEP_MASS
iPLEX	A1oeoe_0413_212	ACGTTGGATGTGGTTTCGTCGTTGGATCAC	ACGTTGGATGGTTTTCCGTATTTGCGTGCC	94	99.9	70.7	46.0	60.0	d	F	4553.0
iPLEX	A2oeoe0450_200	ACGTTGGATGAGTTGTATAAAGCGGCATGG	ACGTTGGATGTACACGCGATCGCAATCATC	109	98.2	70.7	55.0	73.3	D	R	4665.0
iPLEX	A3oeoe_0425_112	ACGTTGGATGAGCAAGGTGCTTTTTCCTCC	ACGTTGGATGTGGCAATCATCTGATCTTGG	119	97.1	70.7	47.8	56.2	D	R	5057.3
iPLEX	A3oeoe_0529_139	ACGTTGGATGGCCTCTTGAATCTGCTGCTT	ACGTTGGATGGGATAACTTGGAGGCGATTG	119	96.1	70.7	46.8	41.2	ds	R	5120.4
iPLEX	A3oeoe_0433_150	ACGTTGGATGGGTGTTTTCAGCTCTTTGCC	ACGTTGGATGAGCGAACCAAAGGCTTCCTG	109	98.2	70.7	46.2	53.3	D	F	5217.4
iPLEX	A5oeoe_0326_101	ACGTTGGATGATCGATATGCCCATGAACGG	ACGTTGGATGAAGGTTACCCTCCAACAGTC	100	100.0	70.7	49.4	56.2		R	5244.4
iPLEX	Boeoe_0402_105	ACGTTGGATGGCTCAAGATGATGCTTTTCC	ACGTTGGATGCGCTTAAATCAGCACGTTCC	111	98.1	70.7	46.1	47.1	D	F	5265.4
iPLEX	Boeoe_0340_216	ACGTTGGATGGGGATTTTTATGGATCGTGG	ACGTTGGATGACCAGGCCATCCAAAAGAAC	100	98.6	70.7	47.7	50.0	ds	F	5616.6
iPLEX	A4oeoe_0344_196	ACGTTGGATGCCGATTTTTGCGTACTTGCC	ACGTTGGATGTGCGTCATCCTCACATTGCC	111	98.1	70.7	46.9	36.8		R	5777.8
iPLEX	A5oeoe_0420_106	ACGTTGGATGCGCATTTCGCTGGGAATTCT	ACGTTGGATGGGTTATGCTTATGAAACCTG	107	91.8	70.7	46.0	42.1	D	R	5802.8
iPLEX	A2oeoe0450_176	ACGTTGGATGCGATGTTCCTGAAAATTGGG	ACGTTGGATGATTGCCAATTCGATGGCACC	94	98.4	70.7	48.0	44.4		F	5900.9
iPLEX	Boeoe_0456_151	ACGTTGGATGGGACATCCCAGTGGAAAATG	ACGTTGGATGGAATCAACTCCGAAGATCCG	102	100.0	70.7	47.2	35.0	D	R	6073.0
iPLEX	B1oeoe_0360_186	ACGTTGGATGTCTTGCGGAGTTGTTTTCGG	ACGTTGGATGTCTTCCAAAACCATTCGATG	97	94.3	70.7	46.0	35.0	d	F	6207.1
iPLEX	Aoeoe_0558_100	ACGTTGGATGTGTATCGTTCATCTGACCGC	ACGTTGGATGACCACCGCAACATATGCAAG	104	99.9	70.7	48.2	38.1	d	R	6349.2
iPLEX	A2oeoe0450_97	ACGTTGGATGAGAAGTGGATTGGTCTTCCC	ACGTTGGATGCCCAAACTGTTGCCCATATC	99	100.0	70.7	49.8	58.8	D	F	6376.2
iPLEX	A3oeoe_0424_156	ACGTTGGATGCCGGTCACAATAGTTGTATG	ACGTTGGATGAACAGGGGACACATGTCAAG	99	94.2	70.7	45.0	35.0	g	R	6500.2
iPLEX	A1oeoe_0449_29	ACGTTGGATGGTGCAGTAACCTGCACAATC	ACGTTGGATGGAAGATTTCGTTCTTATCG	85	86.8	70.7	45.2	36.8	D	R	6565.3
iPLEX	B1oeoe_0384_211	ACGTTGGATGTTTTTTTTGCTGCCAAGCGG	ACGTTGGATGGGGTCGACAAACTAATTGGG	87	97.9	70.7	49.1	31.8		R	6730.4
iPLEX	Aoeoe_0642_106	ACGTTGGATGGCATCCCAATCATTAAGGGC	ACGTTGGATGTCGGGTCGTATACAAAGGTC	106	99.9	70.7	46.7	38.1		F	6742.4
iPLEX	A2oeoe0450_37	ACGTTGGATGTTTGGGATTGGGTCGACCAG	ACGTTGGATGCGCCTCCATAGGCATAAAAG	92	98.3	70.7	47.1	44.4	d	F	6848.5
iPLEX	Aoeoe_0563_200	ACGTTGGATGTACTCGATTTGTCGTATCTC	ACGTTGGATGAATGCCTTTCAACACGCTGG	102	94.3	70.7	47.2	35.0	D	R	6949.5
iPLEX	B3oeoe_1166_150	ACGTTGGATGACCAAGTATCGGACCGATTG	ACGTTGGATGCCGAAAAATCGTCAAGCCTC	98	100.0	70.7	46.5	42.1	D	R	6952.5
iPLEX	B3oeoe_0574_239	ACGTTGGATGTTTGGAGATTAGCTTGGAAG	ACGTTGGATGCTATGCCTCCTGATTTAACG	111	92.6	70.7	48.8	50.0		F	7095.6
iPLEX	B1oeoe_0375_150	ACGTTGGATGAGCCACAAAGACAGGCAAAC	ACGTTGGATGGTCTGCTTGGTCAAAACCAG	108	99.7	70.7	49.3	29.2		F	7312.8
iPLEX	B1oeoe_0379_150	ACGTTGGATGGCCGTTTTTATCGGTTTGAC	ACGTTGGATGATCGCCGGTAACTATGAAGG	119	97.1	70.7	47.0	30.4		F	7381.8
iPLEX	A4oeoe_0390_191	ACGTTGGATGTTCTTAGCAGCAAAAGAGCG	ACGTTGGATGAACGACACTGCCTTTGAACG	112	98.0	70.7	51.0	38.1	DS	R	7560.9
iPLEX	A3oeoe_0370_150	ACGTTGGATGCCCTCTGTCGATATTTGTTG	ACGTTGGATGTCTACAACTCAAACAGAGGG	117	96.0	70.7	48.9	28.0		R	7612.0
iPLEX	Boeoe_0622_105	ACGTTGGATGCTTGCTTTATTGATCGTTCAG	ACGTTGGATGAAGAGAAAAGATAATATCAG	115	62.2	70.7	45.4	28.6	D	F	7742.0
iPLEX	B3oeoe_0490_154	ACGTTGGATGTTTGCCGACGATTTGTTGGG	ACGTTGGATGCGCCATGATTTGCTGGAAAC	116	99.0	70.7	48.7	36.4	D	R	7913.2
iPLEX	A6oeoe_0378_102	ACGTTGGATGGAAAAGCTACGTTATGGACTG	ACGTTGGATGTATTTTCTTGAGCCAGGCCC	120	93.0	70.7	49.4	38.1	h	F	8014.2
iPLEX	A1oeoe_0391_241	ACGTTGGATGTTAACAAGAGCCGAACAGAG	ACGTTGGATGTTCCGATTGAAACCGGAGTG	114	97.8	70.7	47.4	33.3	Ds	F	8048.3
iPLEX	A6oeoe_0423_179	ACGTTGGATGCAACCTTTTCAACAATTGGG	ACGTTGGATGGTTCGTGGCTCATTAGTTGG	114	93.6	70.7	53.8	47.8	Dg	R	8171.3
iPLEX	Aoeoe_0663_109	ACGTTGGATGAGCTCTGCCTCAAGAGAAAC	ACGTTGGATGGCGGCATCATACCCTAAATC	107	99.8	70.7	45.1	20.8		F	8317.5
iPLEX	B3oeoe_1057_150	ACGTTGGATGGCAACAACGCCTTTCATTAG	ACGTTGGATGGTTAAAGGATCGAGGCTCAC	110	98.2	70.7	45.9	30.4	D	F	8402.5
iPLEX	Boeoe_0357_114	ACGTTGGATGTGGACACATCGGATGAATGG	ACGTTGGATGGAGGCAGTCGTTTCATCAAC	99	100.0	70.7	54.4	47.8	D	F	8404.5
iPLEX	B1oeoe_0428_164	ACGTTGGATGTGCTGATTTTGTTTCACCAC	ACGTTGGATGCCTGAAAAAACAAGAGACGG	116	92.1	70.7	45.9	28.0	DH	F	8488.5
iPLEX	A1oeoe_0440_163	ACGTTGGATGTCAGTCATTGACCTCTTGGC	ACGTTGGATGCGCTGCCAAATCAATCAATG	113	97.9	70.7	50.9	33.3	DH	R	8553.6
iPLEX	Boeoe_0327_114	ACGTTGGATGGAACTCGCTTTCCAAATCTC	ACGTTGGATGTAACCGGAACCCAAATGACG	106	98.4	70.7	48.3	25.0	dh	R	8631.6
iPLEX	A4oeoe_0483_150	ACGTTGGATGGTTCTGGCTAATTGTGAAAC	ACGTTGGATGACCAAGTACCGGATTTGGAC	110	94.0	70.7	47.7	29.2	d	F	8710.7
iPLEX	A1oeoe_0469_150	ACGTTGGATGCCTGAAAACAGCTGTTAAAC	ACGTTGGATGTCAAGCCGCTTTCGGAAATC	97	88.2	70.7	53.4	40.0	dh	F	8878.8

Extension primer

TERM	SNP_ID	UEP_SEQ	EXT1_CALL	EXT1_MASS	EXT1_SEQ	EXT2_CALL	EXT2_MASS	EXT2_SEQ
iPLEX	A1oeoe_0413_212	CACCGATGGCCTATG	C	4800.2	CACCGATGGCCTATGC	T	4880.1	CACCGATGGCCTATGT
iPLEX	A2oeoe0450_200	GCGGCATGGTTGCGG	G	4912.2	GCGGCATGGTTGCGGC	A	4992.1	GCGGCATGGTTGCGGT
iPLEX	A3oeoe_0425_112	gCCTCCACCACTTTTGC	G	5304.5	gCCTCCACCACTTTTGCC	T	5328.5	gCCTCCACCACTTTTGCA
iPLEX	A3oeoe_0529_139	TCTGTTCAATTGCCACA	T	5391.6	TCTGTTCAATTGCCACAA	C	5407.6	TCTGTTCAATTGCCACAG
iPLEX	A3oeoe_0433_150	ggTTGGCGATCATGCTC	C	5464.6	ggTTGGCGATCATGCTCC	T	5544.5	ggTTGGCGATCATGCTCT
iPLEX	A5oeoe_0326_101	cTGAGGTCGACGACAGA	G	5491.6	cTGAGGTCGACGACAGAC	A	5571.5	cTGAGGTCGACGACAGAT
iPLEX	Boeoe_0402_105	GTTTTGGACAACGATGG	C	5512.6	GTTTTGGACAACGATGGC	T	5592.5	GTTTTGGACAACGATGGT
iPLEX	Boeoe_0340_216	tgTGGATCGTGGTTGGAT	C	5863.8	tgTGGATCGTGGTTGGATC	T	5943.7	tgTGGATCGTGGTTGGATT
iPLEX	A4oeoe_0344_196	GCGTACTTGCCAATTTTAA	G	6025.0	GCGTACTTGCCAATTTTAAC	A	6104.9	GCGTACTTGCCAATTTTAAT
iPLEX	A5oeoe_0420_106	CTGGGAATTCTTTCAGAAC	G	6050.0	CTGGGAATTCTTTCAGAACC	A	6129.9	CTGGGAATTCTTTCAGAACT
iPLEX	A2oeoe0450_176	tAAAATTGGGCAGATCGAG	A	6172.1	tAAAATTGGGCAGATCGAGA	T	6228.0	tAAAATTGGGCAGATCGAGT
iPLEX	Boeoe_0456_151	ACAGATTTTATTTTTCCGGC	G	6320.1	ACAGATTTTATTTTTCCGGCC	A	6400.1	ACAGATTTTATTTTTCCGGCT
iPLEX	B1oeoe_0360_186	AATATGGACAAAACGATGAG	C	6454.3	AATATGGACAAAACGATGAGC	T	6534.2	AATATGGACAAAACGATGAGT
iPLEX	Aoeoe_0558_100	GACCGCCATAAATACCTTTAT	G	6596.3	GACCGCCATAAATACCTTTATC	A	6676.3	GACCGCCATAAATACCTTTATT
iPLEX	A2oeoe0450_97	cccaGTCTTCCCGGAGAAACG	C	6623.3	cccaGTCTTCCCGGAGAAACGC	T	6703.2	cccaGTCTTCCCGGAGAAACGT
iPLEX	A3oeoe_0424_156	cATAGTTGTATGGCTAGGATA	T	6771.5	cATAGTTGTATGGCTAGGATAA	C	6787.5	cATAGTTGTATGGCTAGGATAG
iPLEX	A1oeoe_0449_29	cccCACCTCATTTTCCGATAAT	G	6812.5	cccCACCTCATTTTCCGATAATC	A	6892.4	cccCACCTCATTTTCCGATAATT
iPLEX	B1oeoe_0384_211	AGCGGATCACTTTTTTTGATAT	G	6977.6	AGCGGATCACTTTTTTTGATATC	A	7057.5	AGCGGATCACTTTTTTTGATATT
iPLEX	Aoeoe_0642_106	tGGCCTATACGGAAAATTAATC	A	7013.6	tGGCCTATACGGAAAATTAATCA	G	7029.6	tGGCCTATACGGAAAATTAATCG
iPLEX	A2oeoe0450_37	gaggCCAGGGACTTTTGAAGAA	A	7119.7	gaggCCAGGGACTTTTGAAGAAA	G	7135.7	gaggCCAGGGACTTTTGAAGAAG
iPLEX	Aoeoe_0563_200	cccTCTCTTAAATAACTTGGCGT	T	7220.7	cccTCTCTTAAATAACTTGGCGTA	C	7236.7	cccTCTCTTAAATAACTTGGCGTG
iPLEX	B3oeoe_1166_150	tccgGCATAACCTAAATTCCAGC	G	7199.7	tccgGCATAACCTAAATTCCAGCC	A	7279.6	tccgGCATAACCTAAATTCCAGCT
iPLEX	B3oeoe_0574_239	gggtcGCTTGGAAGTTTCACCAG	C	7342.8	gggtcGCTTGGAAGTTTCACCAGC	T	7422.7	gggtcGCTTGGAAGTTTCACCAGT
iPLEX	B1oeoe_0375_150	AACAAACTGTAACAATCGATTACT	A	7584.0	AACAAACTGTAACAATCGATTACTA	T	7639.9	AACAAACTGTAACAATCGATTACTT
iPLEX	B1oeoe_0379_150	gGATAATGATTTATTTCCTGCAGA	G	7669.0	gGATAATGATTTATTTCCTGCAGAG	T	7708.9	gGATAATGATTTATTTCCTGCAGAT
iPLEX	A4oeoe_0390_191	ccctAGCGCAATTTTTCAATCGAAC	G	7808.1	ccctAGCGCAATTTTTCAATCGAACC	A	7888.0	ccctAGCGCAATTTTTCAATCGAACT
iPLEX	A3oeoe_0370_150	CAACATTTTCTTGATTTTCGGATAT	G	7859.2	CAACATTTTCTTGATTTTCGGATATC	A	7939.1	CAACATTTTCTTGATTTTCGGATATT
iPLEX	Boeoe_0622_105	ggagAATTAATTGGTTTGTTTCCAG	C	7989.2	ggagAATTAATTGGTTTGTTTCCAGC	T	8069.1	ggagAATTAATTGGTTTGTTTCCAGT
iPLEX	B3oeoe_0490_154	ttgaAACTCTTCAATCGTATAAACCG	C	8200.4	ttgaAACTCTTCAATCGTATAAACCGG	A	8240.3	ttgaAACTCTTCAATCGTATAAACCGT
iPLEX	A6oeoe_0378_102	gggtgTTTGATTTTTGTCCTGACCAG	C	8261.4	gggtgTTTGATTTTTGTCCTGACCAGC	T	8341.3	gggtgTTTGATTTTTGTCCTGACCAGT
iPLEX	A1oeoe_0391_241	taCGAACAGAGATTATATTTAGTTGG	C	8295.4	taCGAACAGAGATTATATTTAGTTGGC	T	8375.4	taCGAACAGAGATTATATTTAGTTGGT
iPLEX	A6oeoe_0423_179	ccccCAATTGGGGTAACCTTACCTTCG	T	8442.5	ccccCAATTGGGGTAACCTTACCTTCGA	C	8458.5	ccccCAATTGGGGTAACCTTACCTTCGG
iPLEX	Aoeoe_0663_109	ccgGAATTAATTAAAAAAGCCAAAGAT	A	8588.7	ccgGAATTAATTAAAAAAGCCAAAGATA	G	8604.7	ccgGAATTAATTAAAAAAGCCAAAGATG

iPLEX	B3oeoe_1057_150	ggtgGCAAGAATTTTATTAAGGGATAC	A	8673.7	ggtgGCAAGAATTTTATTAAGGGATACA	G	8689.7	ggtgGCAAGAATTTTATTAAGGGATACG
iPLEX	Boeoe_0357_114	gggtGATGAATGGATTCGCAGTCGAAC	C	8651.6	gggtGATGAATGGATTCGCAGTCGAACC	T	8731.6	gggtGATGAATGGATTCGCAGTCGAACT
iPLEX	B1oeoe_0428_164	cccCTTTTCTATAATCATATGGCTAATG	A	8759.7	cccCTTTTCTATAATCATATGGCTAATGA	G	8775.7	cccCTTTTCTATAATCATATGGCTAATGG
iPLEX	A1oeoe_0440_163	ccacTTTTATGGCCTTGATAGTCAATGA	G	8800.8	ccacTTTTATGGCCTTGATAGTCAATGAC	T	8824.8	ccacTTTTATGGCCTTGATAGTCAATGAA
iPLEX	Boeoe_0327_114	agtaTTTATTTTTATTGCGCGAAAGATA	T	8902.9	agtaTTTATTTTTATTGCGCGAAAGATAA	C	8918.9	agtaTTTATTTTTATTGCGCGAAAGATAG
iPLEX	A4oeoe_0483_150	agttAAACAAATCAAGAAGTTAGAAGAG	C	8957.9	agttAAACAAATCAAGAAGTTAGAAGAGC	T	9037.8	agttAAACAAATCAAGAAGTTAGAAGAGT
iPLEX	A1oeoe_0469_150	ctgaCTGAAAACAGCTGTTAAACAAGCTC	A	9150.0	ctgaCTGAAAACAGCTGTTAAACAAGCTCA	G	9166.0	ctgaCTGAAAACAGCTGTTAAACAAGCTCG

TABLE S3. Concatenated SNPs sequences specific for the different genetic groups

Group	Concatenated sequence of 40 SNPs
A0	TCGAAGACATGCTGACGGCCACGATAGAACCGGTCCTAT
A0-1	TCGAAGACATGCTGACGGCCACGATAGAACCGGTCCCAT
A1	CTTGAGACATGCTGACGGCCACGATAGAACCGGTCCTAT
A1-1	CCTGAGACATGCTGACGGCCACGATAGAACCGGTCCTAT
A1-2	TTTGAGACATGCTGACGGCCACGATAGAACCGGTCCTAT
A1-3	TC-GAGACATGCTGACGGCCACGATAGAACCGGTCCTAT
A2	TCGATAGTATGCTGACGGCCACGATAGAACCGGTCCTAT
A2-1	TCGATAGTATGCTGACGGCCATGATAGAACCGGTCCTAT
A2-2	TCGATAGTATGCTAACGGCCACGATAGAACCGGTCCTAT
A2-3	TCGATAGTATGCTGGCGGCCACGATAGAACCGGTCCTAT
A2-4	TCGGTAGTATGCTGACGGCCACGATAGAACCGGTCCTAT
A2-5	TTGGTAGTATGCTGACGGCCACGATAGAACCGGTCCTAT
A2-6	TCGATAGTATGCTGACGGCCACGATAGAACCGGTCCCAT
A2-7	TCGATAGCATGCTGACGGCCACGATAGAACCGGTCCTAT
A2-8	TCGAAAGTATGCTGACGGCCACGACAGAACCGGTCCTAT
A3	TCGAAGACGCTTCGACGGCCACGATAGAACCGGTCCTAT
A3-1	TCGAAGACGTGTCGACGGCCACGATAGAACCGGTCCTA-
A4	TCGAAGACATGCTAGTGGCCACGATAGAACCGGTCCTAT
A4-1	TCGAAGACATGCTGGCGGCCACGATAGAACCGGTCCTAT
A5	TCGAAGACATGCTGACAACCACGATAGAACCGGTCCTAT
A5-1	TCGAAGACATGCTGACGACCACGATAGAACCGGTCCTA-
A6	TCGAAGACATGCTGACGGTTACGATAGAACCGGTCCTAT
B1	TCGAAGACATGCTGACGGCCGTAGCTTGGCCGGCTTCGC
B1-1	TC-AAGACATGCTGACGGCCGTAGCTTGACCGG-TTCG-
B1-2	TCGAAGACATGCTGACGGCCGTAGTTTAGCCGG-T-CG-
B2	TCGAAGACATGCTGACGGCCGTAGTAGAACCGGCTTCGC
B3	TCGAAGACATGCTGACGGCCGTAGTAGAAATAACTTCGC
B3-1	TCGAAGACATGCTGACGGCCGTAGTAGAAATGG-TTCG-
B3-2	TCGAAGACATGCTGACGGCCGTAGTAGAAATAG-T-CG-
B4	TCGAAGACATGCTGACGGCCGTAGTAGAACCGA-TTCG-
B5	TC-AAGACATGCTGACGGCCGTAGTAGAACCGGTTTTG-
C52	TCGAAGACATGCTGACGGCCGTAGTAGAACCGGTCCTAT
N1	TC-AAGACATGCTAACGGCCGCGGTAGAACCGGTCCTA-
N2	TC-AAGACATGCTGACGGCCGCGGTAGAACCGGTTCCA-
N3	TC-AAGACATGCTGACGGCCGCGGCAGGACCGGTTCTG-
N4	TC-AAGACATGCTGACGGCCGTGGTAGAACCGGTCCCA-
N5	TC-AAGACATGCTAACGGCCGTGGTAGAACCGG-CCTA-
N6	TC-AAGACATGCTAACGGCCGTGGTAGAACCGGTTCTA-
N7	TCGAAGACATGCTAACGGCCGTAGTAGAACCGGTCCCA-
N8	TC-AAGACATGCTGACGGCCGTAGTAGAACCGG-CTCGC
N9	TC-AAGACATGCTAACGGCCGTGGC-GAACCGGTTTTG-
N10	TC-AAGACATGCTAACGGCCGTGGTAGAACCGGTCTTG-
N11	TC-AAGACATGCTGACGGCCGTGGTAGAACCGGTTTTG-

References

1. **Campbell-Sills H, Khoury ME, Favier M, Romano A, Biasioli F, Spano G, Sherman DJ, Bouchez O, Coton E, Coton M, Okada S, Tanaka N, Dols-Lafargue M, Lucas**

PM. 2015. Phylogenomic analysis of *Oenococcus oeni* reveals specific domestication of strains to cider and wines. Genome Biol Evol **7**:1506–1518.

2. **Bilhère E**, **Lucas PM**, **Claisse O**, **Lonvaud-Funel A**. 2009. Multilocus sequence typing of *Oenococcus oeni*: detection of two subpopulations shaped by intergenic recombination. Appl Environ Microbiol **75**:1291–1300.