Table S1 The distribution information of the shared haplotypes (Hm1-Hm 94) (COI + 16S) in *Monodonta labio* and *M. confusa*. P indicate the number of the private haplotypes in each population. The bold text represents the haplotypes found in *M. confusa*.

	AD	CF	CG	GJ	KM	MZ	OK	PH	SI	SY	TD	WW	YG
P	12	10	11	4	8	12	10	16	6	14	5	6	12
Hm1	1												
Hm2	1												
Hm3	1					1							
Hm4	1												
Hm5	1							1					
Hm6	1												
Hm7	1												
Hm8	1												
Hm9	1												
Hm10	1												
Hm11	1												
Hm12	1												
Hm13		1											
Hm14		1											
Hm15		4		1									
Hm16		1											
Hm17		1											
Hm18		1											
Hm19		1											
Hm20			1										
Hm21			1										
Hm22			1										
Hm23			1										
Hm24			1		2	1							
Hm25			2			1							
Hm26			1										
Hm27			1										
Hm28			1										
Hm29			1		1	1		1				1	
Hm30				1									
Hm31				1									
Hm32				1									
Hm33					1								
Hm34					1								

	1	2	3	4	5	6	7	8
Hm35	1							
Hm36	1							
Hm37	1							
Hm38		1						
Hm39		**1**						
Hm40		**1**						
Hm41		1						
Hm42		**1**						
Hm43		**1**					**1**	
Hm44		1						
Hm45		1		3				
Hm46			2					
Hm47			1					
Hm48			1					
Hm49			1					
Hm50			1					
Hm51			1					
Hm52			1					
Hm53			1					
Hm54			1					
Hm55				1				
Hm56				1				
Hm57				1				
Hm58				**1**				
Hm59				**2**				
Hm60				**1**				
Hm61				**1**				
Hm62				**1**				
Hm63				1				
Hm64				1				
Hm65					1			
Hm66					2			3
Hm67					1			1
Hm68					1			
Hm69					1			
Hm70						4		
Hm71						1		
Hm72						1		
Hm73						2		
Hm74						2		
Hm75						1		

Hm76	1			
Hm77	2			
Hm78		**1**		
Hm79		**1**		
Hm80		**1**		
Hm81		**1**		
Hm82			1	
Hm83			1	
Hm84			1	
Hm85			1	
Hm86			1	
Hm87				1
Hm88				1
Hm89				1
Hm90				**1**
Hm91				**1**
Hm92				**1**
Hm93				1
Hm94				1

Table S2. The haplotype information downloaded from NCBI.

IA	IB	ALONE	IIA	IIB	IIC
LC316325.1	KU849166.1	LC316297.1	KU848845.1	KU848844.1	KU848833.1
LC316492.1	KU849198.1	LC316475.1	KU849468.1	KU849426.1	KU849559.1
3089mlya1	ZH19	1252mlhiro4	DS10	DS09	CD22
LC316326.1	KU849169.1	LC316281.1	KU849101.1		KU848943.1
LC316493.1	KU849180.1	LC316462.1	KU849255.1		KU849377.1
3090mlya2	ZH22	1421MLhmnk	XP13		JZ14
KU848794.1	KU849025.1	LC316296.1	KU848840.1		KU848818.1
KU849521.1	KU849343.1	LC316474.1	KU849419.1		KU849560.1
BH09	PT15	1251mlhiro3	DS05		CD06
KU848795.1	KU848843.1	LC316282.1	KU849097.1		KU848814.1
KU849494.1	KU849462.1	LC316463.1	KU849246.1		KU849558.1
BH10	DS08	1423MLhmnk	XP09		CD02
KU848798.1	KU849007.1	LC316298.1			KU849048.1
KU849531.1	KU849283.1	LC316476.1			KU849572.1
BH13	NB21	1255mlhiro6			QD17
KU848797.1	KU848897.1	LC316318.1			KU849038.1
KU849525.1	KU849231.1	LC316488.1			KU849581.1
BH12	DT14	67Mltsushima			QD07
	KU848896.1	LC316319.1			KU848945.1
	KU849172.1	LC316489.1			KU849335.1
	DT13	68Mltsushima			JZ16
	KU848774.1	LC316322.1			KU848946.1
	KU849303.1	LC316490.1			KU849318.1
	AJ06	3648mlfuku1			JZ17
	KU849167.1	LC316323.1			KU848944.1
	KU849207.1	LC316491.1			KU849323.1
	ZH20	3650mlfuku3			JZ15
	KU849005.1				KU848829.1
	KU849331.1				KU849565.1
	NB19				CD17
	KU848842.1				KU848826.1
	KU849453.1				KU849557.1

DS07	CD14
KU849024.1	KU848947.1
KU849325.1	KU849366.1
PT14	JZ18
	LC316264.1
	LC316450.1
	Monodonta confusa mcak1
KU849004.1	LC316264.1
KU849368.1	LC316450.1
NB18	*Monodonta confusa* mcak1
	LC316261.1
	LC316448.1
	Monodonta confusa 779mcawa
KU848841.1	
KU849460.1	
DS06	
KU848771.1	
KU849374.1	
AJ03	
KU849022.1	
KU849391.1	
PT12	
KU849008.1	
KU849312.1	
NB22	
KU848772.1	
KU849381.1	

AJ04

KU848894.1

KU849193.1

DT11

KU848894.1

KU849193.1

DT11

KU849023.1

KU849250.1

PT13

KU849006.1

KU849345.1

NB20

U849021.1

KU849393.1

PT11

MF979254.1

MF979294.1

DCL4

KU849102.1

KU849363.1

XP14

KU848895.1

KU849230.1

DT12

KU849098.1

KU849401.1

XP10

KU848893.1

KU849209.1

DT10

KU848773.1

KU849376.1

AJ05

MF979253.1

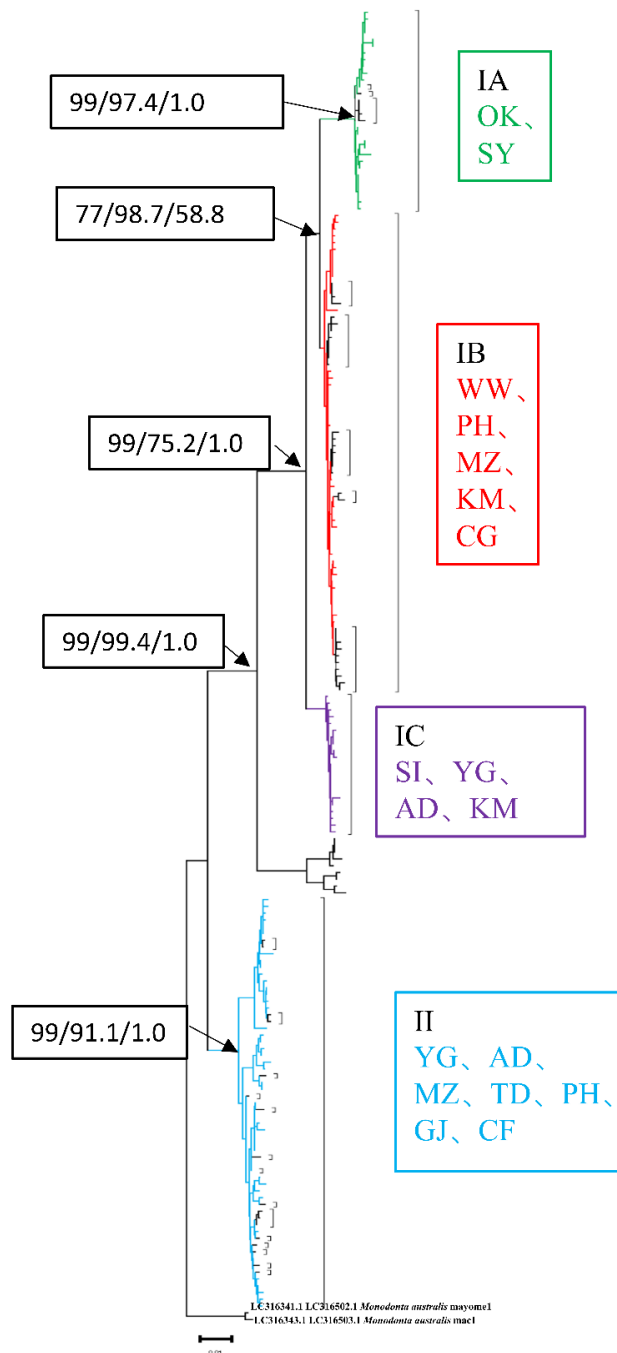MF979293.1

DCL3

KU849170.1

KU849192.1

ZH23

Figure S1. The phylogeny of *Monodonta labio* (Lineage I) and *M. confusa* (Lineage II) was reconstructed using neighbor-joining (NJ) analyses based on the mitochondrial COI + 16S gene. This analysis involved a total of 126 haplotypes, including 68 sequences obtained from NCBI and 94 haplotypes derived from our study. The numbers above each branch are the posterior probabilities for bootstrap values for the NJ, ML, and Bayesian analyses. The haplotypes marked in black on the phylogenetic tree are haplotypes downloaded from NCBI. Please refer to the table S2 for the haplotype information downloaded from NCBI.