functions. From all 19 variables used in this study, the highest coefficient value was observed for variables B, C, A, K, L, S, and D, with the values of 0.356, -0.336, 0.531, -0.407, 0.658, 0.571 and 0.718, respectively. The variable B represents the measurement from snout to insertion of the pelvic fin, variable C represents above the eye to insertion of the pelvic fin, variable A represents snout to above the eye, variable K represents the origin of the anal fin to the origin of anal soft rays, variable L represents origin of dorsal soft rays to origin of anal soft rays, variable S represents the end of anal soft rays to the caudal fin, and variable D represents above the eye to the origin of the dorsal fin.

Stock identification is fundamental to fisheries and hatchery management. Fish stock is referring to a group of fish large enough to be self-reproduce and the members of the group having similar life history (Deka and Gupta, 2013). Fish stocks are identified based on differences between characteristics belonging to different groups (Dantas et al., 2013).

Morphological characteristic is among other methods used in stock identification. Body shape and measurement of particular morphological features of various dimensions in the body part is included as morphological characteristics.

From 19 truss measurement used in this study, it shows evidence of a highly significant morphological difference in *A. testudineus* populations. The DFA analysis (Figure 2) shows the significance level of differentiation between wild and hatchery populations. Based on the DFA analysis of wild and hatchery *A. testudineus* population in this study, these populations showed different morphological characteristics that enable them to be discriminated from each other. This evidence suggested that wild and hatchery *A. testudineus* belonged to a different stock. Even though the hatchery population may be originated from wild populations, but they have morphologically changed due to several factors affecting their changes (Pimentel, 1967).

Table 2: The summary of eigenvalue, canonical correlation, and Wilk's lambda attained from morphological differences between hatchery and wild populations of *A. testudineus*

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation	Wilks' Lambda	Chi-square	df	Sig.
1	134.137[a]	91.6	91.6	0.996	0.000	1090.358	133	0.000
2	6.299[a]	4.3	95.9	0.929	0.008	543.307	108	0.000
3	3.781[a]	2.6	98.5	0.889	0.056	321.673	85	0.000
4	1.982[a]	1.4	99.8	0.815	0.267	147.204	64	0.000
5	0.104[a]	0.1	99.9	0.307	0.796	25.390	45	0.992
6	0.081[a]	0.1	100.0	0.273	0.879	14.379	28	0.984
7	0.053[a]	0.0	100.0	0.224	0.950	5.725	13	0.956

a. First seven canonical discriminant functions were used in the analysis

Table 3: Functions at group Centroids/ Means of canonical variances scores from morphological differences between hatchery and wild populations of *A. testudineus*

Region	F1	F2	F3	F4	F5	F6	F7
Johor	1.986	-1.147	0.110	**3.635**	0.046	-0.012	0.000
Kedah	11.792	1.973	**2.897**	-0.453	-0.011	0.004	-0.008
Kelantan	-0.799	**5.123**	-3.210	0.052	-0.002	-0.047	-0.017
Selangor	**13.432**	-2.920	-1.830	-0.877	-0.006	0.012	0.016
Wild Johor	-13.213	-0.816	0.532	-0.397	-0.528	-0.386	**0.384**
Wild Kedah	-12.775	-0.766	0.293	-0.332	-0.490	0.452	-0.375
Wild Kelantan	-13.043	-0.369	0.371	-0.538	**0.530**	0.456	0.336
Wild Selangor	-12.901	-1.125	0.544	-0.681	0.466	**0.479**	-0.341

* Unstandardised canonical discriminant functions evaluated at group means

Table 4: Standardised Canonical Discriminant Function Coefficients scored based on morphometric characters of hatchery and wild *A. testudineus* populations

Variables	F1	F2	F3	F4	F5	F6	F7
B	**0.356**	-0.102	-0.074	-0.162	0.081	0.080	-0.117
C	0.351	**-0.336**	-0.094	-0.031	-0.154	0.331	-0.212
A	0.069	0.168	**0.531**	-0.304	0.495	0.016	-0.075
K	0.102	0.063	-0.039	**-0.407**	0.157	0.065	0.257
L	0.043	-0.004	0.104	-0.291	**0.658**	0.215	-0.138
H	0.274	-0.066	-0.083	-0.184	0.650	-0.019	0.034
E	0.093	-0.162	0.180	-0.175	0.530	0.112	0.096
I	0.216	-0.062	0.029	-0.297	0.509	0.116	0.079
R	0.100	0.048	-0.213	0.024	0.463	0.118	-0.222
J	0.109	-0.009	0.176	-0.307	0.437	0.194	0.163
G	0.166	-0.022	0.028	0.116	0.396	-0.50	0.293
P	0.039	0.034	0.105	0.104	-0.280	-0.175	-0.057
F	0.165	-0.198	-0.010	-0.221	0.225	0.055	-0.076
M	0.095	0.014	0.153	-0.048	0.202	0.017	-0.090
S	0.103	0.081	-0.238	0.017	0.221	**0.571**	-0.041
O	0.051	0.020	-0.070	-0.085	-0.114	-0.133	-0.014
D	0.206	0.012	0.059	0.031	-0.353	-0.053	**0.718**
N	0.098	0.010	0.121	-0.213	0.198	0.188	-0.441
Q	0.069	-0.160	-0.070	-0.009	0.251	-0.100	0.393

Wild and hatchery condition is far apart from each other. The hatchery provides almost everything to ensure the survival of rear fish, there was enough food, water quality was monitored and shelter for the fish to stay alive. In a natural environment, the conditions are uncertain and providing natural selection for the fittest (Yang et al., 2014). Fish are known to be very sensitive to environmental changes, and they will quickly adapt to the new environment. Changes in water condition, source of food, and stress will demonstrate variation between different environments. They are more susceptible to environmental induce morphological variation. Coupled with every difference between wild and hatchery conditions, the morphology between these two populations was discrete from each other, as displayed in this study.

To make the deviation clearer, in a natural environment, each population experience natural selection and evolutionary process. Natural environments influence changes in the wild population by a random process of mutation, genetic drift, and gene flow. Each of these forces contributes to the variation among the wild population (Yang et al., 2014). Furthermore, in the wild population, only the fittest will survive natural selection such as disease, environmental challenge, and predatory. However, selection in the hatchery population was done by artificial selection based on criteria decided by a human. Fishes with criteria favorable by commercial need were selected. These selections have deviated from natural selection and, in the end, exhibited in morphological differences between wild and hatchery populations.

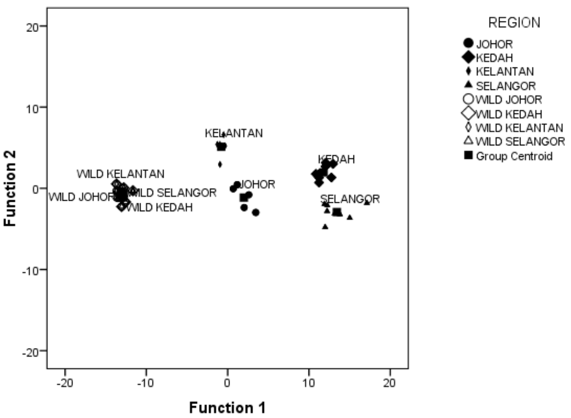

Figure 2: Scatter plot of discriminant functions analysis (DFA) scored based on morphometric characters of hatchery and wild *A. testudineus* populations

Therefore, this study suggested that wild populations can be used to supplement different variations in selective breeding programs to increase variations within the hatchery population. Wild populations have been used as reservoirs in species variation, and this practice has been carried out extensively in aquaculture (Kim et al., 2011). It is also well known that there are higher variations within the wild population due to natural selection, and on this basis, the wild population contained a fitter individual compared to the hatchery population. However, hatchery populations that have gone through artificial selection have an adaptive value of commercial need. Conversely, artificial selection may also reduce the fitness of the hatchery population (Nikolsky, 1963). The selection of wild populations as a supplement to the hatchery population has been used in some selective breeding programs to improve fitness in hatchery populations, especially to increase resistance to disease (Davies et al., 2012; Pitcher, 2012).

4. Conclusion

Morphological analysis between hatchery and wild populations showed that *A. testudineus* populations were from a different stock of populations, where, each population was not closely related to each other. Thus, the mating of individuals from different populations suggested in this study will not lead to inbreeding as they are not closely related to each other.

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