

## Supplementary Material

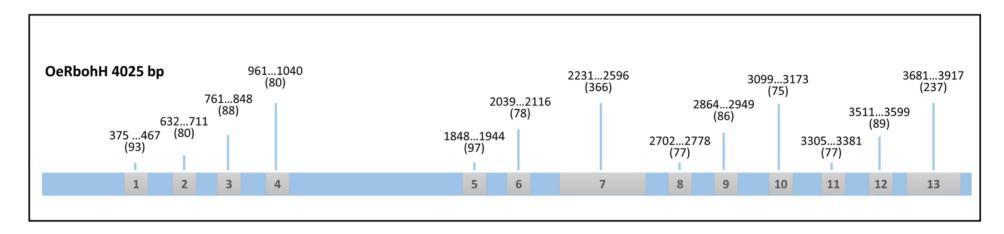
## Generation of superoxide by OeRbohH, a NADPH oxidase activity during olive (Olea europaea L.) pollen development and germination.

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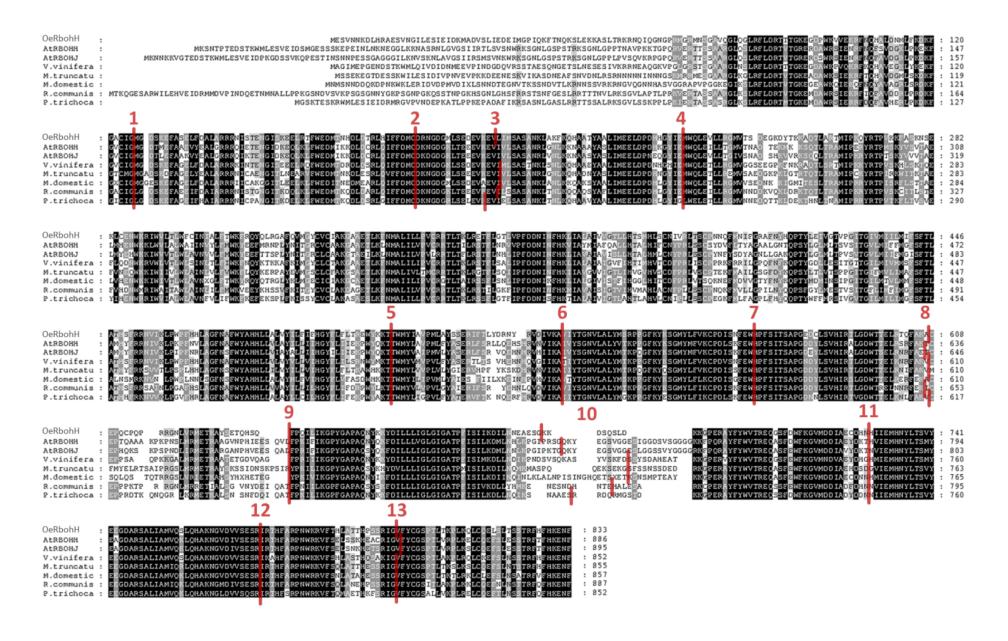
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OeRboh1804F							
AtrbohH	1787	AAAATTTGAATGGCATCCATTCTCCATCACTTCTGCACCAGGAGATGACTATTT	1841				
AtrbohJ	1817	CAAATTCGAATGGCATCCATTCTCCATCACTTCTGCACCCGGAGATGAATATTT	1871				
PtB9HCK1	1823	AAGTTTTGAATGGCATCCCTTCTCCATCACTTCTGCACCAGGAGATAACAATTT	1877				
PtB9IG58	1730	CAAGTTTGAATGGCATCCCTTCTCCATCACTTCTGCACCAGGAGATAACAATTT	1784				
OsA2WWR0	1709	TCCTTTCGAATGGCATCCCTTCTCCATCACTTCTGCACCTGGAGATGACTACCT	1763				
OsQ8S1T0	1709	TCCTTTCGAATGGCATCCCTTCTCCATCACTTCTGCACCTGGAGATGACTACCT	1763				
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AtrbohH	2249	TCAAAGAGCATATTTTTTTTGGGTGACAAGAGAACAAGCTTCCTTTGATTGGTT	2303				
AtrbohJ	2327	ACAAAGAGCATATTTTTATTGGGTGACAAGAGAACAAGCTTCTTTCGAATGGTT	2381				
PtB9HCK1	2129	AGAAAGAGCATACTTTTACTGGGTCACAAGAGAACAAAGCTCTTTTGATTGGTT	2183				
PtB9IG58	2147	AGAAAGAGCATACTTTTACTGGGTCACAAGAGAACAAAGTTCTTTTGATTGGTT	2201				
OsA2WWR0	2120	AGGAAGAGCTTACTTCTACTGGGTGACCAGAGAGCAAGGGTCCTTCGAGTGGTT	2174				
OsQ8S1T0	2120	AGGAAGAGCTTACTTCTACTGGGTGACCAGAGAGCAAGGGTCCTTCGAGTGGTT	2174				
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OeRboh2286R							

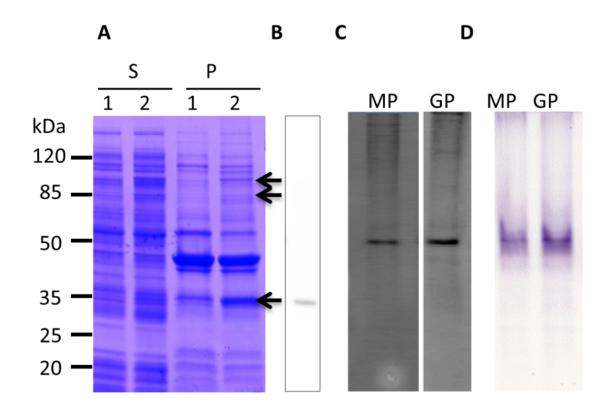
**Supplementary Figure 1.** Partial ORF alignment of homologous plant NOXs *from A. thaliana* (At5g60010, At3g45810), *P. trichocarpa* (PtB9HCK1, PtB9IGS8) and *O. sativa* (OsA2WWR0, OsQ8S1T0). Arrows indicate the conserved domains used to design degenerated primers forward and reverse.



**Supplementary Figure 2.** Genomic sequence of olive pollen *OeRbohH* with introns location (grey boxes). Location and length in bp (in brackets) are indicated.



**Supplementary Figure 3.** OeRbohH introns are conserved. Amino acid alignment of Rbohs from *A. thaliana*, *V. vinifera*, *M. truncatula*, *M. domestica*, *R. communis*, and *P. trichocarpa*. Introns location is conserved (red boxes).



**Supplementary Figure 4.** (A) SDS-PAGE of crude protein extracts of *E.coli* after induction of the expression. S: soluble fraction. P: precipitate; 1: negative control (pET51b); 2: expression construct (pET51b-OeRbohH). Arrows indicate the 3 bands which were later identified by LC-ESI-MS as such OeRbohH. (B) Western-blot using an anti-HisTag antibody in the insoluble fraction of the extract. (C) Western-blot using the anti-OeRbohH antibody in olive pollen protein extracts subjected to native-PAGE. The imuno-reactive band in the blot match the NADPH oxidase activity band in parallel in gel activity assays (D). MP, mature pollen; GP: germinated pollen.

Primer name	Sequence	Use	
OeRboh1804F	GAATGGCATCCMTTCTCCATCACTTC		
OeRboh2286R	TCTCTKGTSACCCARWARAARTAWGCTCTT	Degenerated primer plant Rbohs	
UPM long	CTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGT	Universal Primer for RACE 5' y RACE 3'	
UPM short	CTAATACGACTCACTATAGGGC		
PoliT24(A)	TTTTTTTTTTTTTTTTN	Race 3'	
OeRbohFW2	CTAATTGGTTTGGGAATTGGAGCAACCCC	RACE 3'	
OeRbohRW2	CTGACTAAGTTTCCCCTTCTTGGTTGTGGACACTGAGG	RACE 5'	
OeXbaRbohF	CGCTCTAGAATGGAATCAGTGAACAATAAAGATC	For coding genomic, pET51b and GFP vector cloning	
OeSacRbohR	GCCGAGCTCCAAAGTTTTCCTTGTGAAAATG	For coding genomic and pET51b vector cloning	
UTRRbohF	ATTGATATTCGTACTAGTATCTCAACAG		
UTRRbohR	AAAATGCGAGAATTTTACAAGTATTCAC	Gene expression studies	
Oe18S-F	TTTGATGGTACCTGCTACTCGGATAACC		
Oe18S-R	CTCTCCGGAATCGAACCCTAATTCTCC	Olive Housekeeping gene (ribosomal 18S)	
OeA-F	TTGCTCTCGACTATGAACAGG	Olive Housekeeping gene (actin)	
OeA-R	CTCTCGGCCCCAATAGTAATA		
OeqF	AGTGTCCACAACCAAGAAGG		
OeqR	ATGGGGTTGCTCCAATTC	For quantitative PCR	
OeRbohR	ACGTTCTAGAGAAAGTTTTCCTTGTGAAAATG	For GFP Vector cloning	
OeRboh-Ngo-F	ATAGCCGGCATGGAATCAGTGAACAAT		
OeRboh-Xma-RS	TATCCCGGGTCAAGCTCCAAAGTTTTC	For YFP Vector cloning	
OeRboh-Xma-RNS	TATCCCGGGTCCAGCTCCAAAGTTTTC		
OeRbohRW8	CCCATTTACAGATTCTGCTCTATGTAGATCTTTATTGTTC		
OeRbohRW7	GAAACATCAGCCATTTTATCAATCTCAATGCTCTCC		
OeRbohRW9	ATGAATTGTCCTGTCAAGGTGCTTATTGAGTCTTAGC	For OeRbohH promoter isolation	
OeRbohRW10	CGTCTCTCAAGATACAGCGAAATCTCCTTGCAGCAG		
pRboh1.8F	ATACTCGAGGCCCGGGGAGGTAT		
pRboh1.5F	TGCACTCGAGCGGGGGGGTACTTCTGCT		
pRboh0.7F	GCGCTCGAGTCCGAATTACGAGT	For pBI101 cloning	
pRboh0.2F	TGCACTCGAGGTAAGTTGGGGATCT		
pRbohR	TGCAAGATCTGACACTGACTGATTTCTCTGTTGAG		

	PROTEIN HITS	NAME [ORGANISM]	PEPTIDE
1	gi 56201942	Putative respiratory burst oxidase [Oryza sativa Japonica Group]	R.IGVFYCGSPTLTK.Q
	g1 30201942	Futative respiratory burst oxidase [Oryzu sutivu supomicu Group]	R.SALIAMVQSLQHAK.N
2			K.NGVDVVSESR.I
	gi 225435144	PREDICTED: putative respiratory burst oxidase homolog protein H-like [Vitis vinifera]	K.FN <u>M</u> ALILIPVCR.R +
			Oxidation (M)
			R.SALIAMVQSLQHAK.N
			R.SALIA <u>M</u> VQSLQHAK.N
			+ Oxidation (M)
	gi 171903618	Respiratory burst oxidase-like protein J [Hordeum vulgare subsp. vulgare]	R.IGVFYCGSPTLTK.T
			R.SALIAMVQSLQHAK.N
			R.SALIA <u>M</u> VQSLQHAK.N
			+ Oxidation (M)
		NOX1 [Striga asiatica]	K.NGVDVVSESR.I
	gi 109631188		R.EQGSFDWFK.G
			R.IGVFYCGSPTLTKPLK.K
			R.FHFHK.E
	gi 225435144		K.NGVDVVSESR.I
		[Vitis vinifera]	R.SALIAMVQSLQHAK.N
		PREDICTED: putative respiratory burst oxidase homolog protein H-like [Brachypodium distachyon]	R.FHFHK.E
	gi 357131247		R.EQGSFDWFK.G
			R.SALIAMVQSLQHAK.N
	gi 357505521	Respiratory burst oxidase-like protein [ <i>Medicago truncatula</i> ]	R.FHFHK.E
			K.NGVDVVSESR.I
			R.THFARPNWK.K
	gi 294462658 gi 18389310	Unknown [ <i>Picea sitchensis</i> ]  Respiratory burst oxidase protein F [ <i>Solanum tuberosum</i> ]	R.EEGSFDWFK.G
3			R.SALIA <u>M</u> LQALNHAK.H
			+ Oxidation (M)
			K.GIIELHNYCTSVYEEGDA
			R.S
			R.EQGSFDWFK.G R.THFARPNWK.K
	-	Danklanda Full Dansinskam kunsk suida a kanada suuskais Da	
	gi 166199744	RecName: Full=Respiratory burst oxidase homolog protein D; AltName: Full=NADPH oxidase RBOHD; AltName: Full=StRBOHD	R.EQGSFDWFK.G
			R.SALIAMLQSINHAK.N
	gi 356527324	PREDICTED: respiratory burst oxidase homolog protein C-like	R.EQGSFDWFK.G
		isoform 1 [Glycine max]	R.SALIAMLQSLNHAK.N
	gi 326491643	Predicted protein [Hordeum vulgare subsp. vulgare]	R.SALIAMLQSLNHAK.H
			K.GIIELHNYCTSVYEEGDA R.S
			K.AYFYWMTR.E
	gi 168011242	Predicted protein [Physcomitrella patens subsp. patens]	R.THFARPNWK.S
	1911100011747		IVITITI VIVE IN MIN'S

**Supplementary Table 2.** Identification from samples 1, 2 and 3 and peptide summary obtained by LC-ESI-MS/MS. Taxonomy: Viridiplantae (Green Plants).