

Genome-scale signatures of adaptive gene expression changes in an invasive seaweed *Gracilaria vermiculophylla*

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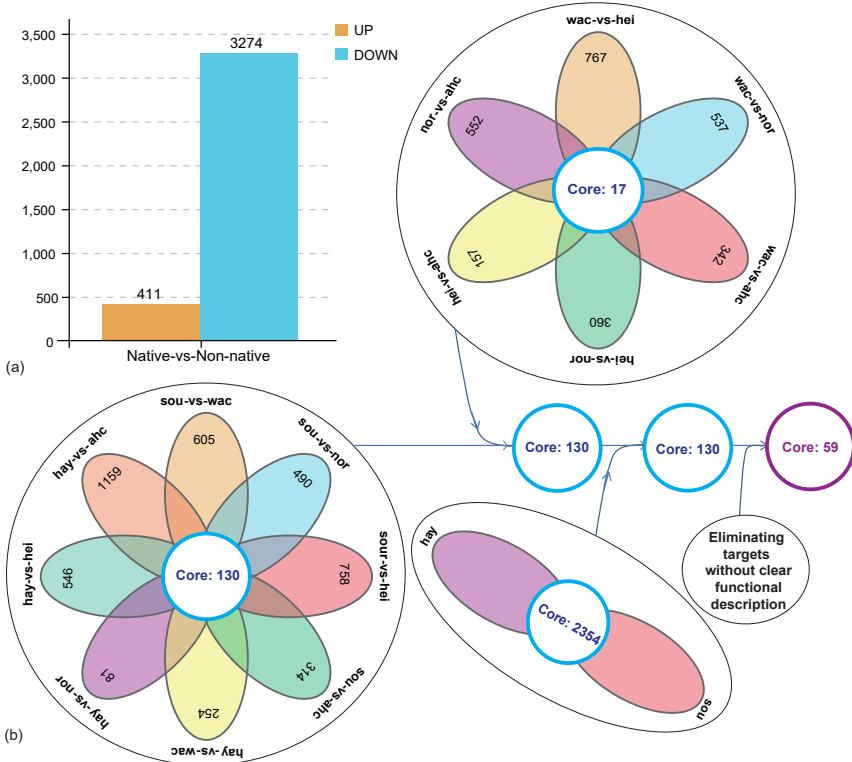
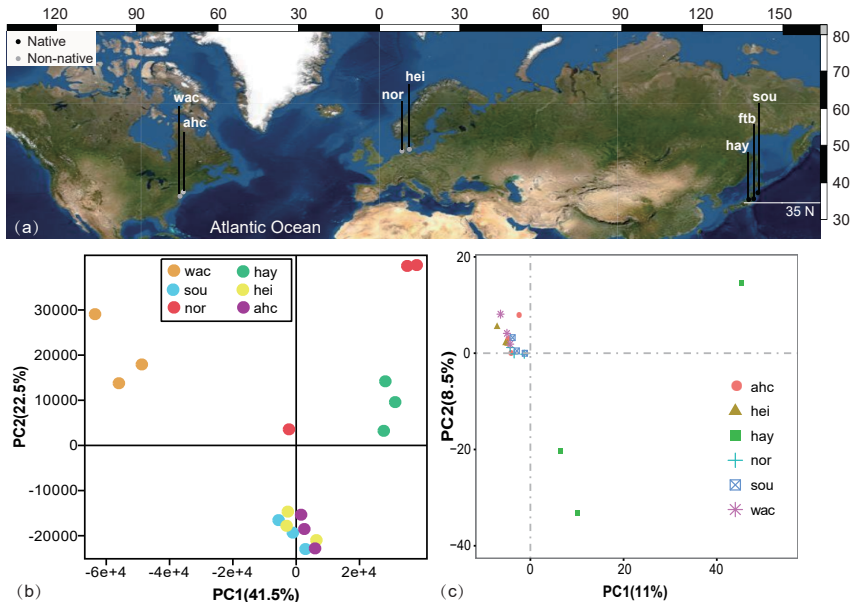
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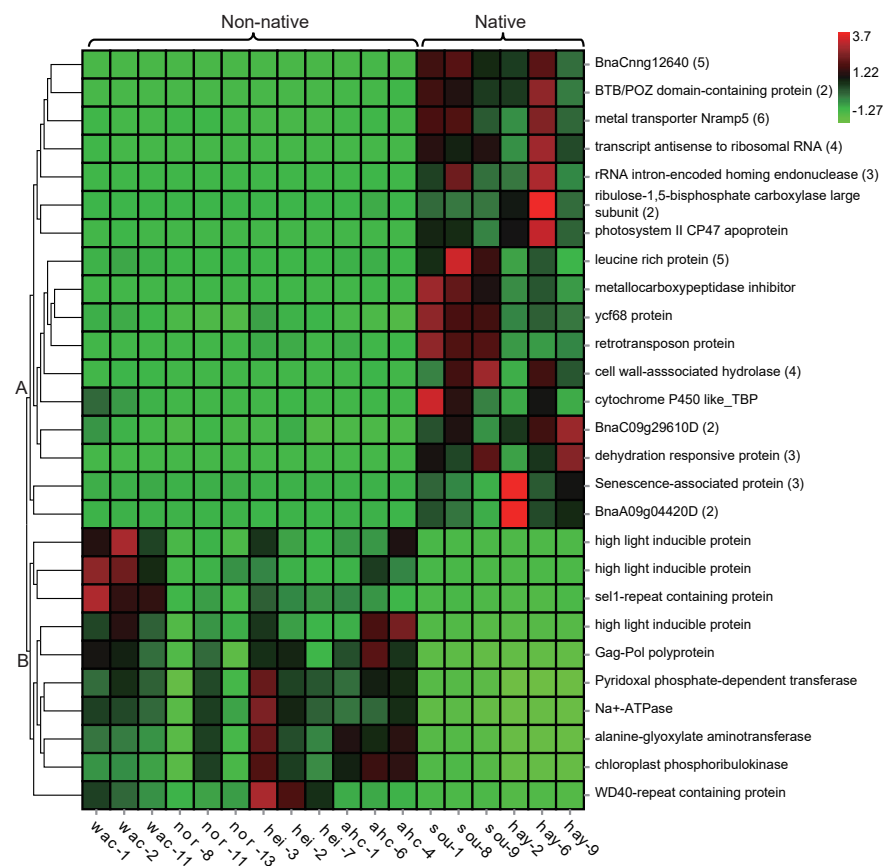
Abstract

Invasive species can successfully and rapidly colonize new niches and expand ranges via founder effects and enhanced tolerance towards environmental stresses. However, the underpinning molecular mechanisms (i.e., gene expression changes) facilitating rapid adaptation to harsh environments are still poorly understood. The red seaweed *Gracilaria vermiculophylla*, which is native to the northwest Pacific but invaded North American and European coastal habitats over the last 100 years, provides an excellent model to examine whether enhanced tolerance at the level of gene expression contributed to its invasion success. We collected *G. vermiculophylla* from its native range in Japan and from two non-native regions along the Delmarva Peninsula (Eastern United States) and in Germany. Thalli were reared in a common garden for four months at which time we performed comparative transcriptome (mRNA) and microRNA (miRNA) sequencing. mRNA-expression profiling identified 59 genes that were differently expressed between native and non-native thalli. Of these genes, most were involved in metabolic pathways, including photosynthesis, abiotic stress, and biosynthesis of products and hormones in all four non-native sites. MiRNA-based target-gene correlation analysis in native/non-native pairs revealed that some target genes are positively or negatively regulated via epigenetic mechanisms. Importantly, these genes are mostly associated with metabolism and defense capability. Thus, our gene expression results indicate that resource reallocation to metabolic processes is most likely a predominant mechanism contributing to the range-wide persistence and adaptation of *G. vermiculophylla* in the invaded range. This study therefore provides a novel molecular insight into the speed and nature of invasion-mediated rapid adaptation.

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(a)

Target genes	Description	sou	ahc		miRNAs	sou	ahc
Unigene0024406	rRNA intron- encoded homing endonuclease				miR10516-x		
Unigene0058350	Senescence - associated protein						
Unigene0089397					novel- m0070-5p		
Unigene0050668							
Unigene0003570	Cell wall - associated hydrolase				miR156-y		
Unigene0026853							
Unigene0003104							
Unigene0026840	Metal transporter Nramp5				miR8725-y		
Unigene0012348	Cytochrome P450- like TBP protein						
Unigene0019443							
Unigene0022103	Chlorophyll a-b binding protein CP24				miR2092-y		
Unigene0014240	Filamin				miR319-y		
Unigene0052343	LMYC1				miR384-x		
Unigene0007833	Zinc finger CCCH domain-containing protein 66				miR5564-x		
Unigene0019057	Ammonium transporter						

(b)

Target genes	Description	sou	hei		miRNAs	sou	hei
Unigene0069598	Metal transporter Nramp5				novel- m0007-3p		
					novel- m0008-3p		
Unigene0019913	Senescence - associated protein				novel- m0093-3p		

(a)

Target genes	Description	sou	hei		miRNAs	sou	hei
Unigene0001428	Metal transporter Nrap5				novel-m0007-3p		
Unigene0001741							
Unigene0002142							
Unigene0002574							
Unigene0002605							
Unigene0002756							
Unigene0002853					novel-m0008-3p		
Unigene0003064							
Unigene0015867							
Unigene0020594							
Unigene0034874							
Unigene0088927							
Unigene0090229							
Unigene0098833							
Unigene0119838							
Unigene0003167	PLC-like phosphodiesterase				novel-m0036-3p		
					novel-m0037-3p		
Unigene0048040	Ycf68 protein				novel-m0059-3p		
Unigene0081535							
Unigene0103594							

(b)

Target genes	Description	sou	ahc		miRNAs	sou	ahc
Unigene0049942	Senescence - associated protein				miR10516-x		
Unigene0074598					miR2092-y		
Unigene0095101					novel-m0204-5p		
Unigene0034760	Glycine dehydrogenase				miR156-y		
Unigene0002813	Ycf68 protein				miR414-y		
Unigene0048040					novel-m0059-3p		
Unigene0086427	Arginine kinase				miR7772-x		

(a)

Target genes	Description	sou	nor	miRNAs	sou	nor
Unigene0099127	Malate dehydrogenase			miR10436-x		
Unigene0078047	Na-ATPase			miR-172-x		
Unigene0002853	Metal transporter Nramp5			novel-m0007-3/novel-m0008-3		
Unigene0000360	Senescence-associated protein			novel-m0024-3		
Unigene0002313						
Unigene0002442						
Unigene0020936						
Unigene0020937						
Unigene0127920						
Unigene0012348	Cytochrome P450 like-TBP			novel-m0070-5		
Unigene0019443				novel-m0084-5		
Unigene0001023	Cell wall-associated hydrolase			novel-m0070-5		
Unigene0050668				novel-m0073-3		
Unigene0003058						
Unigene0008053						
Unigene0009393						
Unigene0029684						
Unigene0042638				novel-m0201-3		
Unigene0043650						
Unigene0045152						
Unigene0054537						
Unigene0066486						
Unigene0073511						
Unigene0081855						

(b)

Target genes	Description	sou	wac	miRNAs	sou	wac
Unigene0122308	Cytochrome P450 like-TBP			miR4405-y		
Unigene0001878				miR164-y		
Unigene0009487	Heat shock protein 90-2					
Unigene0052316	WD40-repeat containing protein			miR8725-y		
Unigene0026840	Metal transporter Nramp5			novel-m0007-3p		
Unigene0000836				novel-m0008-3p		
Unigene0002142				novel-m0093-3p		
Unigene0002547	Senescence-associated protein					
Unigene0049942						

(a)

Target genes	Description	sou	nor	miRNAs	sou	nor
Unigene0065108	GTP-binding protein			miR894-x		
Unigene0001428	Metal transporter Nrmp5			novel-m0007-3p		
Unigene0002574						
Unigene0002605						
Unigene0002756						
Unigene0003064				novel-m0008-3p		
Unigene0034874						
Unigene0088927						
Unigene0098833						
Unigene0000172	Senescence-associated protein			novel-m0024-3p		
Unigene0000823						
Unigene0002713						
Unigene0002808						
Unigene0003004						
Unigene0010949						
Unigene0013261						
Unigene0034337						
Unigene0056345						
Unigene0001878	Cytochrome P450 like-TBP			novel-m0070-5p		
Unigene0091064						
Unigene0002052	ATP synthase subunit alpha			novel-m0073-3p novel-m0201-3p		
Unigene0026718						
Unigene0036522						
Unigene0090761						

(b)

Target genes	Description	sou	wac	miRNAs	sou	wac
Unigene0003071	Cytochrome P450 like-TBP			miR4405-y		
Unigene0126402	WD40-repeat containing protein			miR5021-x		
Unigene0007833	Zinc finger CCCH domain-containing protein			miR5564-x		
Unigene0017715	Beta-lactamase domain protein			miR8614-y		
Unigene0002574	Metal transporter Nrmp5			novel-m0007-3p novel-m0008-3p		
Unigene0002756						
Unigene0002853						
Unigene0003064						
Unigene0088927				novel-m0169-5p novel-m0170-5p		
Unigene0068938						
Unigene0078047	Na⁺-ATPase					
Unigene0019355	Leucine rich protein					