

Table S1. Blind test: PCR-RFLP and analysis of the ITS2 sequences from eighteen pearls of unknown identity.

Pearl sample	Pearl weight (carats / mg)	Sample weight (mg) ^a	ITS2-RFLP ^b results	ITS2 ^b rRNA sequence match	GenBank accession number	Correctly identified?
BL1	16.8 / 3358	103	<i>P. maxima</i>	<i>P. maxima</i> (AY883851.1) ^c 461 bp (100 %) ^d	KF284027	yes
BL2	10.5 / 2092	158	<i>P. margaritifera</i>	<i>P. margaritifera</i> (AY877506.1) 292 bp (100 %)	KF284028	yes
BL3	10.1 / 2012	61	<i>P. maxima</i>	<i>P. maxima</i> (AY877504.1) 492 bp (99 %)	KF284029	yes
BL4	9.2 / 1834	115	<i>P. margaritifera</i>	<i>P. margaritifera</i> (AY877506.1) 437 bp (100 %)	KF284030	no
BL5	9.1 / 1816	165	Not determined	Not determined		no
BL6	8.8 / 1754	146	<i>P. radiata</i>	<i>P. fucata</i> ^e (AB214478.1) 207 bp (100 %)	KF284031	yes
BL7	8.3 / 1658	417	<i>P. radiata</i>	<i>P. fucata</i> (AY877582.1) 538 bp (99 %)	KF284032	yes
BL8	7.8 / 1550	672	<i>P. margaritifera</i>	<i>P. margaritifera</i> ^f		yes
BL9	7.3 / 1456	178	<i>P. radiata</i>	<i>P. fucata</i> (AY877582.1) 511 bp (99 %)	KF284033	yes
BL10	6.8 / 1354	38	<i>P. margaritifera</i>	<i>P. margaritifera</i> ^f		yes
BL11	6.6 / 1324	547	<i>P. margaritifera</i>	<i>P. margaritifera</i> (AY877506.1) 437 bp (100 %)	KF284034	yes
BL12	6.0 / 1198	154	<i>P. margaritifera</i>	<i>P. margaritifera</i> (AY877506.1) 435 bp (100 %)	KF284035	yes
BL13	5.8 / 1154	615	<i>P. margaritifera</i>	<i>P. margaritifera</i> (AY877506.1) 437 bp (100 %)	KF284036	yes
BL14	4.3 / 868	142	<i>P. maxima</i>	<i>P. maxima</i> (AY877505.1) 494 bp (100 %)	KF284037	yes

BL15	4.3 / 856	84	<i>P. maxima</i>	<i>P. maxima</i> (AY877505.1) 494 bp (100 %)	KF284038	yes
BL16	4.1 / 818	184	<i>P. radiata</i>	<i>P. fucata</i> (AY877582.1) 489 bp (99 %)	KF284039	yes
BL17	3.3 / 652	170	<i>P. radiata</i>	<i>P. fucata</i> (AY877582.1) 538 bp (99 %)	KF284040	yes
BL18	2.5 / 504	88	<i>P. radiata</i>	<i>P. fucata</i> (AY877582.1) 489 bp (99 %)	KF284041	yes

^a the sample used for DNA extraction consisted of material extracted from the interior of the pearl, including ground nacre and OM.

^b ITS2: nuclear internal transcribed spacer 2 located between the 5.8S and 28S ribosomal RNA genes. RFLP: restriction fragment length polymorphism.

^c *Pinctada* species assignment was based on the highest BLAST score (highest query coverage and maximal base pair identity). GenBank accession number shown in brackets.

^d amplicon size (base pair) and maximal identity (%) of the sequence to the BLAST query.

^e *P. fucata* is conspecific to *P. radiata* according to their ITS sequences [50].

^f sample had low sequence quality, but the BLAST query in GenBank recovered the correct *Pinctada* species.