SUPPLEMENTARY 1

Confirmation of Ceriops tagal by cpDNA

The genus *Ceriops* is composed of several morphological-similar species: *C. tagal*, *C. decandra*, and *C. australis*. Except the *C. australis* that distributed in the Australia, Papua New Guinea, and Indonesia (Sheue, Yang *et al.* 2009), *C. tagal* and *C. decandra* were sympatrically distributed in the tropical coasts from the eastern Africa to the northern Australia (Tomlinson 1986), including the area of the South China Sea. The confirmation of the accurate sampling is necessary and the cpDNA *trn*L-*trn*F was used firstly for distinguishing them by constructing a neighbor joining (NJ) tree. The NJ trees were preformed by MEGA4 (Kumar, Tamura *et al.* 2004) with the settings of pairwise deletion for indels and maximum composite likelihood model for generating distance matrix. The amount of support for monophyly of clades was evaluated with 1000 bootstrap replicates.

Five *C. decandra* samples that collected at the Trat (TR) and Surat Thani (ST) were composed of two haplotypes (trnLF 18 and trnLF 19) that grouped well with 93% supports in bootstrapping. All the other samples that identified as *C. tagal* in morphology were also grouped in one clade that was composed of 17 haplotypes in the NJ tree (Fig. S1). We assumed that the samples that identified as *C. tagal* came from a single evolutionary lineage in cpDNA and did not introgressed from other species based on the inference from the NJ tree. Based on this assumption, the population genetic structures of the lineage of *C. tagal* were analyzed and discussed then.

References

Kumar S, Tamura K, Nei M (2004) MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. *Briefings in Bioinformatics* **5**, 150-63.

Sheue CR, Yang YP, *et al.* (2009) Reevaluating the taxonomic status of *Ceriops australis* (Rhizophoraceae) based on morphological and molecular evidence. *Botanical Studies* **50**, 89-100.

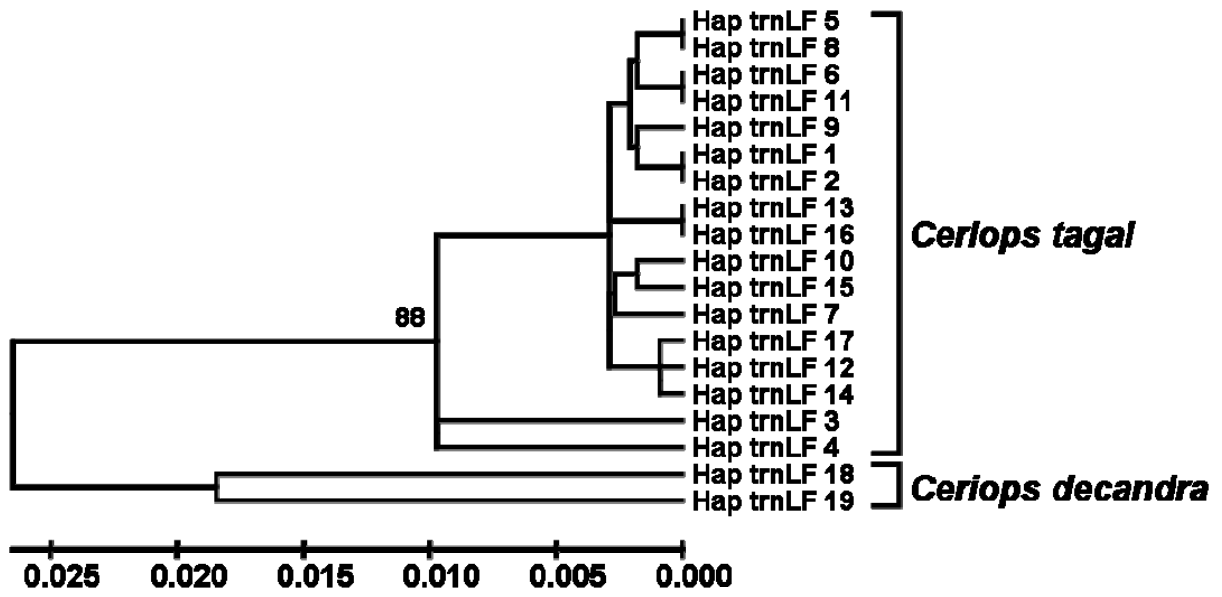Tomlinson PB (1986) 'The Botany of Mangroves.' (Cambridge of University Press: Cambridge)

Figure S1 Haplotype Unweighted-Pair-Group-Method-with-Arithmetic-mean (UPGMA) tree of *trn*L-*trn*F spacers of cpDNA in confirming the single evolutionary lineage of samples of *Ceriops tagal* from the sister species *C. decandra*.

Sampling strategy

Populations of *Ceriops tagal* in the Gulf of Thailand are distributed in a limited manner along the east and west sides of the gulf. The coasts of Bangkok, located around the upper Gulf of Thailand, are overdeveloped and lack natural populations of *C. tagal*. Despite the abundant resources of mangroves around the Gulf of Thailand, many mangrove forests are afforestation or nearby them. For preventing the artificial interference on the genetic analyses, those forests which might be gene mixed with the afforested trees were abandoned for sampling. Only the forests which were confirmed as natural populations were selected as sampling sites. Because of the limited distribution of the remnant *C. tagal* populations in the Gulf of Thailand, only six populations were available: Trat (TR), Khlung (KH), Mu Ko Chumphon National Park (MK), Surat Thani (ST), Thungkra-Swi Amphur Sawi (SW), and Tumethong Amphur Patew (PT) (Table 1 and Fig. 1 in the main text). The other populations were assuming as extinct populations in nature in this study. TR and KH are located in the eastern Gulf of Thailand, which contains a very small number of populations. The other four populations are located in the western Gulf of Thailand. These four populations are remnants of natural populations of eastern gulf, while other populations due to modern restoration efforts. On the other hand, populations of *C. tagal* in the north boundary of distribution in the Hainan Island were sampled in comparative with the indicative of diversity centre (the Gulf of Thailand). The Hainan Island is distributed at the northern South China Sea and has an area *c.* 32,000 km^2, about one tenth the size of the Gulf of Thailand. Like the Gulf of Thailand, the coasts of the Hainan Island are over-exploitation and several estuaries are developed as harbors. Five populations of *C. tagal* located at the northwestern [Guantsun (GT) and Lingao (LG)], northeastern [Wenchang (WCH) and Donzhaigan (DJ)], and the southern Hainan [Yalongwang (YL)] were sampled (Table 1 and Fig. 1). The sampling was along rivers and only adult individuals with diameter at breast height (DBH) over 5 cm were collected in preventing the sampling bias (identical by descent). Due to the limitation of the salty-tolerance, there is very narrow width of the distribution of *C. tagal* around the riversides. Between 6 and 19 samples and between 8 and 25 samples were collected per population in the Gulf of Thailand and in the Hainan Island, respectively, depending on the overall population size. A total of 126 samples (61 in the Gulf of Thailand and 65 in the Hainan Island) were collected across all populations. The coasts of the Vietnam (the western South China Sea) which locates between the Hainan Island and the Gulf of Thailand are mostly composed of

rocky coasts and unsuitable for the growth of mangrove forests. The distribution of the *C. tagal* at the Hainan Island and the Gulf of Thailand becomes a disjunct distribution in fine scale.

SUPPLEMENTARY 3

Hierarchical clades of the TCS network

Haplotypes of the TCS network were sorted according to hierarchical clades with the assistance of the ANeCA software (Panchal, 2007). Six levels of hierarchical clades were constructed (Figure S2). The third-level clades were used for drawing the haplotype frequency in Figure 1, and the third-level clades were represented in Figure 3.
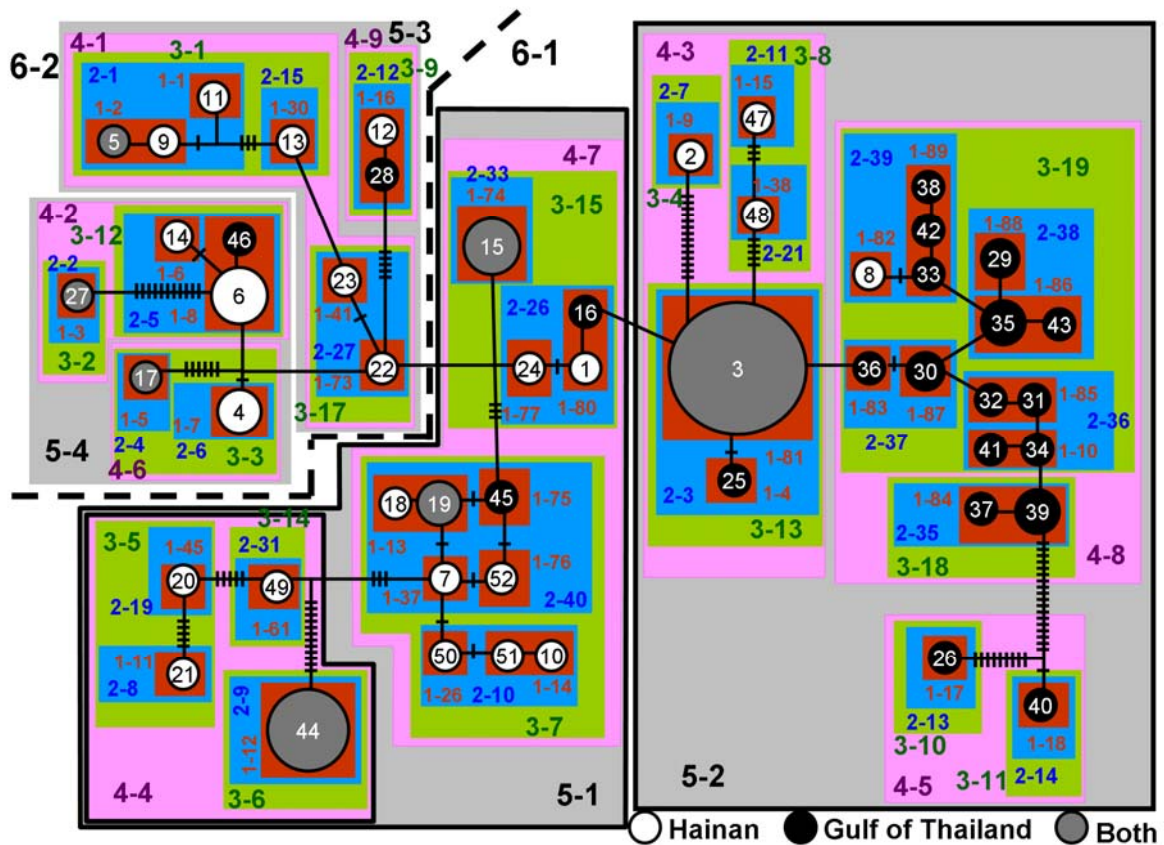

Figure S2. TCS network of *Ceriops tagal* haplotypes in the Gulf of Thailand obtained by combining *atp*B-*rbc*L and *trn*L-*trn*F spacer data. Hierarchical clades that have biogeographic inferences with significant supports are shown in black frame.

Reference

Panchal M. 2007. The automation of nested clade phylogeographic analysis. *Bioinformatics,* **23**: 509-510.