# Taxonomy of the Brown Algal Genus *Padina* With the Description of the New Species *Padina* sp. PG nov. (Dictyotales, Pheaophyceae) from the Northern Coast of Persian Gulf

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### Abstract

Padina is a marine brown macro algal genus, comprising of about 37 species. Representatives genus data along the Persian gulf coast is limited to a few floristic survevs. The present study introduces the Padina species along the Persian gulf coast, with emphasis on the molecular taxonomy. Sequences of the large subunit of RuBis-Co (rbcL) have been used in the molecular analysis of species and for phylogenetic purposes. Based on the rbcL sequences, four species are recognized along the Persian gulf coast: Padina sp. FA, Padina sp. PG, Padina sp. INDEGRO32 and Dictyota ciliolata. A new species, Padina sp. PG nov. is described based on morphology and molecular analyses. Twelve new sequences were generated among the samples examined.

**Keywords**: Macroalgea, *Padina* sp. PG nov., Molecular Systematic

### Introduction

Species of the marine brown algal genus *Padina* are widely distributed through out the tropics and recognize in the field with

their "fan-like" blade. According to Algae-Base (Guiry and Guiry, 2011) 37 species are currently recognized worldwide, in which 6 species were recorded in the northern of Persian gulf coast of Iran based on morphological studies (Børgesen, 1939; Nizamuddin and Gesner, 1970; Sohrabipour and Rabiei, 1996, 1999, 2005, 2008). Several studies about systematic of macroalgae in Persian gulf along Arabian coasts heve been done (Al-Hasan and Jones, 1989; Basson et al., 1992, 1989; Basson, 1979a, 1979b; Børgesen, 1939; DeClerk et al., 1997; Newton, 1955a, 1955b; Abdel-Kareem, 2009). Taxonomic studies of *Padina* species in the coast of Persian gulf, until recently were usually consisting of revisions or descriptions of the genus in this area, exclusively based on morphological characters (e.g. thallus shape, size and color) which might be variable (Trono, 1969; Ni-Ni-Win et al., 2011 a,b). Furthermore, several recent studies dealing with European and Mediterranean taxa have indicated that common morphological data without the support of DNA sequence data are an insufficient basis for estimates species diversity and knowl-

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edge of species boundaries (De Clerck et al., 2005, 2006). However a few papers, based on taxonomic sources, were published dealing with the marine algal flora of the Persian gulf, like the molecular studied on three Sargassum species that were done by Noormohammadi et al. (2011 a, b) in which they used RAPD and ISSR markers for analyses. In addition, Padina could be employed as a possible environmental bioindicator in Persian gulf (Amini et al., 2013). In this study, we execute molecular phylogenetic analyses using chloroplast rbcL gene sequences. The chloroplast encoded large subunit of the Ru-BisCo gene (rbcL) has been used in molecular phylogenetic studies of brown algae and has been demonstrated to be a useful molecular marker by authors (Cho et al., 2004; Hoshina et al., 2004; De Clerck et al., 2006; Cho et al., 2007; Bittner et al., 2008; Ni-Ni-Win et al., 2008, 2010, 2011b; Phillips et al., 2008). The aim of the present study was to characterize the molecular diversity from the new sequences of *Padina* species for the first time in Persian gulf and compare them with the *Padina* species in the other regions. Additionally, to describe the genus based on newly generated sequences from already available sequence data and describe two new species based on morphological and molecular analyses.

#### **Materials and Methods**

*Padina* samples (Phaeophyceae, Dictyotales, Dictyotaceae) were collected from the intertidal regions along the southern coast of Iran (the northern coast of Persian gulf) that showed in Figure 1 namely: Kish island (26° 51' N, 53°59' E), Lengeh area (26° 28' N, 54°78' E), Qeshm island include Shib Deraz (26° 42' N, 56°04' E), Messen (26° 49' N, 53°23' E), Behind Farmandari (27° 04' N, 56°59' E) from Persian gulf during May, June, August, September 2011 and March 2012 (Figure 1). The samples were obtained by hand and diving. Standard collecting and preserving proceeds follow Tsuda (1972) and molecular procedures carried out according



**Fig. 1.** Location of sampling for seaweeds on the intertidal Coast of Persian Gulf of Iran. 1-Kish island, 2- Lengeh area, 3-ShibDeraz (Qeshm island), 4-Messen (Qeshm island), 5-Behined Farmandari (Qeshm island).

to Siemer et al. (1998) and Ni- Ni-Win et al. (2008, 2011a). Collected samples were deposited in HSBU (Herbarium of Shahid Beheshti University). All specimens used for this study are listed in Tables 1 and 2.

Total genomic DNA was extracted from tissue samples, dried in a silica gel. DNA extraction, amplification (PCR) of the rbcL region and sequencing carried out using an extraction protocol detailed by Ni-Ni-Win et al. (2008 and 2011b). PCR conditions for rbcL were as follows: an initial denaturation step at 94°C for 3 min, followed by 94°C for 0.5 min, annealing at 58°C for 0.5 min, extension at 72°C for 2 min for 28 cycles, and final extension at 72°C for 10 min. PCR products were checked for length and yielded by electrophoresis on 1.5% agarose gels dyed with ethidium bromide. In order to minimize possible errors during PCR, three independent PCR reactions were performed for each DNA sample. Primer sequences, annealing temperatures, and bibliographic sources are provided in Table 3.

For anatomical observations, specimens were sectioned by hand and micrographed using a Dino capture Ver. 3 digital camera attached to a microscope (Olympus, Tokyo, Japan). For each specimen, morphological and anatomical characters (vegetative and reproductive) analyzed. According to Ni-Ni-Win et al. (2011a) some of the morphological characters such as shape, size, color, and thickness of the thallus are highly variable within the species and are depend on environmental conditions and age of the speciemens. But other characters like the number of cell layers, presence or absence and degree of calcification, the position and arrangement of hair lines and sporangial sori, and presence or absence of an indusium, the presence or absence of groups of rhizoid-like hairs on the thallus surface, the structure and arrangement of hair lines and reproductive sori were considered less variable within the species. The main anatomical characters used for species identification have been summarized in Table 4.

DNA sequences are deposited in DNA Data Bank of Japan (DDBJ). The 12 newly generated sequences were complemented with 31 sequences downloaded from GenBank and aligned using Thompson et al. (1994) and the alignment was refined manually. Phylogenetic analyses were carried out by maximum parsimony (MP), maximum likelihood (ML) and neighbor joining (NJ) methods, using MEGA5.1 (Tamura et al., 2011). An appropriate model of sequence evolution for maximum likelihood (ML) analysis was selected the best-fit models based on AICc values criterion with MEGA's built-in model testing suite. A ML tree was inferred using the selected GTR model using nearest neighbor interchange tree rearrangements. A neighbour-joining (NJ) distance-based tree was constructed (Saitou and Nei, 1987) using a Kimura 2-parameter method. Maximum parsimony (MP) analysis was obtained using a standard heuristic search with tree-bisection-reconnection (TBR) branch swapping options. Bootstrap resampling was carried out with 100 replicates for ML and 1000 replicates for NJ and MP (Felsenstein, 1985). Dictvota ciliolata and Dictvota dicoto-

Table1. S Beheshti	Species used in this study, University (HSBU).	from which all new	sequencing is ob	tained. Herbarium	ı of Shahid
Sequence	Species	Origin	Voucher No.	DDBJ code for	Reference
entry				rbcL	
1	Padina sp. PG, haplotype: 1	Qeshm Island, IR Iran	HSBU-2011300	AB793713	This study
2	Padina sp. FA haplotype: 2	Kish Island, IR Iran	HSBU-2011301	AB793714	This study
ω	Padina sp. INDGR032	Kish island, IR Iran	HSBU-2011302	AB793715	This study
4	Padina sp. FA haplotype: 4	Kish Island, IR Iran	HSBU-2011303	AB793716	This study
S	Padina sp. FA haplotype: 5	Kish Island, IR Iran	HSBU-2011304	AB793717	This study
6	Padina sp. FA haplotype: 6	Qeshm Island, IR	HSBU-2011305	AB793718	This study
Γ	Padina sp. FA haplotype: 7	Qeshm Island, IR Iran	HSBU-2011306	AB793719	This study
8	Padina sp. FA haplotype: 8	Kish Island, IR Iran	HSBU-2011307	AB793720	This study
9	Padina sp. FA haplotype: 9	Legeh Port, IR Iran	HSBU-2011308	AB793721	This study
10	<i>Padina</i> sp. FA haplotype: 57f	Kish Island, IR Iran	HSBU-2011309	AB793724	This study
11	Padina sp. FA haplotype: 2	Kish Island /LengehPort/ Qeshm Island, IR Iran	HSBU-2011310	AB775783	This study
12	Dictyota ciliolata	Qeshm Island, IR Iran	HSBU-2011311	AB775782	This study

Sequence entry	Species	Urigin	Voucher No.	DDBJ code for rbcL	
	Padina antillarum	India	INDGR032	AB096907	
2	Padina antillarum	Diani Beach, Kenya	ODC1508	JQ364044	Silberfeld et al., 2013
.3	P. australis Hauck	Baie de Gadji, Île des Pins, New Caledonia	IRD233	JQ364054	Silberfeld et al., 2013
4	P. australis Hauck	Sawang, Siquijor, Philippines	ODC1459	JQ364056	Silberfeld et al., 2013
S	P. australis Hauck	Japan	OKNNG019	AB096901	Hoshina et al., 2004
6	P. australis Hauck	Awase, Okinawa I., Okinawa Pref., Japan	SAP105579	AB358907	Ni-Ni-Win et al., 2008
7	P. australis Hauck	New Caledonia	IRD241	JQ364055	Silberfeld et al., 2013
8	P. australis Hauck	Urazoko, Okinawa I., Okinawa Pref., Japan	SAP105580	AB358906	Ni-Ni-Win et al., 2008
9	Padina australis	Awase, Okinawa I., Okinawa Pref., Japan	SAP105579	AB358907	Ni-Ni-Win et al., 2008
10	P. australis Hauck	Ngapalibeach, Thandwel (Sandoway), Myanmar		AB489914	Ni-Ni-Win et al., 2010
11	P. australis Hauck	Newcastle, NSW, Australia		AB489913	Ni-Ni-Win et al., 2010
12	Padina australis	Karang Jong E, Kepulauan Seribu, Indonesia	L0609534	AB489912	Ni-Ni-Win et al., 2010
13	Padina australis			AB512524	Ni-Ni-Win et al., 2011b
14	Padina australis	Ouano, New Caledonia	IRD167	JQ364052	Silberfeld et al., 2013
15	Padina australis	Australia		AB512525	Ni-Ni-Win et al., 2011b
16	Padina australis	Poindimié, New Caledonia	IRD158	EU579959	Silberfeld et al., 2013
17	Padina australis	Balabio, New Caledonia	IRD172	JQ364053	Silberfeld et al., 2013
18	Padina boergesenii	Dickwella, Sri Lanka	HEC15869	JQ364057	Silberfeld et al., 2013
19	Padina boergesenii	Dickwella, Sri Lanka	HEC15913	JQ364058	Silberfeld et al., 2013
20	Padina boergesenii	Cahuita, Costa Rica	LBC0930	JQ364059	Silberfeld et al., 2013
22	Padina boergesenii	Nungwi, Zanzibar, Tanzania	TZ0520	JQ364061	Silberfeld et al., 2013
23	Padina boergesenii	Paje, Zanzibar, Tanzania	TZ0848	JQ364063	Silberfeld et al., 2013
24	Padina boergesenii	Makunduchi, Zanzibar, Tanzania	TZ0863	JQ364064	Silberfeld et al., 2013
25	Padina boergesenii	Makunduchi, Zanzibar, Tanzania	TZ0872	JQ364065	Silberfeld et al., 2013
26	Padina tetrastromatica	Malaysia		AB512554	Ni-Ni-Win, 2011b
27	Padina tetrastromatica	Indonesia:KepulauanSeribu, Kelor		AB512553	Ni-Ni-Win, 2011b
28	Padina tetrastromatica	Thailand:Nakhon Si Thammarat, Huasai		AB512552	Ni-Ni-Win, 2011b
29	Dictyota ciliolata	Canary Islands	D191	GQ425109	Tronholm, 2010
30	Dictyota dichotoma	Korea		AY748311	Lee, 2004
31	Dictyota dichotoma	Japan: Kanagawa, Aburatsubo		AB358934	Ni-Ni-Win, 2008

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Table 3. The nan	ne and ref	erences of the	primers used in this study.		
Primer name	Gene	Direction	Sequence (5'a→3')	Annealing T°C	Reference
rbcL-P1	rbcL	Forward	GGGTAATTTGTAAGTGGATGCG	64	Ni-Ni-Win et al. (2008) Kawai et al. (2007)
rbcL-D2	rbcL	Reversed	CGACGAAGTCAGGAGTATCTG	61.4	Ni-Ni-Win et al. (2008) Kawai et al. (2007)
Fa(57-76)	rbcL	Forward	GTGGACTGTTGTTTGGACTG	60.6	Present study
Ra500-519	rbcL	Reverse	ACATTTACGAAGAGAAGCCC	59.7	Present study

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*ma* (Dictyotales) were considered as outgroup to root the trees.

#### Results

# Morphological observations

Padinasp.PG,haplotype:1nov.AB793713(HSBU-2011300)Habitat:Qeshm Island

The erect thalli with 2-4 cell layers, (4 cells layered at the base) is yellowish brown in color, the length between 5 to 10cm, and the width up to 4 cm, blades much divided, attached by branched rhizoidal stipe. Thalli moderately calcified on both surfaces. Sporangia rows are closely alternate with hair rows at different intervals without indusia, sometimes as isolated patches between two hair lines on the lower surface when both surfaces are viewed together. The species resembles P. tetrastromatica Hauck but the blades of P. tetrastromatica Hauck showed no calcification (Wynne et al., 1999) but this species has light calcification on two sides. In cross sections of the blades, both in mid region and in more basal portions, showed a 4-layered organization but Padina sp. PG has 2 cell layer and 4 layers at the base. Ecology: This species is a new species, usually grows in the lower portions of the intertidal zone on rocky substrates or shallow subtidal zones.

Etymology: The species epithet refers to Persian gulf.

Padinasp.FAINDGR032, haplotype:3AB793715(HSBU-2011302)Habitat:Qeshm Island, Hormozgan provinceThe thallus is bright brown with 2-4 cell layers,

1 morpho anato	omical c	haracter	s used ir	the taxonomic	; identification	n of Pad	<i>ina</i> species of	Persian gulf.		
Color	Leng th (Cm)	Width (Cm)	Cell layer (thallu s)	Calcify on Lower/Upper surface	Sporangial surface	Indosia	Phaeophyce an hairs	Stip with Rust-colored Fibrous hairs	Origin	Accession number
Yellowish	5-10	4-10	2-4	light / light	Upper/Lower	Absent	Upper/Lower	Present	Qeshm Island	AB793713
Dark brown	4-10	4-10	2	Light/ heavy	Upper	Present	Upper	Present	Kish Island	AB793714
Bright brown	5-9	5-9	2-4	Light/ light	Upper/Lower	Absent	Upper/Lower	Present	Kish Island	AB793715
Dark brown	4-6	5-9	2-6	Light/Light	Upper	Present	Upper	Absent	Kish Island	AB793716
Bright brown	10-15	5-8	2	Light/Heavy	Upper/Lower	Present	Upper	Absent	Qeshm Island	AB793717
Yellowish	4-6	6-10	2-6	Heavy/Heavy	Upper	Present	Upper/Lower	Absent	Qeshm Island	AB793718
Bright brown	5-15	8-15	2	Heavy/Heavy	Upper/Lower	Present	Upper/Lower	Absent	Kish Island	AB793719
Bright Brown	4-6	6-9	2-4-6	Heavy/Heavy	Upper	Present	Upper	Absent	Legeh Port	AB793720
Dark brown	5-9	4-8	2-4	Heavy/Heavy	Upper	Present	Upper/Lower	Absent	Kish Island	AB793721
Darkbrown	10-17	10-13	2-4-6	Heavy/Heavy	Upper	Present	Upper	Absent	Kish Island /Lengeh Port/ Oeshm and	AB793724
Brightbrown	5-7	4-6	2-4-6	Heavy/Heavy	Upper/Lower	Present	Upper	Absent	Kish Island /Lengeh Port/	AB775783
	Color Color Yellowish Dark brown Bright brown Bright brown Bright brown Bright brown Bright Brown Dark brown Dark brown	Colorth (Cm)Yellowish5-10Dark brown4-10Dark brown5-9Bright brown10-15Bright brown10-15Bright brown5-15Bright brown5-15Bright brown5-9Dark brown5-15Bright brown5-15Bright brown5-9Dark brown5-9Dark brown10-17Brightbrown5-9	Yellowish5-104-10Dark brown4-104-10Dark brown4-65-9Bright brown10-155-8Yellowish4-66-10Bright brown5-158-15Bright brown5-158-15Bright brown5-94-8Dark brown5-94-8Dark brown5-94-8Dark brown10-1710-13Bright5-94-6Bright brown5-94-8Dark brown10-1710-13Brightbrown5-74-6	ColorLeng th constant of the functionWidth functionlayer (Cm) functionCell functionYellowish5-104-102-4Dark brown4-65-92-4Dark brown10-158-152Bright brown5-158-152Bright brown5-158-152Bright brown5-92-4-6Dark brown5-92-4-6Darkbrown10-1710-132-4-6Brightbrown5-74-62-4-6	Inmorpho anatomical characters used in the taxonomicColor $\begin{array}{c} Leng \\ cm \\ c$	InterpretationColorCell (Cm)Cell Lower/UpperSporangial Lower/UpperVellowish5-104-102.4light / lightUpper/LowerDark brown4-102.4light / lightUpper/LowerDark brown4-65-92.4Light/ lightUpper/LowerDark brown4-65-92.4Light/ lightUpper/LowerBright brown10-155-82Light/HeavyUpper/LowerBright brown5-158-152Heavy/HeavyUpper/LowerBright brown5-158-152Heavy/HeavyUpper/LowerBright brown5-158-152Heavy/HeavyUpper/LowerBright brown5-94-82-4Heavy/HeavyUpper/LowerBright brown5-94-82-4Heavy/HeavyUpper/LowerBright brown5-94-82-4Heavy/HeavyUpper/LowerBright brown5-94-82-4Heavy/HeavyUpper/LowerBright brown5-94-82-4Heavy/HeavyUpper/LowerBright brown5-94-82-4Heavy/HeavyUpper/LowerBright brown5-94-82-4Heavy/HeavyUpper/LowerBright brown5-94-82-4Heavy/HeavyUpper/LowerBright brown5-94-82-4Heavy/HeavyUpper/LowerBright brown5-74-6 </td <td>Interpret on anatomical characters used in the taxonomic identification (Cm)Cell Laver (Cm)Cell Laver (Laver (Cm)Cell Laver (Laver 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gulf.Color<math>\frac{\mathrm{Leg}}{\mathrm{(Cm)}}</math><math>\frac{\mathrm{Vitth}}{\mathrm{(m)}}</math><math>\frac{\mathrm{Calcity}}{\mathrm{(m)}}</math><math>\mathrm{Calcity}{\mathrm{(m)}}</math><math>\mathrm{Sperangial}{\mathrm{(m)}}</math><math>\mathrm{Indexia}</math><math>\frac{\mathrm{Phaophyce}}{\mathrm{marbar}}</math><math>\frac{\mathrm{Sip}}{\mathrm{marbar}}</math><math>\mathrm{Vitth}}{\mathrm{Super/Lower}}</math><math>\mathrm{Sperangial}{\mathrm{marbar}}</math><math>\mathrm{Phaophyce}{\mathrm{marbar}}</math><math>\mathrm{Spir}{\mathrm{marbar}}</math><math>\mathrm{Origin}{\mathrm{marbar}}</math>Vellowish5-104-102.4light/ lightUpper/LowerAbsentUpper/LowerPresentQeshm IslandDark brown4-102.4Light/ heavyUpper/LowerPresentUpper/LowerPresentUpper/LowerPresentKish IslandDark brown5-95-92.4Light/ HeavyUpper/LowerPresentUpper/LowerAbsentAbsentKish IslandDark brown10-155-82Light/HeavyUpper/LowerPresentUpper/LowerAbsentCeshm IslandBright 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$\mathrm{Indexia}$ $\frac{\mathrm{Phaophyce}}{\mathrm{marbar}}$ $\frac{\mathrm{Sip}}{\mathrm{marbar}}$ $\mathrm{Vitth}}{\mathrm{Super/Lower}}$ $\mathrm{Sperangial}{\mathrm{marbar}}$ $\mathrm{Phaophyce}{\mathrm{marbar}}$ $\mathrm{Spir}{\mathrm{marbar}}$ $\mathrm{Origin}{\mathrm{marbar}}$ Vellowish5-104-102.4light/ lightUpper/LowerAbsentUpper/LowerPresentQeshm IslandDark brown4-102.4Light/ heavyUpper/LowerPresentUpper/LowerPresentUpper/LowerPresentKish IslandDark brown5-95-92.4Light/ HeavyUpper/LowerPresentUpper/LowerAbsentAbsentKish IslandDark brown10-155-82Light/HeavyUpper/LowerPresentUpper/LowerAbsentCeshm IslandBright brown5-158-152Heavy/HeavyUpper/LowerPresentUpper/LowerAbsentCeshm IslandBright brown5-94-82.4Heavy/HeavyUpperPresentUpper/LowerAbsentCeshm IslandBright brown5-94-82.4Heavy/HeavyUpperPresentUpper/LowerAbsentCeshm IslandDark brown5-94-82.4Heavy/HeavyUpperPresentUpper/LowerAbsentKish Island <tr<tr>Coeshm Island</tr<tr>

the range of the wide is the same as the long, 5-9 cm. Thallus attached by a thick, discoid holdfast, stipe short with Rust-colored Fibrous hairs, lightly calcificated on both surfaces of the thallus, sporangial sori without indusium is alternating with hair lines on both surface. Ecology: This species is a new species, usually grows in the lower portions of the intertidal zone on rocky substrates.

## Padina sp. FA

Habitat: Qeshm Island, Hormozgan province The sequences obtained for the rbcL of 11 *Padina* sp. FA samples collected along the coast of Persian gulf yielded 9 distinct haplotypes. There are high similarities among the haplotypes of *Padina* sp. FA and their morphological characters are very similar to those of *P. boergesenii* and *P. australis*. The following characters are similar to more samples of haplotypes. Sporangia with indusium, relatively high calcified on lower and upper surface. They all have more than five blades.

Etymology: The species epithet refers to the name of author.

Ecology: This haplotype is a new reported for the first time in Iran, usually grows in the lower portions of the intertidal zone on rocky substrates.

# *Padina* sp. FA, haplotype: 2 AB793714 (HSBU-2011301)

Habitat: Kish Island, Intertidal

The thallus is two cells thick through out, up to 7 cm high, usually become 3 cells layered at the base. Generally blades dark brown in color, more deep develops from a stipe short withRust-colored Fibrous hairs. Sporangia rows



**Fig. 2.** A and B. Habitat, C. 2 cell layers transverse section of the middle portion of thallus, D. The view of 3 layers with hair lines (arrow) ×40.



Fig. 3. A. Habitat, B. The view surface, C. Longitudinal section of the thallus $\times 100$ .

were always situated on the upper surface with indusium, closely alternate with hair rows at equal intervals. Hairs in concentric lines only on the upper surface. The calcification is heavy on upper surface and light calcificated on the lower surface.

# *Padina* **sp. FA**, haplotype: 4AB793716 (HSBU-2011303)

Habitat: Kish Island, Intertidal

The erect dark brown thalli with 2-6 cell layers, are relatively small, wider than tall at 4-6 cm long and 5-9cm wide. Calcification islight on both surfaces. Sporangia with indusium principally on the outer surfacealternating with hair lines, usually in small clusters with a thin indusium. Concentric hair lines on the upper surface of the thallus.

# *Padina* **sp. FA**, haplotype: 5AB793717 (HSBU-2011304)

Habitat: Qeshm Island, Intertidal

The bright brown thallus (2 cell layers) is relatively large with 10-15 length and 5-8 width, lightly calcified on the lower surface and moderately to heavily on the upper surface, sporangia principally on the outer surface and sometimes also on the inner surface, usually in small clusters with indusium, hair lines on upper

*Padina* **sp. FA**, haplotype: 6AB793718 (HSBU-2011305) Habitat: Qeshm Island, Intertidal



**Fig. 4.** A. Habitat, B. The surface view with the length of cell  $\times$ 40, C. Cross section showed two cell layers  $\times$ 40.

The yellowish thallus (2-6 cell layers) has 4-6 cm long and 6-10 cm wide. Upper and lower surfaces with heavy calcification. Sporangial sori is alternating with hair lines.

# *Padina* sp. FA, haplotype: 7 AB793719 (HSBU-2011306)

Habitat: Kish Island, Intertidal

Thalli is bright brown with 2 cell layers and 5-15 cm long and 8-15 cm wide , stipe short without rust-colored fibrous hairs, heavily calcified on both surfaces except for hair lines, indusium present, hair lines on both surfaces sporangial sori alternating with hair lines, sporangial sori on both surface.

## Padina sp. FA, haplotype: 8AB793720

#### (HSBU-2011307)

Habitat: Lengeh Port, Intertidal

Thalli (2-4-6 cell layers) with bright brown in color,4-6 cm long and 6-9 cm wide, hair lines on upper surface and alternating with sporangial sori without indusium, heavy calcification is on upper and lower surfaces.

# *Padina* **sp. FA**, haplotype: 9AB793721 (HSBU-2011308)

Habitat: Kish Island, Intertidal

The length of bright brown thallus (2-4 cell layers) is 5-9 cm and the width is 4-8cm. Calcification is heavy on Upper and lower surfaces, sporangial sori on upper surface. Thallus dark brown with 2-4cell layers, 5-9 length, 4-8 width, high calcified on two sides spo-



**Fig. 5.** A. Habitat, B. Longitudinal section×40, C. Hair lines (arrowhead) sporangium line (arrow) ×40.

rangial on upper surface, reproductive organs and Phaeophycean hairs present in concentric zones.

# *Padina* **sp. FA**, haplotype: 57FAB793724 (HSBU-2011309)

Habitat: Kish Island, Lengeh Port, Qeshm Island, Intertidal

Thallus color is dark brown with 2-6 cell layers, up to 10-17cm length and 10-13cm width, hair lines on upper surface, sporangial sori alternating with hair, calcification is on upper and lower surfaces heavily.

*Padina* **sp. FA,** haplotype: 2AB775783 HSBU-2011310 Habitat: Qeshm island, Intertidal Thalli (2-6 cell layers) has 5-7 long and 4-6 wide color is bright brown, hair lines on upper surface sporangial sori alternating with hair lines sporangial sori on upper and lower surfaces, upper and lower surfaces is heavily calcified. They are yellow greenish in color. Apices are acute to round and sometimes somewhat incurved is completely erect with more than 10 cm.

#### Molecular phylogenetic analysis

The chloroplast-encoded rbcL gene has been extensively used in molecular phylogenetic studies of brown algae and has been demonstrated to be a useful molecular marker by authors (Hoshina et al. 2004; De Clerck et al., 2006; Lane et al., 2006; Cho et al., 2007; Bittner et al., 2008; Ni-Ni-Win et al., 2008 and



**Fig. 6.** *Padina* sp. FA haplotype 6: A. Habitat, B. Longitudinal section×40.



**Fig. 7.** *Padina* sp. FA haplotype 7: A. Habitat, B. Hair lines (arrow head) sporangium line (arrow) ×40.

2010). The rbcL alignment consisted of 12 sequences representing three Padina species and one out group taxa, including twelve new sequences and yielded 10 distinct haplotypes along the coast of Persian gulf (Table 1). Figures 13 and 14 showed the main monophyletic groups were constant in performed analyses. The first clade (Fig. 14) presented high bootstrap values (99-100% support) in all analyses (ML, NJ, MP) and included 9 haplotypes

of *Padina* sp. FA from Persian gulf which grouped with *Padina boergessenii*.

Phylogenetic trees constructed from the ML and NJ analyses showed a similar topology. P. boergessenii specimens and *Padina* sp. FA haplotypes were closely allied, and formed a strongly supported monophyletic group with high bootstrap confidence of 90%. Padina boergesenii with JQ364063 and JQ364065 accession numbers are clearly separated from the



**Fig. 8.** *Padina* sp. FA haplotype 8: A. Habitat, B. view surface hair lines (arrow head) of tetrasporangium line (arrow) ×40.

strongly monophyletic group consisting of the other P. boergessenii specimens and Padina sp. FA haplotypes. Padina sp. FA haplotypes are morphologically similar to Padina australis which have 2-6 layers but they are molecularly similar to P. boergesenii from Zanzibar, Tanzania which has 0-7 nucleotide differences. However, these similarities cover the partial of the nucleotides. In other words, all nucleotides of this study are almost 490 bp, but this is a comparison among 275 nucleotides. Padina sp. FA haplotypes are morphologically similar to Padina australis which have 2-6 layers but they are different from P. Australis with more than 10 nucleotides.. Other taxa Padina sp. PG and Padina sp. INDEGRO32 included in clade 2 in Figure 13 and in calde 3 of Figure 14. Morphological study showed that Padina sp. PG is closely to P. antillarum (P. tetrastromatica). As previously noted the differences between species are the calcification of blades and the number of cell layers. The phylogenetic trees confirmed Padina sp. PG was always nested in the diverse clade of the P. antillarum.

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This placement was highly supported with 92% bootstrap confidence (Fig. 14). *Dictyota ciliolata* and *Dictyota dicotoma* is used as outgroup.

#### Discussion

Molecular phylogenetic analyses using rbcL sequences, combined with morphological observations, showed the occurrence of two undescribed Padina species in Persian gulf coasts. Padina sp. FA most closely related P. australis and P. boergesenii. The members of the P. boergesenii and Padina sp. FA haplotypes are the most strongly grouped in the trees constructed in the present study (Fig. 14). This result suggests that these species might have evolved closely to each other, but separately from the other species of the P.boergessenii. Given the close similarity of Padina sp. FA haplotype sequences to the P.boergessenii sequences, it seems safe to assume that these samples are conspecific, in addition, there are some differences in nucleotides between 0 to 8 positions. In order to investigate wheth-



**Fig. 9.** *Padina* sp. FA haplotype 9A: Habitat, B. Longitudinal section Transverse section of tetrasporangial sori, showing obovate tetrasporangia (arrow) ×40.



**Fig. 10.** *Padina* sp. FA haplotype 57FA: Habitat, B. view surface view surface hair lines (arrowhead) Tetrasporangium line (arrow) ×40.

er the *Padina* sp. FA is a new species or the conspecific with the *Padina boergesenii* it is necessary to make further studies. Also more samples and using different molecular markers is needed. Until further studies clarifing their taxonomic status, we prefer to set the *Padina* sp. FA samples as a new species, since they were indistinguishable in morphology and positioned in a monophyletic clade in all analyses of rbcL gene and other markers.

Phylogenetic relationships among the Padina

sp. INDEGRO32 and *P. antillarum* species can be clear. The phylogenetic analyses of the rbcL data show the monophyly groupings. The monophyly of Padina was fully supported (De Clerck, 2006).

*Padina* sp. PG is very similar to *Padina antillarum* (Kützing) Piccone = *P. tetrastromatica* Hauck but the blades of *P. tetrastromatica* showed no calcification (Wynne et al., 1999). In cross sections of the blades, both in mid region and in more basal portions, *Padina* sp.



**Fig. 11.** *Padina* sp. FA haplotype 2: A. Habitat, B. Transverse section of tetrasporangial sori, showing obovate tetrasporangia and C. Tetrasporangium on surface *Dictyota ciliolata* AB775782.



**Fig. 12**. Dictyota ciliolate AB775782: A. Habitat, B. Transverse section.



Fig. 13. Maximum likelihood tree (-1n L = 531.2360) based on rbcL gene sequences. Numbers at each node indicate bootstrap values (>50%) for maximum



Fig. 14. Maximum likelihood tree (-1n L= 702.1252) based on rbcL gene sequences. Numbers at each node indicate bootstrap values with only values>70% being shown for maximum likelihood (ML) (left), maximum parsimony (MP) (middle) and neighbor joining (NJ) (right). The Persian gulf specimens whose sequenced were determined in the present work are in green boxes.

PG showed a 4 layered organization but this species has 2 cell layer and 4 layers at the base. Molecular studies confirmed this dividing. A sequence of *Padina* sp. FA is genetically identical with those of *P. australis* and *P. boergesenii*. Therefore, we consider *Padina* sp. FA to be conspecific with *P. boergessenii*. Many Padina species may remain to be discovered. This species is possibly endemic to Persian gulf. However, additional sampling in other regions might be able to confirm either its endemism northern or southern of Persian gulf.

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