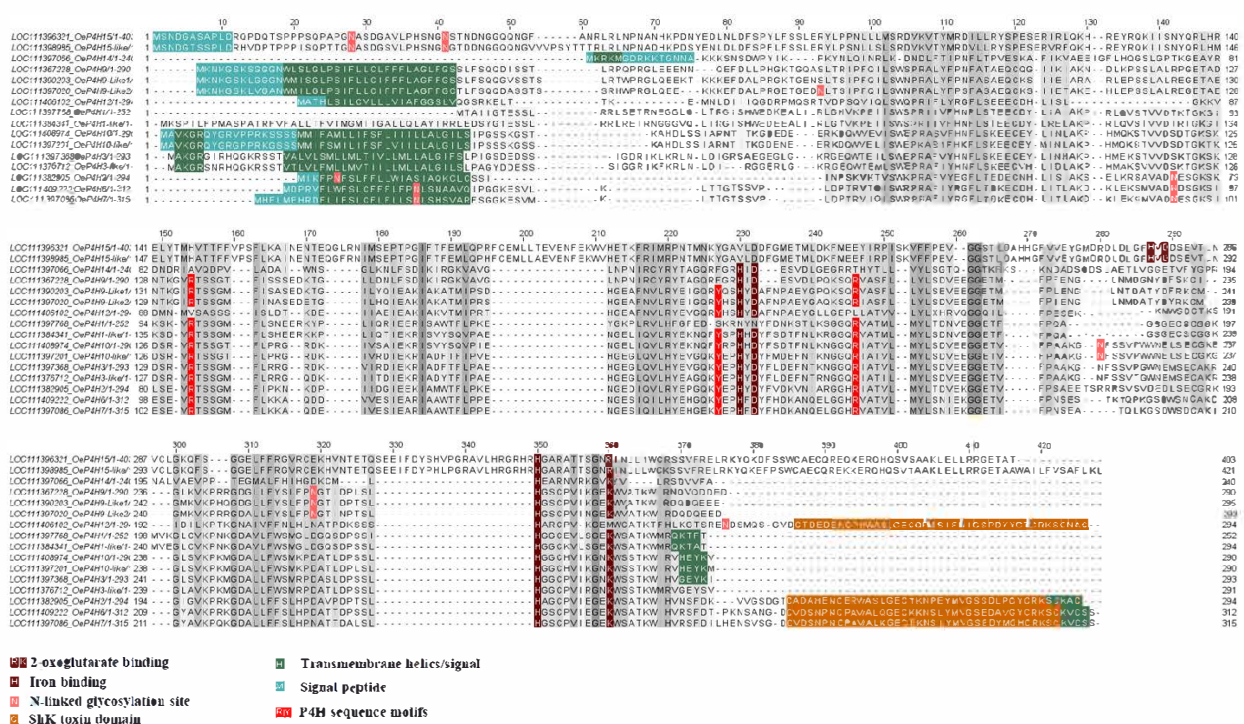




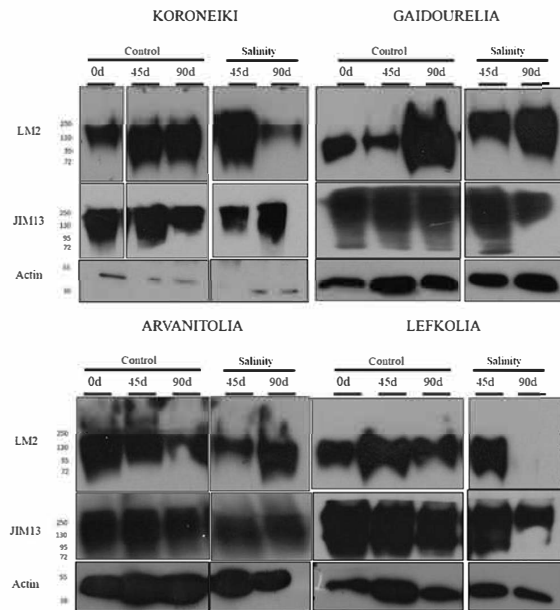
**Supplementary Figure S1.** Olive trees of Koroneiki, Lefkolia, Arvanitolia and Gaidourelia were placed in barrels of 90 cm long in four fertigation lines randomly for approximately one year to adapt to this environment and afterwards were subjected to NaCl treatment.



**Supplementary Figure S2.** CLUSTAL multiple sequence alignment of the *Olea Europea* putative P4Hs (OeP4Hs) amino acid residues highlighting the catalytic domain with its distinct functional domains and ER signal. The multiple sequence alignment shows the high similarity between P4H and P4H-like deduced amino acid sequences.



3<sup>rd</sup> Biological  
Replicate



**Supplementary Figure S5.** Western blot analysis of LM2- and JIM13-bound AGPs in roots of Arvanitolia, Lefkolia, Koroneiki and Gaidourelia olive cultivars under a salinity time course of the third biological replicate. Total proteins were extracted from roots of four cultivars olive trees after 45 (45d) and 90 days (90d) of control (untreated) and salinity treatment and 15  $\mu$ g from each sample were fractionated in SDS-PAGE for immunoblot analysis using LM2 and JIM13 antibodies and the actin antibody for loading control. The 0 day (0 d) refer to the un-treated control. The Molecular masses (kDa) are indicated on the left.

**Supplementary Table S1** Primary Protein sequence analysis of P4Hs and AGPs and protein domain prediction. P4Hc: Prolyl 4-hydroxylase, alpha subunit SM00702 (p4hc), ShKT: ShKT domain (IPR003582) SM00254 (ShkT\_1), Fe2OG\_Oxy: Oxoglutarate/iron-dependent dioxygenase (IPR005123) PF13640 (2OG-FeII\_Oxy\_3)

<i>Olea europaea</i>	Gene ID	Chromosome	Protein length	Exons Number	Homology to Arabidopsis	P4Hc	Fe2OG_Oxy	ShKT
Oe_P4H1	LOC111397768	7	253 aa	11	At_P4H1	54 - 248	132 - 249	-
Oe_P4H1-like	LOC111384341	un	294 aa	12	At_P4H1	95 - 290	177 - 289	-
Oe_P4H3	LOC111397368	7	293 aa	7	At_P4H3	89 - 288	169 - 287	-
Oe_P4H3-like	LOC111376712	un	291 aa	7	At_P4H3	87 - 285	167 - 285	-
Oe_P4H2	LOC111382905	un	294 aa	7	At_P4H2	40 - 241	120 - 240	284 - 294
Oe_P4H6	LOC111409222	14	312 aa	8	At_P4H6	58 - 256	139 - 255	302 - 312
Oe_P4H7	LOC111397086	7	315 aa	8	At_P4H7	62 - 258	143 - 257	305 - 315
Oe_P4H9	LOC111367228	18	293 aa	8	At_P4H9	88 - 286	172 - 285	-
Oe_P4H9-like1	LOC111390203	un	295 aa	8	At_P4H9	91 - 289	175 - 288	-
Oe_P4H9-like2	LOC111397020	7	293 aa	8	At_P4H9	89 - 287	173 - 286	-
Oe_P4H10	LOC111408974	14	290 aa	7	At_P4H10	86 - 285	166 - 284	-
Oe_P4H10-like	LOC111397201	7	290 aa	7	At_P4H10	86 - 285	166 - 284	-
Oe_P4H12	LOC111406102	12	293 aa	7	At_P4H12	63 - 236	172 - 293	253 - 293
Oe_P4H14	LOC111397066	1	240 aa	5	At_P4H14	40 - 238	118 - 240	-
Oe_P4H15	LOC111396321	6	403 aa	9	At_P4H15	176 - 355	257 - 356	-
Oe_P4H15-like	LOC111398985	8	421 aa	9	At_P4H15	182 - 361	263 - 362	-
Oe_AGP4-like	LOC111390511	un	142 aa	1	-	-	-	-
Oe_AGP10-like	LOC111400351	10	182 aa	3	-	-	-	-

**Supplementary Table S2** Protein sequence analysis and protein localization prediction \* XXRR-like motif in the N-terminus; \*\* KKXX-like motif in the C-terminus; cytoplasmic domain: membrane topology, type 2 cytoplasmic tail.

<i>Olea europaea</i>	Gene ID	N-terminal signal peptide position	Cytoplasmic domain position	ER Membrane Retention Signals	Transmembrane helices position	N- Glycosylation position
OeP4H1	LOC111397768	-	-	QKTF**	-	-
OeP4H1-like	LOC111384341	-	-	QKTA**	-	-
OeP4H3	LOC111397368	-	1 - 19	AKGR*, GEYK**	20 - 42	-
OeP4H3-like	LOC111376712	-	1 - 19	AKGR*	20 - 42	-
OeP4H2	LOC111382905	1 - 19	-	SCKA**	4 - 23	6, 73
OeP4H6	LOC111409222	1 - 23	1 - 5	DPRV*, KVCS**	5 - 23	19, 91
OeP4H7	LOC111397086	1 - 27	-	KVCS**	10 - 29	23, 95
OeP4H9	LOC111367228	1 - 35	-	-	13 - 35	258
OeP4H9-like1	LOC111390203	1 - 35	1 - 20	-	21 - 39	261
OeP4H9-like2	LOC111397020	1 - 35	1 - 11	-	12 - 34	76, 259
OeP4H10	LOC111408974	1 - 45	1 - 20	VKGR*, HEYK**	21 - 44	221
OeP4H10-like	LOC111397201	1 - 45	1 - 20	VKGR*, HEYK**	21 - 44	221
OeP4H12	LOC111406102	1 - 24	-	-	5 - 24	244
OeP4H14	LOC111397066	1 - 15	-	KRKM*	-	-
OeP4H15	LOC111396321	1 - 40	-	-	-	28, 41
OeP4H15-like	LOC111398985	1 - 40	-	AFLK*	-	28, 41

**Supplementary Table S3:** Table of primers used for the qPCR analysis.

Primers for qPCR	Sequence
OeP4H1 F	5' GGGACTTTCTTTGCTAGGTG 3'
OeP4H1 R	5' ACCGTTATTGTCGACCCATC 3'
Oe P4H2 F	5' GCCTTCTGTAGACTCCGTTTG 3'
OeP4H2 R	5' TCCCTGATCCCCATCAACTA 3'
OeP4H3 F	5' CATGGAGGTTGCCAGTTAT 3'
OeP4H3 R	5' TCTGGAAAGCAGTTGACCAC 3'
OeP4H6 F	5' CGGGAATTGACATCGTCGTA 3'
OeP4H6 R	5' CCCCATGCCAAGTGTAATGA 3'
OeP4H7 F	5' GGCCAATCAAGAACTAGGTGGTC 3'
OeP4H7 R	5' TCACTGCCCTTAAGCTGAGTTG 3'
OeP4H9 F	5' AGTGCAGGACGACGAAGATT 3'
OeP4H9 R	5' CTTGTGAGAGATGACGGATG 3'
OeP4H10 F	5' GGCTGCCATGTTATCAAAGG 3'
OeP4H10 R	5' AGTGCTGCTGAAATCCTCGT 3'
OeP4H1-like F	5' TTTTCTGGAGCATGGGGCTT 3'
OeP4H1-like R	5' AGGTCGCAGTTTTCTGTCTC 3'
OeP4H10-like F	5' AACAGAGGGTCAAGAATCGGT 3'
OeP4H10-like R	5' TAACTTGATCTGCCGACGCA 3'
OeP4H3-like F	5' AAGTTTGCATGGTGGTTGCC 3'
OeP4H3-like R	5' ATTCCCCAGGCAGCTAAACC 3'
OeP4H9-like F	5' TCTTCTCTCAGCAGGGAGTGT 3'
OeP4H9-like R	5' CCGTGGCAAAGCATCAAATTCT 3'
OeAGP4-like F	5' TTGCTGTGGCGTTGATGTAGTTT 3'
OeAGP4-like R	5' GGGTGGAGAGAATAAAGACAAGGG 3'
OeAGP9-like F	5' TACTCGGGCTCCAAGAAAGA 3'
OeAGP9-like R	5' CTGATGCGGGACTAGGAGAA 3'
OeAGP10-like F	5' CGCTCCAACACCATCTCCTT 3'
OeAGP10-like R	5' AGGAGCAGGAGGTGAAGACA 3'
Act7a F	5' AACGGAATCTCTCAGCTCCA 3'
Act7a R	5' TTGCTTACGTGGCACTTGAC 3'

**Supplementary Table S4:** Table of antibodies used for immunolocalization of homogalacturonans and arabinogalactan proteins.

Primary antibody	Epitope recognized	Secondary antibody
LM-20	fully methyl-esterified HGs	FITC-conjugated anti-rat IgG
LM-19	demethylesterified HGs and unesterified HGs.	FITC-conjugated anti-rat IgG
LM-18	partially methyl-esterified HGs	FITC-conjugated anti-rat IgG
JIM-7	partially methyl-esterified HGs	FITC-conjugated anti-rat IgG
JIM-5	methyl-esterified and unesterified HGs	FITC-conjugated anti-rat IgG
JIM-13	$\beta$ -Glc pA-(1 $\rightarrow$ 3)- $\alpha$ -GalA-(1 $\rightarrow$ 2)-Rha	FITC-conjugated anti-rat IgG