

Fig. 1: Sampling locations of snakehead wild and culture populations in Cambodia and Viet Nam

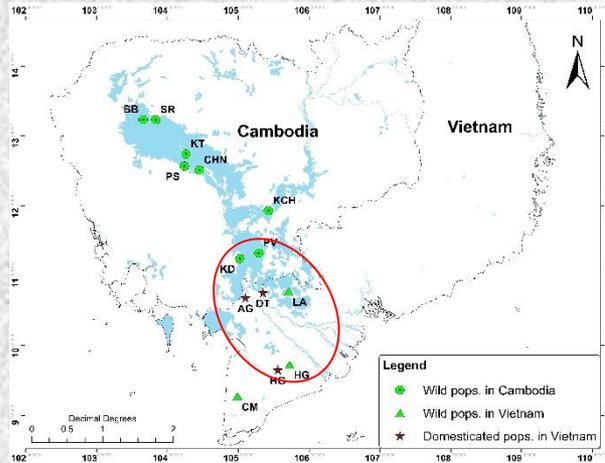


Table 1: Genetic diversity of three groups (Cambodian, VN-cultured and VN-wild) of populations based on cytochrome b gene

Populations	Haplotype number	Haplotype diversity	Nucleotide diversity
Cambodia (N=145)	23	0.760 ± 0.033	0.00239
VN-Wild (N = 58)	8	0.561 ± 0.003	0.00115
VN-Culture (N = 59)	2	0.034 ± 0.033	0.00006
Total	28	0.620 ± 0.034	0.00169

Implications for snakehead domestication and genetic improvement

- Wild snakehead in Cambodia is a good source for domestication and farming.
- VN snakehead sources should not be used for domestication and aquaculture in Cambodia because of lower genetic diversity.
- Genetic diversity of snakehead broodstock in Cambodia should be monitored regularly during the process of domestication and aquaculture.
- Cultured snakehead populations in VN should be genetically improved.

“Genetic diversity of striped snakehead (*Channa striata*) in Cambodia and Vietnam”.

Characterizing and comparing genetic diversity of wild snakehead populations in Cambodia to Vietnamese domesticated and wild populations can provide basic information and wise recommendations for striped snakehead domestication and selection breeding and farming in Cambodia, and Viet Nam.

Snakehead samples were collected from 5 locations in the Tonle Sap floodplains (Siem Reap, SR; Battambang, BB; Kampong Thom, KT; Pursat, PS; and Kampong Chnang, CHN) and three locations in the Mekong River floodplains (Kampong Cham, KCH; Kandal, KD; Prey Veng, PV). In Viet Nam (VN), fish were collected in 3 hatcheries (in Dong Thap DT, An Giang AG, and Hau Giang HG) and wild populations in Long An (LA), Hau Giang (HG), and Ca Mau (CM) (Fig. 1).

Findings from sequence data of mitochondrial DNA genes (Cytochrome b and D-loop region) from 15-20 individuals per each of 14 populations showed consistent results:

- Genetic diversity was highest in Cambodian wild populations, followed by VN wild ones and lowest in VN culture fish (Table 1).
- Genetic differences of Cambodian populations grouped as a whole were significant compared to VN cultured and wild populations. In a smaller scale, however, two populations KD and PV in Mekong River floodplains did not genetically differ from VN cultured and wild populations located along Mekong River (circled, Fig. 1), except one (Ca Mau) far away from the Mekong River.
- VN cultured populations also differed (small magnitude) from VN wild ones.
- No genetic difference observed among VN cultured populations

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