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

Jing-Xi Xiang[1], Saha Mahasweta [2], Kei-Le Zhong[3], Quan-Sheng Zhang[1], Di Zhang[1], Alexander Jueterbock[4], Stacy Krueger-Hadfield[5], Gao-Ge Wang[6], Florian Weinberger[2], and Zi-Min Hu[1]

[1]Yantai University
[2]GEOMAR Helmholtz-Zentrum für Ozeanforschung Kiel
[3]Institute of Oceanology Chinese Academy of Sciences
[4]Nord University
[5]University of Alabama at Birmingham
[6]Ocean University of China

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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 adaption.

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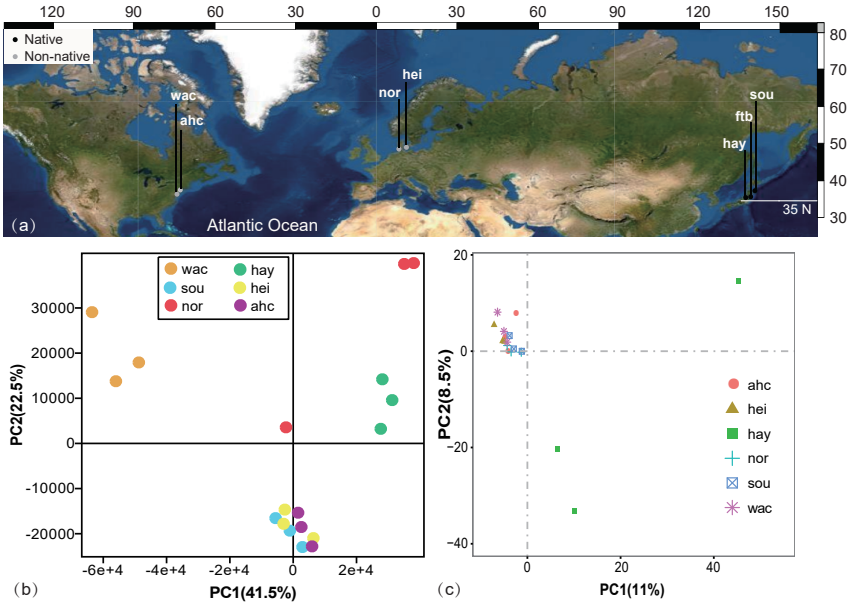

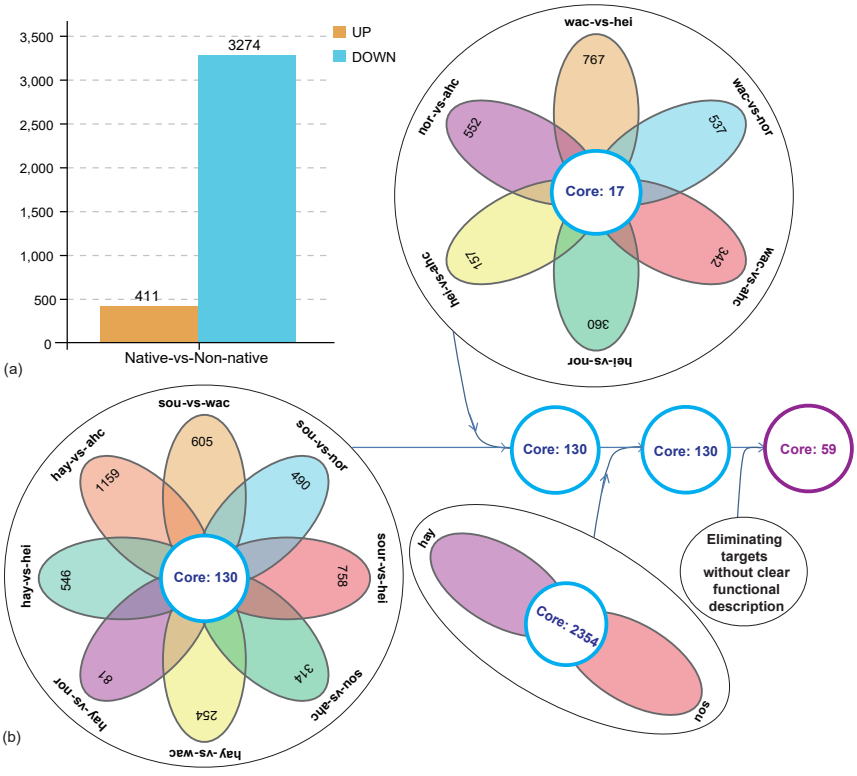

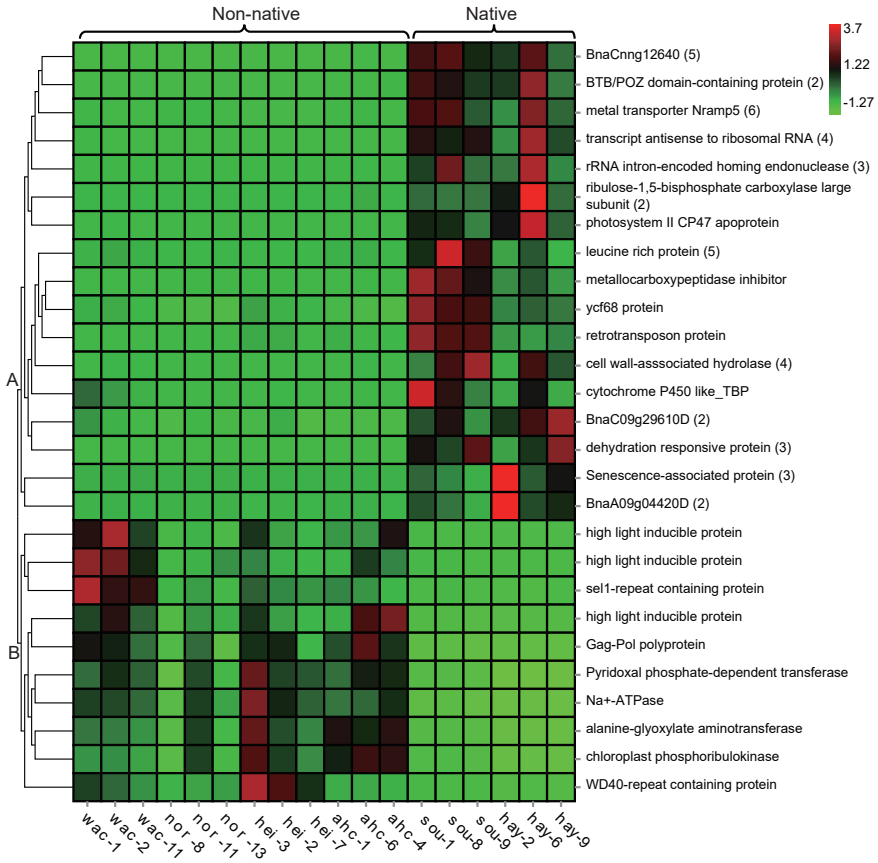

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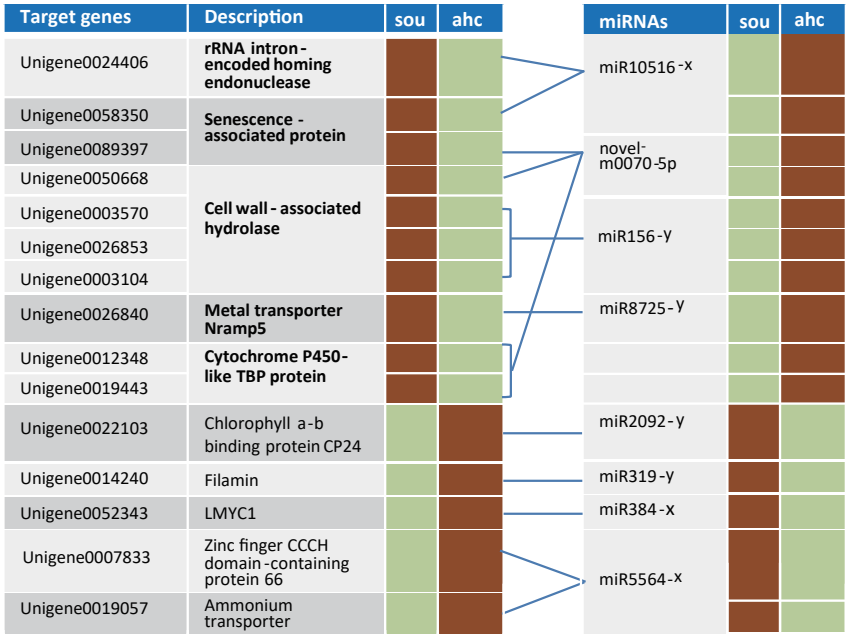

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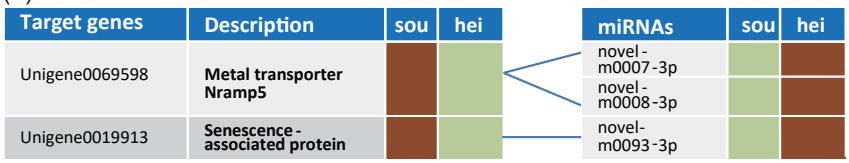

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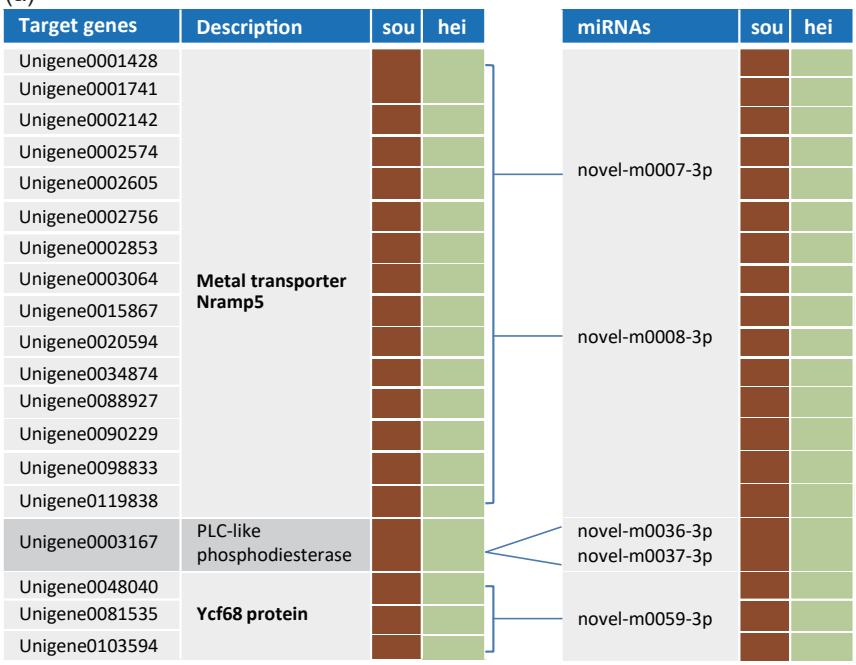

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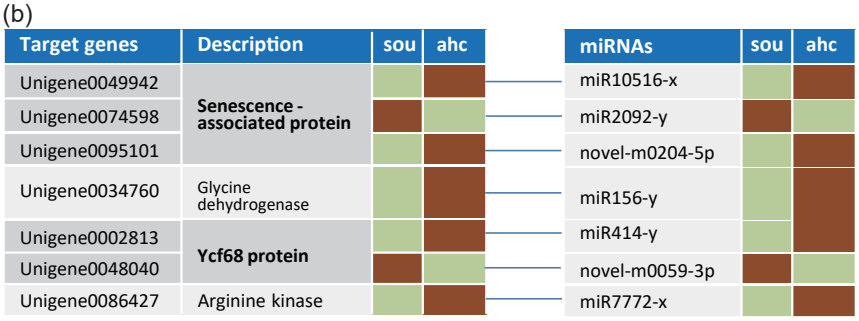

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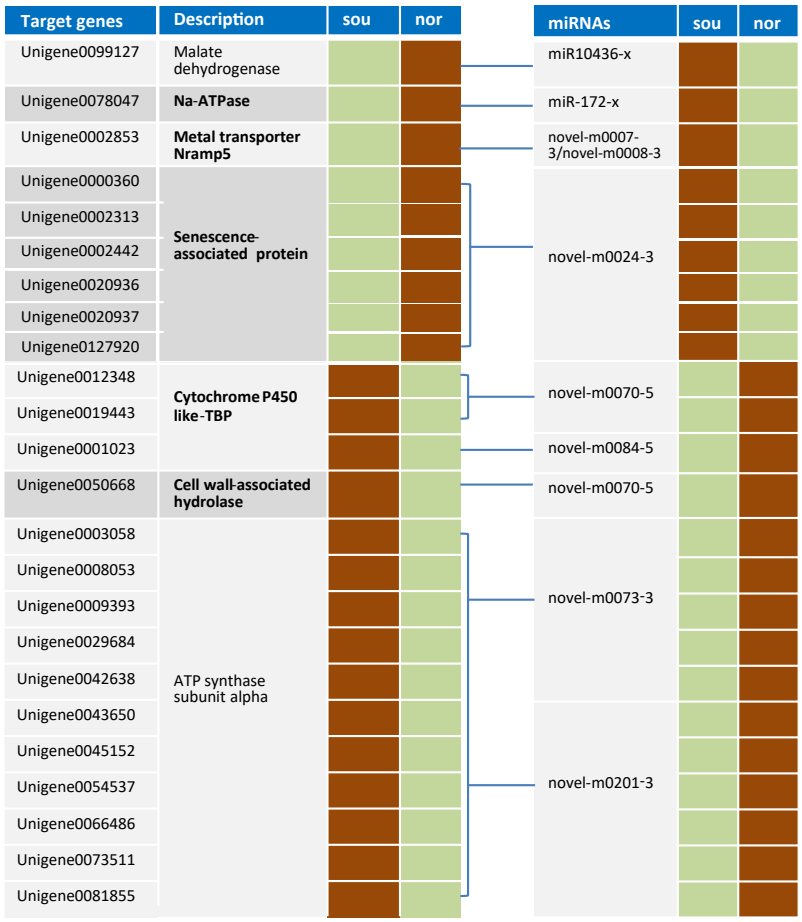

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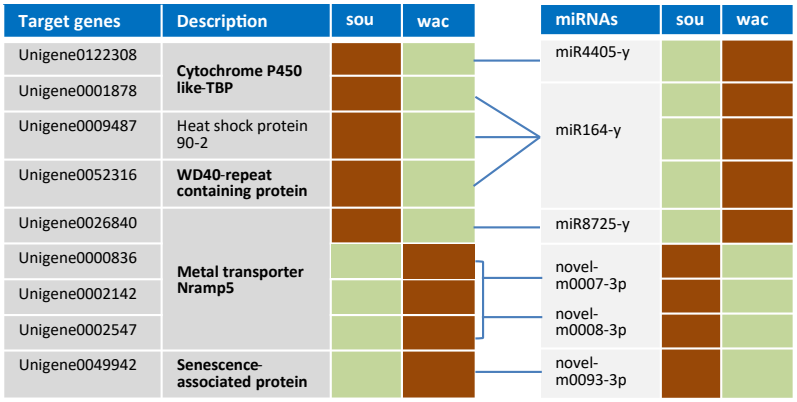

(a)

Target genes	Description	sou	nor	miRNAs	sou	nor
Unigene0065108	GTP-binding protein			miR894-x		
Unigene0001428	**Metal transporter Nramp5**			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		
Unigene0026718				novel-m0201-3p		
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 Nramp5**			novel-m0007-3p		
Unigene0002756						
Unigene0002853				novel-m0008-3p		
Unigene0003064						
Unigene0088927						
Unigene0068938						
Unigene0078047	**Na^+-ATPase**			novel-m0169-5p		
Unigene0019355	**Leucine rich protein**			novel-m0170-5p		