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Stock discrimination of Indian sand whiting *Sillago sihama* (Forsskal, 1775) using truss morphometry along the Maharashtra and Goa coasts of India

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Abstract

The present study aimed to assess the stock structure of *Sillago sihama* (Forsskal, 1775) along the Maharashtra and Goa coasts using truss morphometric analysis. A total of 180 specimens were collected from six locations including Satpati, Mumbai, Harnai, Ratnagiri, Malvan, and Panaji between September 2024 and May 2025.Twenty truss distances, generated from ten anatomical landmarks, were subjected to statistical analyses comprising ANOVA, MANOVA, Principal Component Analysis (PCA), and Discriminant Function Analysis (DFA) to assess morphometric variation among populations. Nineteen out of twenty morphometric traits showed significant variation among locations. PCA revealed that most variation was concentrated in the caudal and dorsal regions, while DFA correctly classified 78.9% of specimens, with 70.6% accuracy in cross-validation. The distinct clustering patterns suggest the presence of multiple morphometric stocks. These results highlight the presence of significant morphological variability among *S. sihama* populations and underscore the effectiveness of truss morphometry in stock discrimination for sustainable fisheries management.

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Introduction

Fish stocks being largely self-sustaining and distinct with comparable life history traits, are fundamental to fisheries management (Hilborn and Walters, 1992). Understanding the stock structure of a target species is crucial for achieving sustainable harvests, preventing recruitment failures, restoring depleted populations, and protecting vulnerable species (SriHari *et al.,* 2019). Morphometric analysis, which examines the geometric form of organisms, reveals variations in growth and maturity patterns that are highly responsive to environmental changes while exhibiting minimal genetic variation. Assessing morphometric traits is a widely used and cost-effective approach towards stock differentiation (Sajina *et al.,* 2011). Truss morphometry is a landmark-based method that utilises geometric morphometrics without imposing limitations on the direction of variation or the localisation of shape changes. The system is highly efficient in capturing detailed shape information of an organism (Cavalcanti *et al.,* 1999). Truss network measurements consist of a series of distances calculated between specific landmarks, creating a structured pattern of interconnected quadrilaterals or cells across the body form (Strauss and Bookstein, 1982). It serves as a classification tool for differentiating species with similar morphology and identifying distinct stocks (Cadrin and Friedland, 1999).

The truss network system serves as an effective fisheries management tool due to its ability to analyse large quantities of samples in a short time. This system utilises a standardised set of measurements to study stock differentiation within a species, facilitating long-term comparisons of morphological changes in stocks. When combined with molecular genetic markers, it enhances stock identification and strengthens the biological foundation for management strategies (Sen *et al.*, 2011).

Fishes of the family Sillaginidae are commonly referred to as ladyfish or sand whitings. In India, eight species of sand whitings have been reported so far, namely *Sillago sihama, S. vincenti, S. parvisquamis, S. argentifasciata, S. maculata, Sillaginops macrolepis, Sillaginopsis panijus* and *Sillaginopodys chondropus* (McKay, 1976; Dutt and Sujatha, 1980). Among these, the Indian sand whiting, *Sillago sihama* (Forsskal, 1775) is commonly found in the coastal waters of Ratnagiri and is considered one of the most economically valuable fish species in the coastal regions of Maharashtra (Sawant *et al.*, 2017). *S. sihama* is widely distributed across tropical and subtropical waters in the western-central Pacific and Indian Oceans (McKay, 1999). It is primarily caught using gill nets, drag nets and cast nets. *S. sihama* is an economically important demersal species that contributes to artisanal and small-scale fisheries along the Maharashtra and Goa coasts. Despite being economically and ecologically important, no comprehensive work on the stock structure of the species has been reported from the region so far.

Brackishwater fisheries in India remain largely data deficient and are increasingly impacted by multiple stressors, including habitat degradation, overexploitation, stock depletion, illegal fishing, and climate change (Kavitake *et al*., 2024). In light of the above, the present study was carried out with the objective of differentiating stocks of *S. sihama* along the Maharashtra and Goa coasts of India with the aim of generating baseline information to support stock-specific management and sustainable exploitation of the species.

Materials and methods

Sample collection

A total of 180 specimens of *S. sihama* were collected from six distinct sampling sites along the Maharashtra and Goa coasts of India between September 2024 and May 2025. About 30 specimens from each location *i.e.* Satpati fish landing center in Palghar (19.71° N; 72.7° E); Versova fish landing centre in Mumbai (19.08° N; 72.48° E); Harnai fish landing centre (17.81° N; 73.09° E); Sarjekot fish landing center in Malvan, Sindhudurg (16.09° N; 73.67° E); and Alto betim fish landing centre in Panaji, Goa (15.50° N; 73.83° E) were collected for the study (Fig. 1). The samples were stored in an ice box and brought to the laboratory for further analysis.

Digitisation of samples

All samples were thoroughly cleaned with running water to remove slime, dirt and drained completely. The specimens were placed on a flat platform with graph paper and the fins were erected to make the origin and insertion points visible. Each individual was labeled with a specific code for identification. A canon EOS 800D camera with a resolution of 24.2 megapixels was used to take digital pictures of each specimen. The landmarks used to obtain truss measurements from the fish body are shown in Fig. 2. A truss network was developed by linking 10 landmark points, resulting in 20 truss measurements for each specimen (Table 1). The '.jpeg' images were converted to '.tps' format using the software tpsUtil (Rohlf, 2006a). Before identifying landmarks, the scale was calibrated in cm for all specimens.

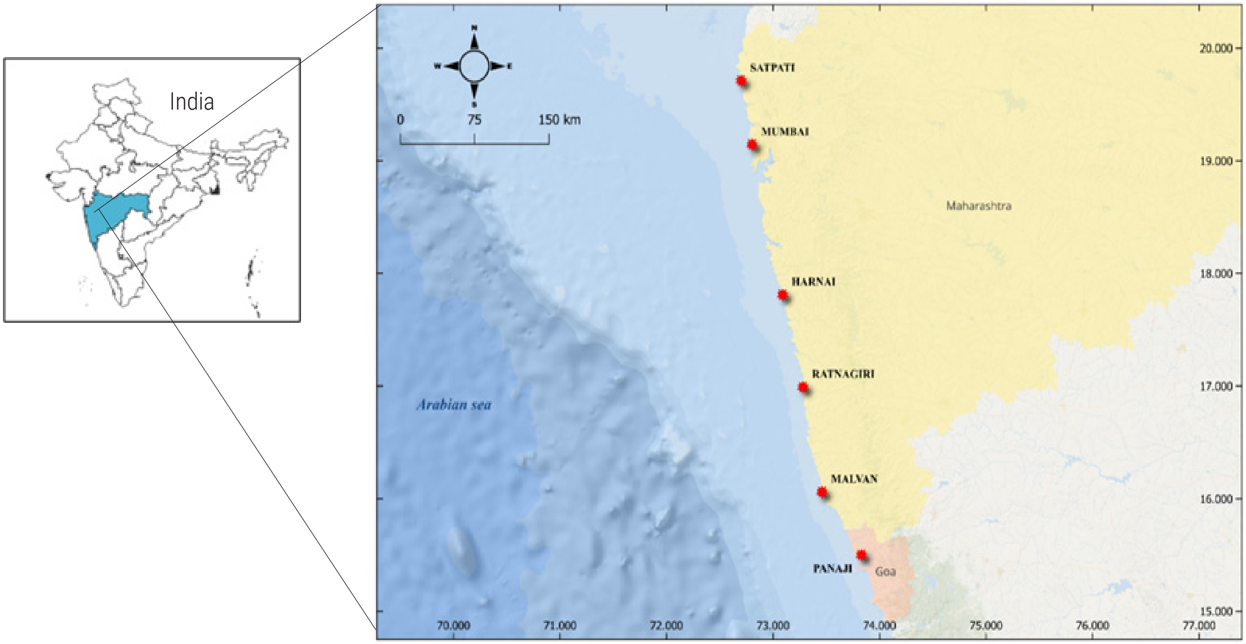

Fig. 1. Map of the study area

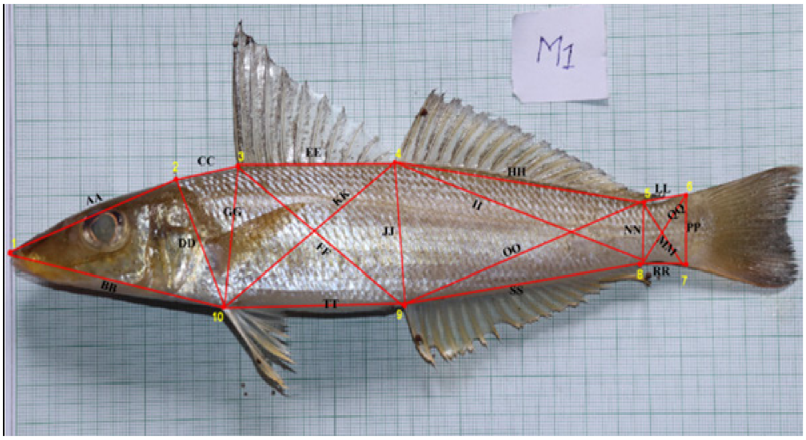

Fig. 2**.** Truss distances and associated landmarks

Table 1. Truss distances and associated landmarks for truss morphometrics

S. No.	Truss distance	Associated landmarks	Description
1	AA	1-2	Anterior tip of snout at upper jaw - Dorsal opercular margin
2	BB	1-10	Anterior tip of snout at upper jaw - Origin of pelvic fin
3	CC	2-3	Dorsal opercular margin – Origin of first dorsal fin
4	DD	2-10	Dorsal opercular margin – Origin of pelvic fin
5	EE	3-4	Origin of first dorsal fin – Origin of second dorsal fin
6	FF	3-9	Origin of first dorsal fin – Origin of anal fin
7	GG	3-10	Origin of first dorsal fin – Origin of pelvic fin
8	HH	4-5	Origin of second dorsal fin - End of second dorsal fin
9	II	4-8	Origin of second dorsal fin - End of anal fin
10	JJ	4-9	Origin of second dorsal fin – Origin of anal fin
11	KK	4-10	Origin of second dorsal fin – Origin of pelvic fin
12	LL	5-6	End of second dorsal fin - Insertion of dorsal lobe of caudal fin
13	MM	5-7	End of second dorsal fin - Insertion of anal lobe of caudal fin
14	NN	5-8	End of second dorsal fin - End of anal fin
15	OO	5-9	End of second dorsal fin – Origin of anal fin
16	PP	6-7	Insertion of dorsal lobe of caudal fin - Insertion of anal lobe of caudal fin
17	QQ	6-8	Insertion of dorsal lobe of caudal fin - End of anal fin
18	RR	7-8	Insertion of anal lobe of caudal fin - End of anal fin
19	SS	8-9	End of anal fin – Origin of anal fin
20	TT	9-10	Origin of anal fin – Origin of pelvic fin

Landmarks on the images were marked using tpsDig2 (Rohlf, 2006b) software and the resulting landmark data was encoded as X-Y coordinates within the TPS files. These TPS-formatted images were then processed using PAST (Hammer *et al.*, 2001) software. By utilising the "all distances from landmark and 2D" and "Geomet menu" options, the distances between landmarks were extracted for further analysis.

Statistical analysis

To accurately compare body shape among individuals or populations, it is important to eliminate the influence of overall fish size on shape variation (Azad *et al.*, 2020; Ramya *et al.*, 2021; Shahana *et al.*, 2024). Hence, size-dependent variation was corrected using the allometric formula proposed by Elliott *et al*. (1995).

$$Ms = M\left(\frac{L_s}{L_0}\right)^b$$

where, M = Original morphometric measurement; Ms = Size corrected morphometric measurement; Ls = Overall mean of the standard length of all the samples; L_0 = Total length of the fish and b = Slope of the regression of log M on log L_0.

Total length (TL) was excluded from subsequent analyses as it served as the basis for size correction. Outliers were detected and removed using the boxplot function in SPSS to minimise the impact of extreme values, which may have resulted from measurement inaccuracies or human error (Shahana *et al.*, 2024). To assess significant morphometric differences among populations, both one-way univariate analysis of variance (ANOVA) and multivariate analysis of variance (MANOVA) were conducted. These were followed by Tukey's *post-hoc* test to identify specific pair-wise differences between locations. In addition, multivariate techniques such as Principal Component Analysis (PCA) and Discriminant Function Analysis (DFA) were employed. PCA was used to reduce data dimensionality while retaining the majority of variation, thereby facilitating the identification of morphometric traits contributing most to population differentiation (Rawat *et al.*, 2017). DFA was then applied to those variables with strong loadings (greater than 0.700) on the principal components to effectively classify individuals into their respective stocks (Bal *et al.*, 2021). The accuracy of classification was assessed by calculating the percentage of correctly assigned specimens, with cross-validation performed using the leave-one-out (Jackknife) method. All statistical analyses were carried out using SPSS software (version 27.0).

Results

The ANOVA results showed that 19 out of the 20 morphometric traits differed significantly among the locations (Table 2). The significant values of Wilk's lambda and Pillai's trace in the MANOVA indicated overall significant shape variations across the locations. Further, Tukey's *post-hoc* test provided detailed insights into pair-wise differences between locations (Table 3).

Table 2. ANOVA - comparison of mean truss distances between locations

Variables	Sum of squares	Mean square	F	Significance
AA	1.761	0.352	20.996	$p < 0.05$
BB	1.868	0.374	20.108	$p < 0.05$
CC	0.938	0.188	14.869	$p < 0.05$
DD	2.887	0.577	40.119	$p < 0.05$
EE	0.128	0.026	2.534	$p < 0.05$
FF	2.379	0.476	33.706	$p < 0.05$
GG	2.579	0.516	32.433	$p < 0.05$
HH	0.927	0.185	9.337	$p < 0.05$
II	0.982	0.196	11.034	$p < 0.05$
JJ	1.339	0.268	19.467	$p < 0.05$
KK	0.116	0.023	1.331	$p = 0.253$
LL	0.902	0.180	16.590	$p < 0.05$
MM	0.281	0.056	9.222	$p < 0.05$
NN	0.216	0.043	12.918	$p < 0.05$
OO	0.314	0.063	3.231	$p < 0.05$
PP	0.053	0.011	3.833	$p < 0.05$
QQ	0.364	0.073	8.661	$p < 0.05$
RR	1.136	0.227	26.831	$p < 0.05$
SS	0.419	0.084	3.529	$p < 0.05$
TT	1.646	0.329	12.291	$p < 0.05$

Table 3. Pair-wise comparison of truss characters from Tukey's *post hoc* test

Measurements	SAT-MUM	SAT-HAR	SAT-RTN	SAT-MAL	SAT-PAN	MUM-HAR	MUM-RTN	MUM-MAL	MUM-PAN	HAR-RTN	HAR-MAL	HAR-PAN	RTN-MAL	RTN-PAN	MAL-PAN
AA	0.001*	1.000	0.069	0.870	0.000*	0.000*	0.753	0.000*	0.000*	0.029*	0.966	0.000*	0.002*	0.000*	0.001*
BB	0.000*	0.000*	0.000*	0.999	0.961	1.000	0.830	0.000*	0.000*	0.732	0.000*	0.000*	0.000*	0.000*	0.997
CC	0.321	0.000*	0.000*	0.998	0.000*	0.000*	0.003*	0.601	0.157	0.997	0.000*	0.444	0.000*	0.753	0.001*
DD	0.982	0.000*	0.000*	0.818	0.026*	0.000*	0.000*	0.995	0.158	0.000*	0.000*	0.006*	0.000*	0.000*	0.423
EE	0.687	0.921	0.165	0.999	0.256	0.997	0.940	0.445	0.981	0.727	0.750	0.845	0.069	1.000	0.117
FF	0.000*	0.962	0.011*	0.034*	0.000*	0.000*	0.000*	0.000*	1.000	0.115	0.246	0.000*	0.999	0.000*	0.000*
GG	0.999	0.000*	0.000*	0.997	0.215	0.000*	0.000*	1.000	0.409	0.000*	0.001*	0.153	0.000*	0.000*	0.474
HH	0.055	0.298	0.002*	0.993	0.000*	0.974	0.902	0.010*	0.293	0.466	0.090	0.053	0.000*	0.899	0.000*
II	0.024*	0.683	0.219	0.713	0.000*	0.557	0.951	0.000*	0.287	0.970	0.048*	0.003*	0.004*	0.037*	0.000*
JJ	0.007*	0.086	0.000*	0.137	0.885	0.000*	0.000*	0.000*	0.151	0.115	1.000	0.003*	0.071	0.000*	0.006*
KK	0.850	0.995	0.841	0.973	1.000	0.987	0.175	0.998	0.942	0.521	1.000	1.000	0.374	0.699	0.996
LL	0.899	0.000*	0.000*	0.014*	0.954	0.000*	0.000*	0.214	1.000	0.924	0.005*	0.000*	0.097	0.000*	0.145
MM	0.088	0.000*	0.000*	0.200	0.058	0.006*	0.300	0.999	1.000	0.672	0.002*	0.010*	0.146	0.394	0.995
NN	0.625	0.000*	0.004*	0.022*	0.989	0.000*	0.000*	0.000*	0.936	0.974	0.800	0.000*	0.996	0.000*	0.003*
OO	0.165	0.107	0.996	0.998	0.816	1.000	0.049	0.367	0.860	0.028*	0.263	0.760	0.939	0.506	0.964
PP	0.985	0.270	0.282	0.061*	0.990	0.061	0.065	0.008*	0.795	1.000	0.985	0.647	0.983	0.663	0.246
QQ	0.041*	0.000*	0.001*	0.802	0.987	0.164	0.908	0.540	0.196	0.747	0.001*	0.000*	0.077	0.013*	0.989
RR	0.049*	0.000*	0.000*	0.033*	0.091	0.000*	0.000*	1.000	1.000	0.097	0.000*	0.000*	0.000*	0.000*	0.999
SS	0.128	0.191	0.968	1.000	0.949	1.000	0.015*	0.179	0.589	0.026*	0.257	0.707	0.934	0.544	0.977
TT	0.000*	0.005*	0.008*	1.000	0.000*	0.705	0.604	0.000	0.936	1.000	0.010*	0.171	0.016*	0.121	0.000
Total Sig. characters	8	10	13	5	7	10	9	8	2	5	10	11	9	11	7
Total characters	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20

The population of Satpati showed a significant difference from that of Ratnagiri, with respect to 13 truss distances. The Panaji population differed from both Harnai and Ratnagiri populations in terms of 11 characters. The populations of Satpati and Mumbai were found to differ significantly ($p<0.05$) in terms of eight truss measurements. The populations of Satpati and Harnai showed a significant difference in 10 truss characters. Satpati and Malvan populations showed differences in only five truss distances. Satpati and Panaji populations differed significantly in terms of seven truss measurements. The populations of Mumbai and Harnai were found to differ significantly in terms of 10 truss distances. Mumbai and Ratnagiri populations showed significant variation in nine truss characters. Mumbai and Malvan populations were found to differ significantly in eight truss measurements. The populations of Mumbai and Panaji were found to differ significantly in terms of only two truss distances. Harnai and Ratnagiri populations showed differences in five morphometric characters. Harnai and Malvan populations showed differences in 10 truss characters. Malvan and Ratnagiri exhibited a significant difference in nine truss morphometric measurements. Malvan and Panaji populations were found to differ significantly in terms of seven truss measurements. PCA extracted six components, which together explained 76.87% of the total variance. The first principal component PC1 was primarily characterised by high loadings of the truss measurements LL, MM, QQ, and RR, representing the caudal region. PC2 had significant loadings on JJ and NN, associated with the mid body region, particularly the distances between the origins of the dorsal and anal fins. PC3 was characterised by HH and II, reflecting distances between the dorsal fin origin and the anal fin. PC4 was largely influenced by SS and TT, which represent the anal and pelvic fin area. PC5 was characterised by AA associated with distances between the anterior tip of snout at upper jaw to the dorsal opercular margin. PC6 accounted for variation primarily in the dorsal fin areas (Table 4). Discriminant Function Analysis (DFA) correctly classified 78.9% of the specimens into their original groups, and cross-validation yielded a correct classification rate of 70.6% using the selected truss morphometric measurements (Table 5).

Table 4. Principal components extracted from the PCA after varimax normalised rotation on truss measurements

Characters	Principal component					
	1	2	3	4	5	6
AA	-.113	.038	-.025	-.102	.849*	.120
BB	-.218	.224	-.291	.147	.663	-.403
CC	-.349	.285	-.560	.196	-.343	-.156
DD	-.323	.646	-.519	.140	.099	-.239
EE	.086	.025	.047	.108	.098	.849*
FF	-.164	.680	.117	-.566	.093	.139
GG	-.364	.648	-.495	-.026	.022	-.064
HH	-.166	.042	.867*	.059	-.186	-.120
II	-.144	.199	.854*	.117	-.056	-.001
JJ	-.133	.824*	-.075	-.254	.018	.043
KK	-.142	.256	-.399	-.239	-.268	.581
LL	.840*	-.228	-.125	.023	-.063	-.012
MM	.857*	.006	.021	-.048	.128	.101
NN	.026	.720*	.060	-.089	.035	.159
OO	-.262	-.040	.388	.665	-.302	.108
PP	.193	.655	.254	.190	.000	-.098
QQ	.820*	.230	.028	.013	-.279	-.073
RR	.860*	-.184	-.063	-.149	-.094	.031
SS	-.225	-.160	.362	.757*	-.117	.212
TT	-.064	.043	.241	-.831*	-.181	.152
Eigenvalues	4.567	3.469	2.615	1.836	1.641	1.247
% Variance	22.834	17.347	13.076	9.179	8.204	6.235
Cumulative	22.834	40.181	53.258	62.437	70.641	76.876

Discussion

One-way ANOVA revealed that 19 out of 20 truss morphometric characters exhibited statistically significant differences across the sampling locations, with the exception of the character KK (Origin of second dorsal fin - origin of pelvic fin). This indicates pronounced inter-population morphometric variation. These findings reflect the influence of localised environmental factors on body shape, consistent with previous studies on morphometric stock identification (Khan *et al.,* 2019; Shahana *et al.,* 2024). The results of the Multivariate Analysis of Variance (MANOVA), particularly the significance of Wilk's lambda and Pillai's trace, further confirmed the presence of overall shape differentiation among the populations. The effectiveness of MANOVA in identifying morphological variations among distinct fish populations agree with the findings of ShriHari *et al*. (2021), Nama *et al.* (2022), and Shahana *et al.* (2024).

Table 5. Number and percentage of individuals classified into their respective groups based on truss measurements

Location		HAR (%)	MAL (%)	RTN (%)	MUM (%)	SAT (%)	PAN (%)	TOTAL(%)
Original (78.9%)	HAR	73.3	3.3	16.7	3.3	0.0	3.3	100
	MAL	6.7	70.0	0.0	0.0	23.3	0.0	100
	RTN	23.3	3.3	66.7	3.3	0.0	3.3	100
	MUM	0.0	0.0	0.0	96.7	3.3	0.0	100
	SAT	0.0	23.3	0.0	6.7	66.7	3.3	100
	PAN	0.0	0.0	0.0	0.0	0.0	100.0	100
Cross-validated (70.6%)	HAR	70.0	0.0	20.0	3.3	3.3	3.3	100
	MAL	10.0	53.3	0.0	0.0	36.7	0.0	100
	RTN	23.3	6.7	63.3	3.3	0.0	3.3	100
	MUM	3.3	0.0	0.0	83.3	10.0	3.3	100
	SAT	0.0	23.3	0.0	13.3	60.0	3.3	100
	PAN	3.3	0.0	0.0	3.3	0.0	93.3	100

PCA reduced the dimensionality of the data and identified six principal components that collectively explained 76.87% of the total variance. The first principal component (PC1) was associated with high loadings from LL, MM, QQ, and RR, representing the caudal region. Variations in the caudal region are particularly important for swimming performance and habitat preference, suggesting adaptive divergence (Bookstein, 1991; Cavalcanti *et al.*, 1999). This implies that tail morphology is a major contributor to shape variation, potentially reflecting adaptation to different hydrodynamic conditions (Bookstein, 1991; Cavalcanti *et al.,* 1999). PC2 was influenced by mid-body truss variables JJ and NN, while PC3 was driven by HH and II, associated with the dorsal-anal fin area. The remaining components (PC4–PC6) captured variation in pelvic-fin and snout regions. These regional shape differences support the view that morphometric traits are sensitive to environmental and ecological gradients such as salinity, substrate type, and hydrology (Tzeng, 2004).

DFA, based on characters with high PCA loadings (>0.700), showed effective group separation among populations, with a classification accuracy of 78.9%, and 70.6% in cross-validation (jackknifed). This high classification accuracy rate affirms the utility of truss morphometrics in population discrimination. The DFA plot (Fig. 3) revealed partial overlaps among several groups, particularly Satpati and Malvan, indicating possible stock mixing or environmental similarity. The Panaji population, in particular, exhibited strong group cohesion with 93.3% correct classification in cross-validation, suggesting it may represent a discrete stock, likely influenced by dynamic estuarine environment and relative geographic isolation. The distinctiveness of the Ratnagiri population is also evident in its divergence from Satpati, Mumbai, and Panaji, confirming the presence of multiple morphometric stocks.

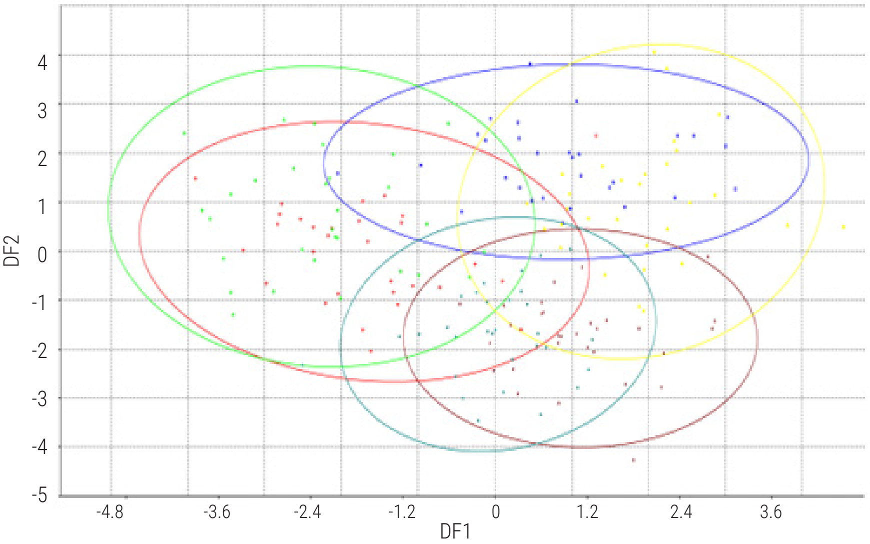

Fig. 3. DFA biplot of truss measurements from the six different locations in Maharashtra and Goa coasts of India

The observed morphometric variation likely reflects a combination of phenotypic plasticity and environmental adaptation**,** as genetic differences are generally minor in coastal fish species (Wimberger, 1992; Cadrin, 2000). The variation in caudal and dorsal-fin regions suggests differences in swimming ability, habitat usage, or current regimes among regions. These results align with previous studies that successfully used truss-based DFA to distinguish fish stocks, such as *Terapon jarbua* along the Indian coast (Shahana *et al.*, 2024), and *Hyporhamphus limbatus* in south-western Bangladesh (Mahfuj *et al*., 2023).

From a management perspective, the observed stock structuring highlights the need for location-specific conservation strategies and fishery management plans**.** In particular, the Ratnagiri and Panaji populations, which exhibit distinct morphotypes, may require recognition as independent management units to prevent overexploitation and ensure the sustainability of local fisheries. According to Cadrin and Friedland (1999), accurate stock identification is essential for aligning harvest limits with biological populations to avoid recruitment failure. In conclusion, the clear morphological separation revealed by DFA and PCA demonstrates that *S. sihama* along the Maharashtra and Goa coasts comprises multiple morphometric stock units, with distinct differentiation between Maharashtra and Goa populations, thereby supporting the need for region-specific fisheries management strategies.

The present study demonstrated significant morphometric heterogeneity among *S. sihama* populations sampled from six coastal locations along Maharashtra and Goa. Truss-based morphometric analysis revealed distinct phenotypic structuring among populations. Discriminant Function Analysis, supported by high classification accuracy and cross-validation rates, confirmed the presence of discrete morphometric stocks. The observed variation, primarily in the caudal and dorsal regions, likely reflects ecological adaptation and phenotypic plasticity driven by localised environmental conditions. These findings highlight the effectiveness of truss morphometry in delineating population structure and contribute essential baseline data for the development of region-specific fisheries management strategies. The recognition of morphometrically distinct stocks supports their consideration as independent management units to ensure the long-term sustainability of *S. sihama* populations in the region.

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