

# Confirmatory factor analysis of seagrass *Thalassia hemprichii* descriptors from coastal waters of Kepulauan Seribu Marine National Park

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**Abstract.** The study was conducted to explore and confirm eight *Thalassia hemprichii* descriptors as indicators of two latent structures and to examine invariance in inhabited and uninhabited locations. Eight seagrass meadows at Kepulauan Seribu Marine National Park (TnLKs) were purposively selected to encompass anthropogenic gradient pressure. The *T. hemprichii* descriptors were analyzed using exploratory factor analysis in the confirmatory factor analysis (CFA) framework (E/CFA strategy), pure CFA model based on E/CFA strategy and multiple indicators multiple causes (MIMIC) modelling or CFA with covariates to examine invariance in two groups (inhabited and uninhabited locations) using the established CFA model. The final results indicated that the measured *T. hemprichii* descriptors have more clearer latent structures than the derived *T. hemprichii* descriptors, showed large effect differences between inhabited and uninhabited locations and *T. hemprichii* potentially could be used as bioindicator for biomonitoring environmental quality for tropical coastal waters.

**Key Words:** anthropogenic pressure, bioindicator, E/CFA, MIMIC model, multi metric index.

**Introduction.** Seagrasses are submerged marine plants that form an integrative relationship with land vegetation (terrestrial vegetations and mangroves) and coral reef (Hogarth 2015). Seagrasses are flowering plants (Angiospermae) that live submerged in water columns and develop well in shallow and estuary sea waters. Seagrass plants consist of leaves and sheaths (shoot), stems that are usually called rhizomes, and roots that grow on the rhizomes. It is known that there are 13 seagrass species in all Indonesian waters, with an estimated seagrass coverage area of 30,000 km<sup>2</sup> (Nienhuis 1993; Kuo 2007). Seagrass is one of the conservation targets of Kepulauan Seribu Marine National Park (TnLKs) at North Jakarta Bay Indonesia. Seagrass beds scattered in almost all shallow waters around small islands in the TnLKs area. There were 6 species identified in TnLKs: *Thalassia hemprichii*, *Enhalus acoroides*, *Holodule uninervis*, *Cymodocea rotundata*, *Halophila ovalis* and *Syringodium isoetifolium*.

*T. hemprichii* is a type of ecological seagrass species with the widest distribution and high abundance in Indonesian waters (Erftemeijer & Herman 1994; Kiswara & Djamali 1995). In the TnLKs water area, *T. hemprichii* is spread almost evenly and is most commonly found (Kiswara 1992; Feryatun et al 2012; Wahab et al 2017). This species of tropical seagrass is most sensitive to environmental stresses (Neckles 1994) and is the primary producer on tropical beaches (Van Tussenbroek et al 2006). This species has the potential and is very suitable for use as an environmental quality bioindicator candidate in Indonesian waters.

Due to seagrass wide distribution, its important role in ecology and its sensitivity to disturbances, seagrasses can be used as bioindicators of environmental ecology (Short & Wyllie-Echeverria 1996; Krause-Jensen et al 2005), especially as indicator of magnitude anthropogenic pressure of coastal waters because its closeness with populated coastal area. The use of seagrass species as bioindicator index for biomonitoring the environmental status of coastal waters related to anthropogenic pressure gradient has

been carried out, mostly in Europe using The European Water Framework Directive (WFD), as Buia et al (2005) using *Posidonia oceanica* with 5 metrics (PoSte index), Romero et al (2007) using *P. oceanica* with 14 metrics (POMI index), Martinez-Crego et al (2008) examined 59 metrics as seagrass indicator candidates; Gobert et al (2009) used *P. oceanica* with 5 metric (PREI index), Lopez y Royo et al (2010) used *P. oceanica* with 5 metric (BiPo index), Oliva et al (2012) used *Cymodocea nodosa* with 37 metric (CYMOX index) and Garcia-Marin et al (2013) used *Zostera noltii* with 9 metrics (ZONI index). Based on the results of above studies, seagrass metric variables affected by anthropogenic pressure can be grouped at physiology, individual, population and community levels. The seagrass descriptors used for assessment of the environmental status of coastal waters ideally should include metric for all levels and the selection of seagrass metric variables that sensitively affected by anthropogenic pressure of all levels is the most important stage for the index development.

The analysis of *T. hemprichii* and other ecological seagrass descriptors in context of anthropogenic pressure gradient have not been widely explored and well documented yet. In this study we analyze six *T. hemprichii* structural metrics (length and width of leaf, rhizome diameter, length of vertical rhizome, shoot density and covering) and two derived metrics (leaf surface area and leaf area index) from four populated area and four non populated areas at TnLKs. From previous studies and theoretical context, these seagrass metric variables represent metric at individual (morphological) level (leaf length, leaf width, rhizome diameter, length of vertical rhizome and leaf surface area) and population level (shoot density and *T. hemprichii* covering).

Our analysis aims to explore and confirm that the eight metric variables (descriptors) could be represented as manifestation (indicator) of two latent structures or two factors (individual and population) using Confirmatory factor analysis (CFA) model and to examine invariance of the CFA model in two groups (inhabited and uninhabited locations) using multiple indicators multiple causes (MIMIC) modelling.

## Material and Method

**Description of the study sites.** The study was conducted on July-September 2018 in TnLKs Jakarta Indonesia (Figure 1), in eight locations spread from the southern to the northern parts of TnLKs, purposively choosed to encompass anthropogenic gradient pressure of the region.

Four locations are densely populated islands (Panggang/Pa, Pramuka/Pr, Harapan/Ha and Kelapa Dua/Kd) with a population ranging from 3000 to 7000 people. These four islands are the main islands that are populated and are domestic recreation islands with a very dense population, massive development and reclamation. The other three islands are uninhabited islands (private property), two of which are islands with limited access (Semut Kecil/Se and Kotok/Kt), one island is a tourist island with a camp site (Semak Daun/Sed). One location (Karang Lebar/KI) is a reef flat area with small lagoons and no island exist. The distance between the southernmost and northernmost locations was 21 km.

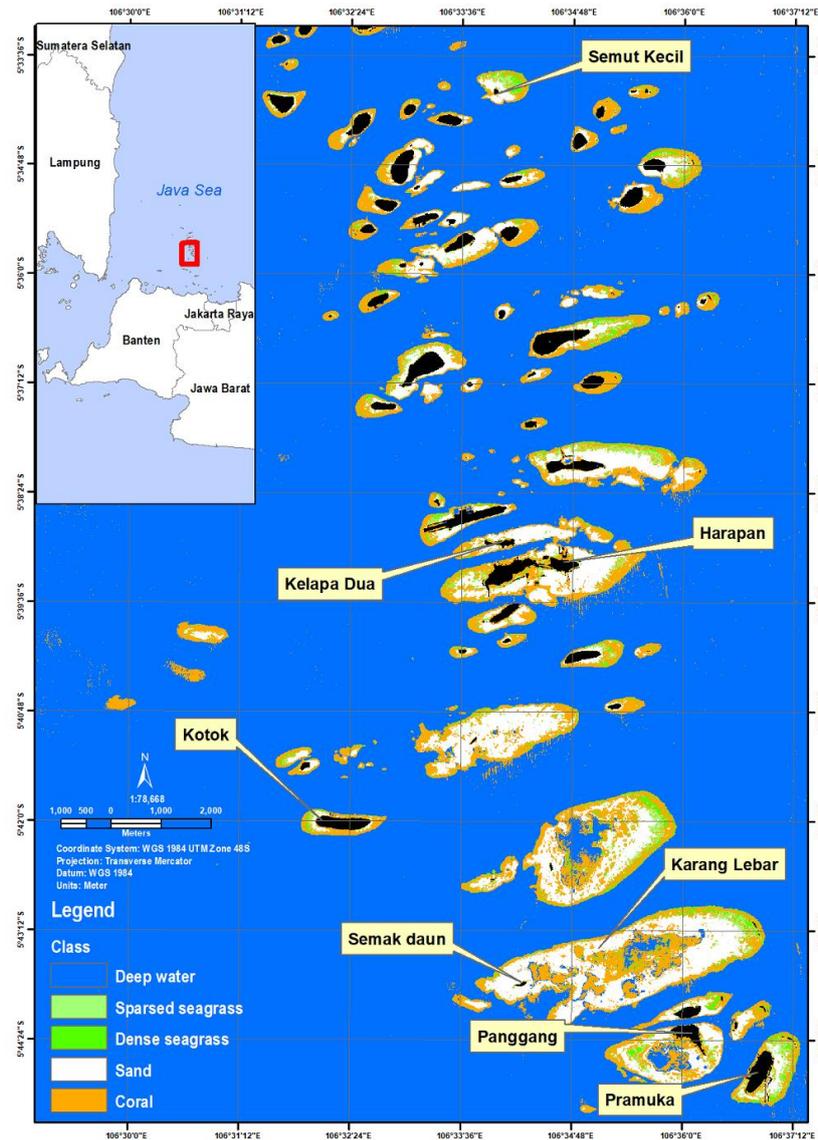


Figure 1. Study sites at Kepulauan Seribu Marine National Park Jakarta Indonesia (satellite image: Sentinel 2 2017; mapping software: arcgis v.10.5; classification method: random forest).

**Sampling design and data acquisition.** Fifteen quadrats ( $0.25 \text{ m}^2$ ) were spread on seagrass meadow at every location (total 121 quadrats; 16 quadrats in Karang Lebar), sampling points for quadrat placements were generated using systematic random pattern of points in R spatstat package (Baddeley et al 2015). Distance between sampling point ranged from 30 to 34 m.

In every quadrat, *T. hemprichii* coverage was estimated visually and all individual shoots were counted (shoot density). Shoot and rhizome of *T. hemprichii* within quadrat were removed using shovel for further measurement of morphological descriptors. Morphological descriptors were measured manually using caliper. Leaf length (cm) were measured from 5-10 leaves (green area of oldest leaf), leaf width (cm) was measured from three part of leaf (top, mid and base). Rhizome diameter (cm) and vertical rhizome (cm) measured from 3-5 individual shoot. Leaf surface area ( $\text{cm}^2$ ) derived from multiplying leaf length and width, and Leaf area index ( $\text{m}^2 \text{ m}^{-2}$ ) was calculated by multiplying the mean surface area by shoot density. The measured morphological structure is shown in Figure 2.

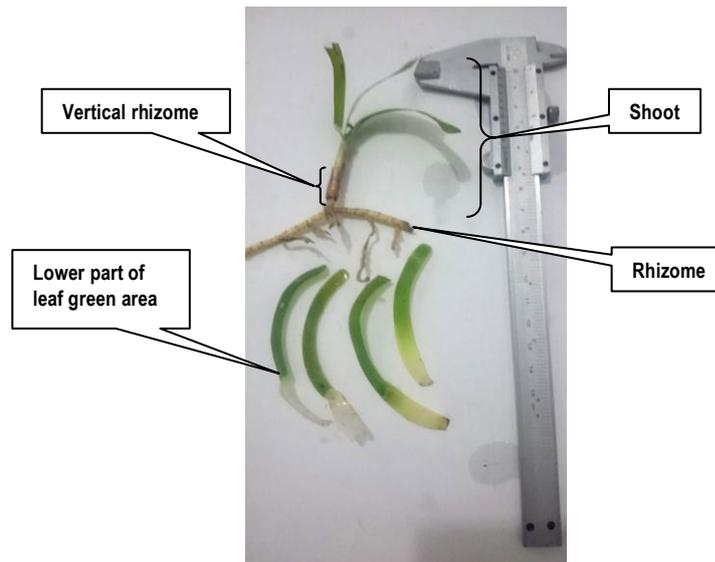


Figure 2. The measured morphological structure of *Thalassia hemprichii*.

**Data analysis.** all data were tested for multivariate normality test prior to the analysis, using Mardia test in MVN R package (Korkmaz et al 2014). The analysis was conducted in three stage using R package lavaan (Rosseel 2012) and semPlot package (Epskamp & Stuber 2017): first analysis was exploratory factor analysis (EFA) in the confirmatory factor analysis (CFA) framework (E/CFA strategy) to explore the dimensionality (latent construct/factor) of eight *T. hemprichii* descriptors. According to Brown (2015) E/CFA strategy was applied by selecting an anchor item (selected from the highest primary loading on the factor based on EFA result) and fixing the factor variances to 1.0 (completely standardized as in EFA). The CFA estimation gives more information about the model fit than EFA (the statistical significance of cross-loadings and the potential presence of salient error covariances). Secondly was developed a model in pure confirmatory framework (CFA) based on E/CFA strategy results. Thirdly was performed multiple indicators multiple causes (MIMIC) modelling or CFA with covariates to examine invariance in two groups (inhabited and uninhabited locations as covariates) using the established CFA model. In MIMIC modelling, individual and population factors become endogenous variables (dependent variable) because both of factors specified as outcomes predicted by the covariates (Status) specified as exogenous variable (independent variable). It is expected that the CFA model will show different characteristics (i.e. factor means and indicator intercepts) of Th descriptors for inhabited and uninhabited locations (Status), with the assumption that factor loadings, error variances–covariances, factor variances-covariances are the same across all levels of the covariates (Brown 2015). This was done to test the hypothesis that Th descriptors would be different in inhabited and uninhabited locations due to different in anthropogenic pressure.

CFA diagram notations was displayed as follows (Bollen 1989; Grace 2006): a square box signifies observed, measured, manifest or indicator variable; circles signifies latent, unmeasured, construct or factor variable; straight arrow indicated assumption that variable at head of arrow "caused by" variable at base of arrow; curved two-headed arrow signifies association (covariance in unstandardized or correlation in standardized variable) between two variables. Variable without arrow pointing at it are called exogenous variable (independent variable) and vice versa are called endogenous variable (dependent variable). An arrow pointing at square box indicated unexplained variance (error) and double head arrow at square box indicated variance.

Maximum likelihood estimation was used to all model and model fit was evaluated based on the fit indices for a single path coefficient (p value at significant level of 0.05) and the overall goodness of fit indices: chi square value ( $\chi^2$ ) not significantly different with null model, standardized root mean square residual (SRMR)  $\leq 0.08$ , root mean square error of approximation (RMSEA)  $\leq 0.06$ , comparative fit index (CFI) and Tucker Lewis Index (TLI)  $\geq 0.95$  (Brown 2015; Fan et al 2016). We used R software v.3.5.1 (R

Core Team 2018) for statistical analysis and  $\Omega$ nyx v.1.0-1010 for visualization (Oertzen et al 2015).

**Results.** Summary statistics showed that in average, except for vertical rhizome value (VR), *T. hemprichii* descriptors in inhabited locations exceed metric values of uninhabited locations (Table 1). Mardia test for multivariate normality showed only one location (Kotok Island) which did not followed multivariate normality (mvn) at significance level 0.05, this abnormality arised from the skewed distribution of *Thalassia* covering (Th\_COV) and shoot density (SD) metrics of Kotok Island (other six parameters of Kotok Island followed univariate normality using Shapiro-Wilk's test at signigifance level 0.05).

Table 1  
Summary statistics of *Thalassia hemprichii* descriptors in eight locations

Loc	St	LL (cm)	LW (cm)	LSA (cm <sup>2</sup> )	VR (cm)	RD (cm)	SD (m <sup>2</sup> )	LAI (m <sup>2</sup> m <sup>-2</sup> )	Th COV (%)	Th Cat
Ha	I	8.10	0.76	6.23	2.09	0.38	230.40	0.14	41.75	moderate
Kd	I	11.31	0.76	9.25	2.94	0.39	132.53	0.12	32.17	moderate
Pa	I	8.02	0.77	6.17	1.40	0.39	160.00	0.10	37.97	moderate
Pr	I	9.59	0.72	7.18	1.81	0.40	285.33	0.23	56.35	dense
Average		9.25	0.75	7.21	2.06	0.39	202.07	0.15	42.06	moderate
KI	U	9.14	0.75	6.99	3.97	0.39	72.50	0.05	18.95	sparse
Kt	U	8.34	0.68	5.67	2.73	0.35	119.47	0.07	35.00	moderate
Sed	U	6.83	0.63	4.34	3.46	0.34	178.93	0.08	38.47	moderate
Sk	U	7.75	0.63	4.95	2.65	0.36	118.93	0.06	27.42	moderate
Average		8.01	0.67	5.49	3.20	0.36	122.46	0.06	29.96	moderate

Loc (Location), St (Status), I (Inhabited), U (Uninhabited), LL (Leaf length), LW (leaf width), LSA (leaf surface area), VR (vertical rhizome), RD (rhizome diameter), SD (shoot density), LAI (leaf area index), Th COV (*T. hemprichii* covering), Th Cat (*T. hemprichii* covering category).

From scatterplot matrix (Figure 3), leaf length (LL) and leaf width (LW) were highly correlated with leaf surface area (LSA) (0.96 and 0.81 respectively).

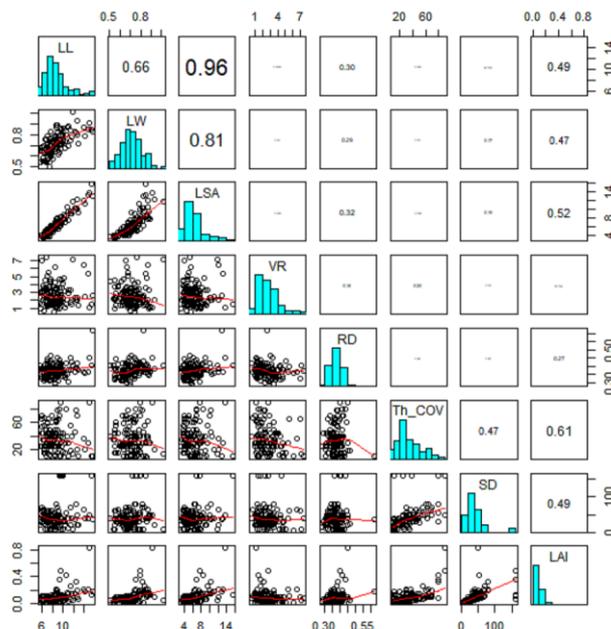


Figure 3. Scatterplot of correlation matrix (the size of numbers font indicates the magnitude of the relationship between variables).

The high correlation from this metrics were expected, since LSA was derived from multiplying LL and LW, but leaf area index (LAI) which is also a derived metric (from SD

and LSA) was not shown high correlation to SD and LSA. The other parameters only showed moderate to low correlations.

**E/CFA analysis.** Based on preliminary EFA analysis, Th\_COV and LL has the highest factor loading values in population and individual respectively. Th\_COV was anchored to population factor (0 value of its factor loading on individual factor) and LL was anchored to individual factor (0 value of its factor loading on population factor). The other parameters were freely estimated on each factor in the E/CFA model. Derived metrics (LSA and LAI) were assumed to have non random error (non random unexplained variance), thus their errors were correlated to their metrics from which they derived (unlike EFA, E/CFA allow to specify correlated error). This meta model intended to capture all patterns in the data. The model and result is displayed in Figure 4.

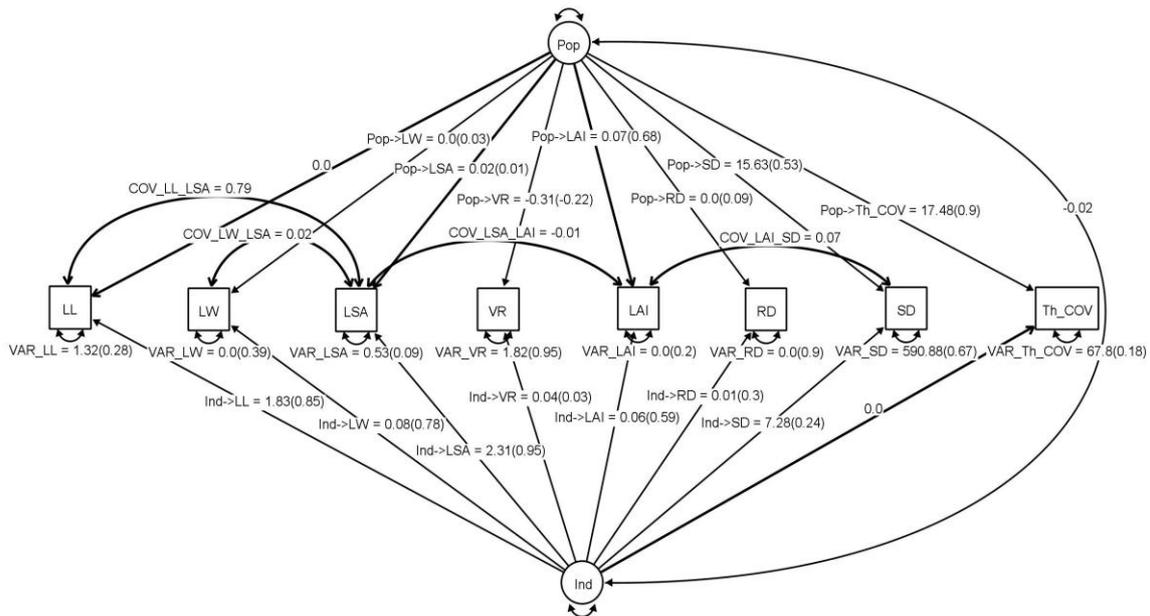


Figure 4. E/CFA model with correlated error (standardized values in parentheses).

From the results of first model above, all of the overall goodness of fit indices suggest that the model fit the data well (Tabel 2), but correlation matrix LSA showed very high correlation with LL and LW thus practically no unique information was gained from LSA.

Table 2

Fit indices from two E/CFA model

<i>Fit Indices</i>	<i>E/CFA without correlated error</i>	<i>E/CFA with correlated error</i>
npar	20.000	27.000
Chi square	4.574	9.475
df	8.000	9.000
pvalue	0.802	0.395
CFI	1.000	0.999
TLI	1.037	0.998
AIC	2103.243	2216.180
BIC	2159.159	2291.667
ntotal	121.000	121.000
RMSEA	0.000	0.021
rmsea.ci.lower	0.000	0.000
rmsea.ci.upper	0.068	0.106
rmsea.pvalue	0.904	0.616
SRMR	0.032	0.037

The covariance estimated from the model showed that only LL-LSA covariance was statistically significant (z-value 2.176, p value 0.03) and the covariance matrix of the residuals of the observed variables was not positive definite. Based on these results LSA was dropped from the model and accordingly was eliminated the need for correlated error in the model (Figure 5). The second model showed improvement of all fit indices (Table 2), more easily interpreted and more parsimonious than the first model with correlated error (lower AIC and BIC values).

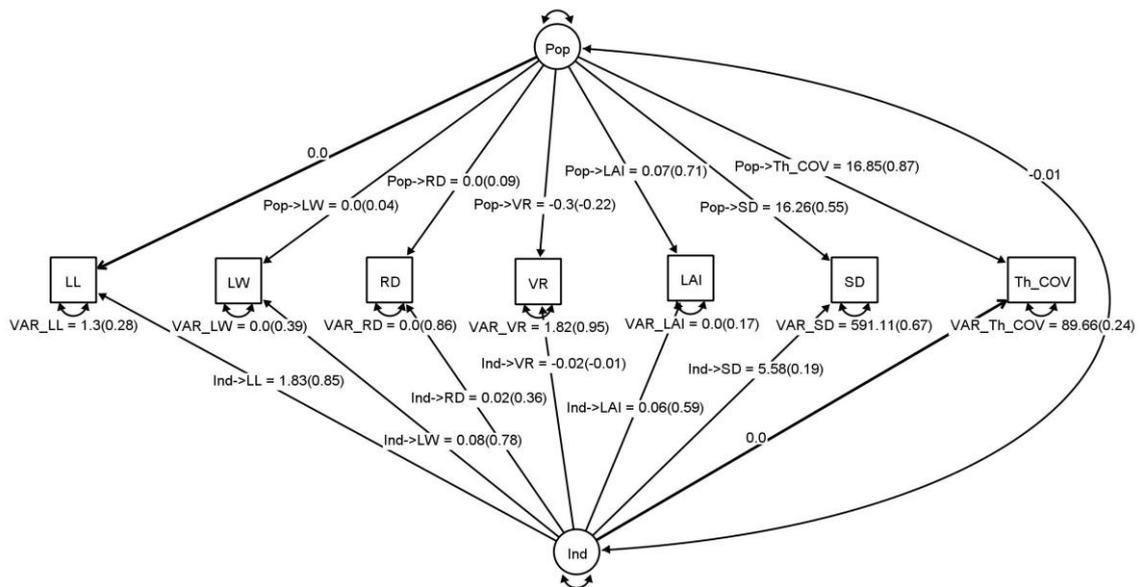


Figure 5. E/CFA model without correlated error (LSA dropped; standardized values in parentheses).

**CFA model.** The results from E/CFA second model showed LL, LW, RD significantly and strongly correlated to individual factor, Th\_COV and SD to population factor (bolded in Table 3).

Table 3  
Estimated factor loadings from E/CFA without correlated error

Factor	Indicator	Factor loading estimate		Std. Err	z-value	P(> z )
		Unstandardized	Standardized			
Individual	LL	1.832	<b>0.849</b>	0.180	10.153	0.000
	LW	0.075	<b>0.778</b>	0.008	9.201	0.000
	VR	-0.020	-0.014	0.135	-0.146	0.884
	RD	0.015	<b>0.360</b>	0.004	3.766	0.000
	SD	5.584	0.188	2.651	2.107	0.035
	LAI	0.058	<b>0.586</b>	0.007	8.321	0.000
Population	Th_COV	16.847	<b>0.872</b>	1.747	9.645	0.000
	LW	0.003	0.036	0.008	0.437	0.662
	VR	-0.303	-0.219	0.135	-2.245	0.025
	RD	0.004	0.087	0.004	0.919	0.358
	SD	16.263	<b>0.547</b>	2.679	6.071	0.000
	LAI	0.070	<b>0.706</b>	0.008	8.693	0.000

LAI moderately correlated to individual and strongly correlated to population. The other metrics showed low correlation (VR) and/or not statistically different. LAI was derived from multiplying SD (population indicator) and LAS (individual indicator), and turned out to be correlated with the two factors (individual and population). Dropping or only

included LAI in one factor in CFA model produced negative variances and poor model fit, also 2 factors with indicator less than 6 (3 indicators per factor) prone to producing unidentified model (Brown 2015; Kline 2016). In CFA model LAI was loaded on individual and population factors (non congeneric model; Figure 6). Model fit indices of CFA model indicated the model fit well with the data and all freely estimated parameters statistically significant:  $\chi^2(7)=5.195$  with  $p$  value=0.636, SRMR=0.049, RMSEA=0.00 (95% CI=0.00–0.092,  $p$  value=0.789), TLI=1.016, CFI=1.00.

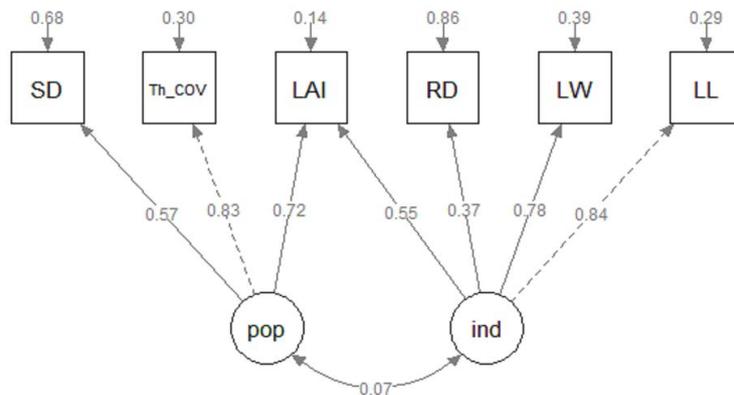


Figure 6. CFA model (standardized values; dash line indicated scaled indicators or anchored indicators in E/CFA).

**MIMIC model.** Status as covariates (two members: inhabited and uninhabited) added to the CFA model in MIMIC modelling (Figure 7), but the model did not provide a quiet good fit to the data. When LAI was dropped from the model (Figure 8), MIMIC model without LAI provided better fit to the data (Tabel 4). Direct effect of Status on both factors was statistically significant in both models (Tabel 5). The negative sign of unstandardized values from status to both of factors indicated that uninhabited location have a lower mean of *T. hemprichii* descriptors than inhabited location on both factors (in the second model the mean of inhabited location was 1.5 and 12.68 units higher than uninhabited location on the individual and the population factors respectively). Standardized factor column in Table 5 indicated inhabited location scored 0.932 and 1.069 standardized scores higher than uninhabited location on the individual and population factors respectively.

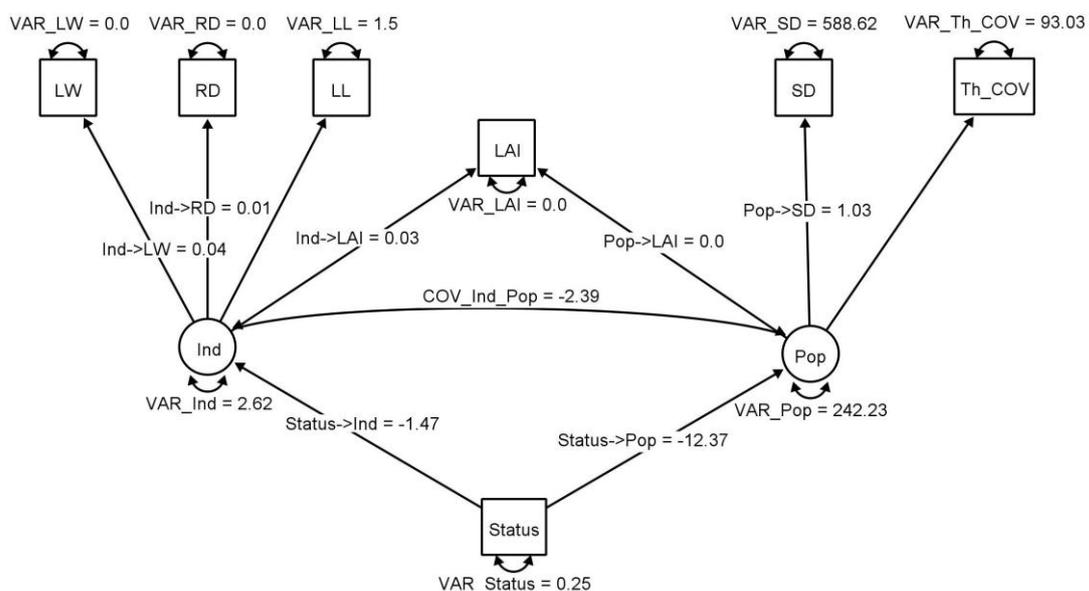


Figure 7. MIMIC model LAI included (unstandardized values).

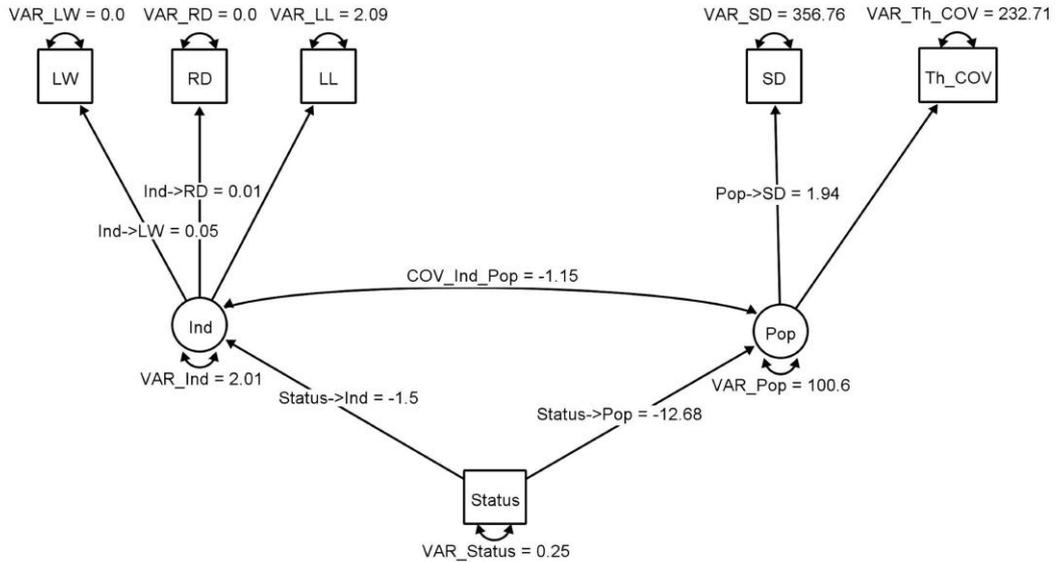


Figure 8. MIMIC model LAI not included (unstandardized values).

Table 4

Fit indices from two MIMIC model

<i>Fit Indices</i>	<i>MIMIC model LAI not included</i>	<i>MIMIC model LAI included</i>
npar	13.000	16.000
Chi square	12.963	27.934
df	7.000	11.000
pvalue	0.073	0.003
CFI	0.963	0.941
TLI	0.921	0.888
AIC	1976.535	1648.825
BIC	2012.880	1693.557
ntotal	121.000	121.000
RMSEA	0.084	0.113
rmsea.ci.lower	0.000	0.061
rmsea.ci.upper	0.154	0.166
rmsea.pvalue	0.189	0.026
SRMR	0.054	0.072

Table 5

Regression of status to the individual and population in the model without LAI

<i>Regressions</i>	<i>Estimate</i>		<i>Std. error</i>	<i>z-value</i>	<i>P(&gt; z )</i>	<i>Standardized factor</i>
	<i>Unstandardized</i>	<i>Standardized</i>				
Ind-Status	-1.495	-0.466	0.345	-4.339	0.000	-0.932
Pop-Status	-12.679	-0.534	3.309	-3.831	0.000	-1.069

**Discussion.** Measured *T. hemprichii* descriptors (LL, LW, VR, RD, SD, Th\_COV) showed clear pattern with their underlying dimensions (factors). CFA model clearly showed that LL, LW and RD could be used as indicators of individual factor and SD, Th\_COV could be used as indicators of population factor. Meanwhile for derived variables (LSA and LAI) their pattern with their underlying dimensions was rather complex to determine. Including LSA in the CFA model required specification of correlated error in the model because its high correlation with LL and LW brought multicollinearity into the model. LAI made non congeneric CFA model (LAI loaded on two factors) because it was derived from

individual and population indicators, and produced model that was not well suited to the data when covariates was added to CFA model (MIMIC model). Dropping LSA and LAI from the model made indicators only five left (VR was not strongly correlated with the two factors and dropped from the beginning), and with two factors specified, the minimum requirement of indicators are six to ensure identified model (although with five indicators the model could be identified but some condition must be met as showed in the MIMIC model). RD only showed marginal correlation on its factor, but dropping RD, VR, LAI and LSA from the CFA model definitely will produce unidentified model. These results emphasized the need for sufficient and reliable number of indicators with appropriate samples size. Another consideration to make related to this results is concept dimensionality of the factor used in the analysis because it will related to sufficient number of indicators needed for each factor (Grace 2006). Individual and population concepts are rather broad concepts thus the selection and combination of indicators of this factor which is sensitive, measurable and reflect the environmental alterations must be carefully determined prior the analysis as suggested by Rice (2003) and Martinez-Crego et al (2008).

In average, *T. hemprichii* descriptors in inhabited locations except for VR, showed greater values than *T. hemprichii* descriptors in uninhabited locations. Table 5 showed large effect of difference between inhabited and uninhabited locations. These results indicated that *T. hemprichii* could be potentially used as bioindicator for biomonitoring the environmental status of coastal waters related to anthropogenic pressure gradient. Nevertheless, our results showed different expected response to increasing anthropogenic disturbances from other seagrass species (*P. oceanica*, *C. nodosa* and *Z. noltii*) in non tropical area as reported by Romero et al (2007), Lopez y Royo et al (2010), Oliva et al (2012), and Garcia-Marin et al (2013). LL, LSA, SD and covering expected to decrease as anthropogenic pressure increasing, but our results showed that in inhabited locations these metrics were higher than in uninhabited locations. Our results about seagrass covering is also supported by long term monitoring (2007-2009) of NGO Terangi (Setyawan et al 2011) at TnLKs and by the Indonesian Institute of Sciences (LIPI) at Kepulauan Riau Province West Indonesia region (2015-2018, unpublished), both reported that in general seagrass was more abundant in residential areas. Based on field survey and observation of our study sites, *T. hemprichii* species scattered and clustered near the beach of islands, mixed with other species to a depth of approximately 3 meters in highest tide, away from populated islands and in more deep water *T. hemprichii* decreased conspicuously. The previous studies (Romero et al 2007; Martinez-Crego et al 2008; Gobert et al 2009) mostly used seagrass species from deep water areas (>5 m), in TnLKs areas at deep of >5 m seagrass are rarely found (mostly absent from the site). The depth was likely to be one of the causes of the different seagrass descriptor responses of this study and the previous studies. These results emphasized the importance of selection of seagrass descriptor to examined response of seagrass to anthropogenic pressure gradient for all ecological levels. The descriptors should be appropriate, sensitive and robust to magnitude of anthropogenic pressure, and confirmed empirically over a whole existing environmental gradient, especially in tropical areas where related studies have not been comprehensively carried out.

**Limitations.** Our study was only involving eight *T. hemprichii* descriptors in two level in analysis, further research is needed to examine all seagrass descriptors that are sensitive to anthropogenic pressure and encompass the multiple levels (individual, population, community) with appropriate descriptors for each level over a whole existing environmental gradient.

**Conclusions.** We have explored and confirmed the latent structures (factors) of eight *T. hemprichii* descriptors using E/CFA, CFA and MIMIC model. The final CFA model showed that the measured *T. hemprichii* descriptors have clearer latent structures than the derived *T. hemprichii* descriptors. *T. hemprichii* descriptors showed large effect differences between inhabited and uninhabited locations. *T. hemprichii* potentially could be used as bioindicator for biomonitoring environmental quality for tropical coastal

waters, nevertheless further comprehensive research is needed to explore, examine and establish *T. hemprichii* descriptors that are sensitive to anthropogenic pressure along different environmental gradient.

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