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HPLC-Based Chemotaxonomy of Florida Bay Phytoplankton: Difficulties in Coastal Environments

J. William Louda^a

^a Organic Geochemistry Group, Department of Chemistry and Biochemistry, Florida Atlantic University, Boca Raton, Florida, U.S.A

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HPLC-Based Chemotaxonomy of Florida Bay Phytoplankton: Difficulties in Coastal Environments

J. William Louda

Organic Geochemistry Group, Department of Chemistry and Biochemistry, Florida Atlantic University, Boca Raton, Florida, U.S.A

Abstract: This report covers high performance liquid chromatography (HPLC) derived pigment based chemotaxonomy for phytoplankton studies in a turbid coastal environment. Sediment resuspension brings detritus with pheopigments and other chlorophyll (CHL) breakdown products into the water column and hampers data interpretation. Two hundred sixty six water samples from Florida Bay were analyzed from monthly collections (Sept. 2000–Aug. 2002). Comparing biomarker estimated CHL*a* to measured CHL*a*, we found a mean of 105.4% (Std. Dev. = 24.7; R² = 0.9547) and when data was restricted to those samples with <10% pheopigments, estimations improved to 102 ± 16%. It is concluded that all HPLC studies on phytoplankton communities must report the percentage pheopigments.

Keywords: HPLC, Pigments, Chlorophyll, Pheopigments, Chemotaxonomy

INTRODUCTION

High performance liquid chromatography (HPLC) derived pigment based chemotaxonomy has been reviewed by Millie and co-workers^[1] and expanded by Paerl and others.^[2] Only through chromatographic advances, such as the ion pairing techniques popularized by Mantoura and Llewellyn^[3] and many others, has dissection of the full range of polar through non-polar lipid

Correspondence: J. William Louda, Organic Geochemistry Group, Department of Chemistry and Biochemistry, Florida Atlantic University, Boca Raton, FL 33431, U.S.A. E-mail: blouda@fau.edu

soluble pigments been possible in a single analytical procedure. The popularity of pigment based chemotaxonomic studies on microalgae is reflected by studies on: (1) the separation of the chlorophylls-*c* to better define the chromophytes;^[4] (2) community structure in lakes,^[5–8] estuaries,^[9–12] or the sea;^{[13– ^{18]} and (3) detailing anoxygenic photosynthesis by purple and green/brown sulfur bacteria in both lakes and the sea.^[6,13,19–21]}

The importance of studies of phytoplankton community structures is easily noted from The Scientific Committee on Oceanic Research (SCOR) of the United Nations Educational, Scientific and Cultural Organization (UNESCO) directing and publishing an in depth study and review of guidelines and recommendations for pigment based chemotaxonomy.^[22]

At the heart of pigment based chemotaxonomic studies is the assertion that, once the overall pigment array has been analytically dissected, the distribution of the primary (chlorophylls) and secondary/accessory (carotenoids, phycobiliproteins) photosynthetic pigments can be mathematically deconvoluted in ways that reflect the taxonomic makeup of the sampled community. That is, specific biomarker pigments (examples in Appendix A) should be present in known ratios to a biomass commonality, such as Chlorophyll-a (CHLa) in the oxygenic photoautotrophs. As an example, a number of diatom species have been studied by the author and many more are reported in the literature^[7,9,15,17] and these, except those reported from the Southern Ocean,^[23,24] yield average chlorophyll-a -to- fucoxanthin molar ratios of 1.2 + 0.3:1 (1.6:1 by wt.). Thus, the moles of diatom (or chrysophyte) contributed CHLa should be about 1.2 times the moles, or about 1.6 times the mass, of fucoxanthin found in a natural phytoplankton sample, if diatoms are the only fucoxanthin contributor in the community. Next, comparison of the 'diatom CHLa' to the CHLa similarly calculated for other taxa (e.g., from chlorophyll-b for chlorophytes, peridinin for dinoflagellates, 19'-hexanovloxyfuxoxanthin and/or 19'-butanovloxy-fucoxanthin for prymnesiophytes/nanoflagellate chrysophytes, alloxanthin for cryptophytes, prasinoxanthin for prasinophytes, and zeaxanthin, echinenone and/or myxoxanthophyll for cyanobacteria), or directly from divinyl-chlorophyll-a for the prochlorophytes (cf. Paerl et al.^[2]), should then allow the relative percentage of each taxon (=taxon-specific CHLa) within the source community to be back calculated. The overall method employs (regression) formulae based upon the study of unialgal cultures, field samples, and/or literature values. Alternatively, CHEMTAX, a matrix factorisation program using a "steepest descent algorithm"^[23–25] may be utilized. A comparison of multiple linear regressions (MLR) and the CHEMTAX algorithm has been published^[26] and problems with CHEMTAX in certain coastal environments have been noted.^[25,27] "Methods that rely more strongly on empirically determined pigment ratios"^[27] are stressed herein, in order to "reflect the dominant phytoplankton species present".^[25]

We have chosen a modified MLR approach for our studies in Florida Bay, the Everglades and Lake Okeechobee as well defined major species are known

and interest here is in rapidly assessing plankton functional groups (PFGs)^[2] as a measure of bulk community dynamics for monitoring purposes.

Given that the Everglades and Florida Bay are linked within the Comprehensive Everglades Restoration plan and that methods for the rapid temporal and spatial monitoring of microalgal communities are needed (CERP-MAP),^[28] an evaluation of HPLC derived pigment based chemotaxonomy in the high light turbid interface of these systems and within the bay proper was undertaken.

EXPERIMENTAL

Study Area and Field Samples

This study sampled sites within north-central and western Florida Bay (Figure 1).

Monthly sampling at thirteen main stations (1-12 plus OS5) occurred between September 2000 and August 2002. Water samples were collected at about 0.3 m into triple rinsed brown 2 L Nalgene bottles, occlusively sealed, and transported to shore in the shade. Water was filtered through Whatman GF/F filters, which were then folded, blotted, refolded (quarters), blotted and sealed in aluminum foil, and flash frozen by immersion in liquid nitrogen. Filtration and all subsequent operations were conducted in dim, usually yellow light. Samples were transported from Flamingo to the FAU lab on dry ice and stored frozen until analyzed within 1-2 weeks.



Figure 1. Map of Florida Bay with sampling sites labeled.

Unialgal Cultures

Numerous unialgal cultures were analyzed for biomarker pigment ratios. These cultures included the following groupings by source: (a) Synechococcus elongatus, Cyclotella choctawatcheeana, and a "2 micron prokaryotic picosphere", all isolated clones from Florida Bay and provided by Carmelo Tomas, then of the Florida Marine Research Institute in St. Petersburg. (b) Isochrysis galbana from John Scarpa at Harbor Branch Oceanographic Institute in Ft. Pierce, Florida. (c) 8 cyanobacteria, 10 chlorophytes, 1 euglenophyte, 4 non-diatom chrysophytes, 7 diatoms, and 4 dinoflagellates purchased from the Living Materials Division of Carolina Biological Supply or the Provasoli-Guillard National Center for Culture of Marine Phytoplankton (CCMP). Several of these were ordered two or more times over the period of several years; and, (d) the dinoflagellates Amphidinium carterae (CCMP#1314), Prorocentrum hoffmanianum (CCMP#683), P. micans (CCMP#1591), Heterocapsa triquetra (CCMP#448), and 3 isolates of Karenia brevis (CCMP# 718, 2228, 2229) were gifts from K. S. Rein of the Advanced Research Cooperation In Environmental Health (ARCH) program at Florida International University.

Pigment Extraction and Analysis

Pigment extractions were performed at ice bath temperatures using pre-chilled solvent, containing a known amount of a procedural internal standard ("IS"; Cu-mesoporphyrin-IX-DME, aka Cu-MESO-IX-DME), by grinding (350-500 rpm) at ice bath temperature ($\sim 2-3^{\circ}$ C) in a Teflon/glass homogenizer (Kontes "Duall"TM, 15 mL) that had been previously stored in a freezer. The extractant/glass fiber mixture, in the mortar or the homogenizer, was sonicated in an ice bath 5-10 times in 3-5 second spurts and then allowed to steep at 2-3°C for 2-3 hours. Steeping for prolonged periods (6-72 h) of time was found to release only minor amounts (<5%) of additional pigment,^[29,30] and likely leads to unwanted isomerizations and other artifacts (e.g., phytol/Mg²⁺ losses etc., cf. Chapters in Jeffrey et al.).^[22] Throughout much of the present study, the extraction solvent was 90% aqueous acetone. We have also explored alternate extraction cocktails and found that both acetone/methanol water (45:45:10, v/v/v) and methanol/ acetone/dimethylformamide/water (aka MADW; 30:30:30:10, v/v/v/v) are also excellent extractants, and lead to much better separation and peak shapes of the early eluting (polar) pigments.^[29,30] The later extractant mixture was used during the last several months of the present study. Extracts were recovered by centrifugation and subsequently filtered through a 0.45 μ m syringe filter. The overall UV/Vis spectrum (330–800 nm) of the filtered extract was recorded on a Perkin-Elmer Lambda-2 instrument, calibrated against holmium oxide for wavelength and absorbance. The

injectate was prepared using 1.00 mL of filtered extract and 0.125 mL of an ion pairing solution ("IP": ammonium acetate plus tetrabutylammonium acetate) made according to Mantoura and Llewellyn.^[3]

Separation and identification of chlorophylls, chlorophyll derivatives, and carotenoids was by the 2D analytical technique of reversed-phase high performance liquid chromatography (RP-HPLC), coupled with full spectral (190-800 nm) photodiode array detection (PDA, also called diode array detection = DAD). RP-HPLC was performed using $3.9 \times 150 \text{ mm}$ (or 300 mm) Waters NovaPak 4-micron C₁₈ columns, developed with a ternary gradient (Table 1) close to that we previously reported.^[8,20-21,29] Prepared extracts were loaded and injected with a Rheodyne 7125 injector and solvents were delivered with a Thermo-Separations Products Model 4100 quaternary HPLC pump at 1.00 mL min⁻¹. The present HPLC method was developed using over 85 known carotenoids, chlorophylls, and chlorophyll derivatives. the known amount of Cu-MESO-IX DME (IS) in the injectate was divided by the detected amount and the response correction factor $(=IS_{added}/IS_{detected})$ which averaged 1.2 \pm 0.1 was then applied to all peaks. The exact times of elution of the internal standardfucoxanthinzeaxanthinchlorophyll-a and β -carotene were utilized to adjust for slight run-to-run retention time drift due to operatorinjectionand solvent differencesas well as column aging. HPLC-PDA responses were standardized versus known pigments^[21,31] Overall response (QA/QC) of the system was monitored with the procedural internal standard (IS) added to the extracting solvent mixture. Here the known amount of Cu-MESO-IX DME (IS) in the injectate was divided by the detected amount and the response correction factor (=IS_{added}/IS_{detected}) which averaged 1.2 ± 0.1 was then applied to all peaks. The exact times of elution of the internal standard, fucoxanthin, zeaxanthin, Chlorophyll-a and b-carotene were utilized to adjust for slight

Time (minutes)	Solvent "A"	Solvent "B"	Solvent "C"
0	60	40	0
5	60	40	0
10	0	100	0
40	0	30	70
45	0	30	70
46	0	0	100
47	0	100	0
48	60	40	0

Table 1. Solvent profile used with RP-HPLC

Solvents: "A" = 0.5 M ammonium acetate in methanol/water (85:15, v/v); "B" = Acetonitrile/water (90:10, v/v); "C" = ethyl acetate.

All gradients were linear. Column stored in methanol/water (85:15, v/v). Profile as modified from Kraay et al.^[4] (Mantoura and Llewellen^[3]).

run-to-run reterntion time drift due to operator, injection, and solvent differences as well as column aging. HPLC-PDA responses were standardized versus known pigments^[31] that were isolated from unialgal cultures, formed by in vitro derivatizations, purchased (Sigma, VKI-Denmark) or received as gifts (Hoffman-LaRoche). Periodic co-injections, notably with alloxanthin, were made as part of our routine QA/QC protocol.

Quantitation relied on the Beer-Lambert relation wherein peak areas at an appropriate wavelength (440 nm = chlorophylls, carotenoids; 410 nm = pheopigments, 394 nm = internal standard, 360 nm = bacteriochlorophyll/bacteriopheophytin-*a*, etc.) were divided by an extinction coefficient from the literature.^[22,32] Extinction coefficients that were used but did not correspond to the exact maximum for which it was reported were adjusted by the ratio of the HPLC monitoring/integrating wavelength to the wavelength of the reported coefficient. This quantitation protocol was verified using solutions of authentic known pigments that were prepared using standard spectrophotometric techniques (Chapters in Jeffrey et al.).^[22] Multiplication by the effective volume adjusted for dilutions, such as the addition of an ion pairing solution to the injectate, gave the overall yield of individual pigments.

Microscopic Examinations

Aliquots (\sim 125 mL) from several of the water samples analyzed for pigments were sent to two separate commercial phytoplankton laboratories for cell counts and biovolume estimates to the species level and were totaled into Divisional values by the author. These aliquots were added to 125 mL brown Nalgene bottles, made up to a final concentration of 0.25–0.50% glutaraldehyde for preservation, occlusively sealed, placed on ice, and mailed to the microscopy laboratories (Labs "A" and "B") for identification to division and provision of cell numbers and estimated biomass.

RESULTS AND DISCUSSION

Chemotaxonomic Equation(s) Development

In order to convert HPLC pigment data into (chemo-) taxonomic groupings, one must relate the individual biomarker relationships to a commonality, such as chlorophyll-*a*. To that end, literature surveys, analyses of unialgal cultures, and interpretations of field data were performed.

The present compilation (Table 2) is not meant to be an all encompassing survey of pigment ratios. In each case, these data are given here both as the weight and molar ratios. In our studies, we prefer to use molar ratios as those data may eventually reveal additional insight concerning underlying pigment relationships in taxon-specific photosynthetic reaction centers.

Table 2. Biomar	ker pigmer	nt-to-chloroph	ıyll-a (weight	ratios)						
CYANOS	GR	EENS	-	CHRYS-NAI	0N	DIATS	DINOS	CRYPTO	PRASIN	
ZEA	LUT	CHLb	HEX	BUT	Hex + But	FUCO	PERI	ALLO	PRAS	Ref.
0.83		1.24			1.05	1.84	2.25	3.34		[81]
		06.0	1.14			1.34	2.79	3.60		[82]
0.69		2.95	0.73			1.72				[34]
1.32		0.70			0.68	1.07	2.50	3.34		[62]
		2.40	06.0	1.20		1.90	1.40	4.20	2.50	[17]
5.50	4.29					0.89	0.77	1.58		[83]
								2.50		[84]
0.63	5.56					0.87	2.22	4.00		[85]
		1.13	0.67			1.24	2.02			[86]
		2.5 - 3.0	1.23	1.12		1.3 - 1.9		2.1 - 2.7		[63]
		1.3 - 2.3	0.7 - 3.2	0.9 - 3.9		1.3 - 2.3	1.4 - 2.8	1.8 - 4.2	2.3 - 4.3	[17]
2.8	4.9	3.8	0.61			1.0	0.9	4.4	4.4	[87]
0.7		3.26				0.89	1.05	2.39		[88]
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Table 2. Continue	d (molar r	atios)								
CYANOS	GRE	BUS	0	CHRYS-NAN	Q	DIATS	SONIC	CRYPTO	PRASIN	
ZEA	LUT	CHLb	HEX	BUT	Hex + But	FUCO	PERI	ALLO	PRAS	Ref.
1.30		1.22			1.24	2.50	3.20	5.28		[81]
		0.88	1.32			1.82	3.96	5.69		[82]
1.08		2.89	0.85			2.34				[34]
2.07		0.69			0.80	1.46	3.55	5.28		[79]
		2.35	1.04	1.44		2.58	1.99	6.64	3.73	[17]
8.64	6.74					1.21	1.09	2.50		[83]
								3.95		[84]
0.99	8.73					1.18	3.15	6.32		[85]
		1.11	0.78			1.69	2.87			[98]
		2.4 - 2.9	1.43	1.30		1.8 - 2.6		3.3 - 4.3		[63]
		1.5 - 2.6	0.8 - 3.7	1.1 - 4.7		1.8 - 3.1	2.04.0	2.8 - 6.6	3.4 - 6.4	[17]
4.4	T.T	3.9	0.7			1.4	1.3	7.0	6.6	[87]
1.10		3.20				1.20	1.50	3.80		[88]
Abbreviations, se	e Appendi	ix B.								

Most of the data in Table 2 are 'CHLa/taxonomic biomarker' values derived by the taking the reciprocal of published 'biomarker-to-CHLa' weight ratios with the exceptions of data reported as pM xanthophyll to nM CHLa (ref. [6] in Table 2) and values obtained by the author (ref. [13] in Table 2) directly as molar ratios.

Gieskes and Kraay^[33] published one of the first mathematical chemotaxonomic descriptions of phytoplankton communities using multiple regression formulae to back calculate taxon-specific chlorophyll-*a* contributions. Gieskes et al.,^[34] then published seasonal regression formulae for phytoplankton in the Banda Sea of Indonesia.

Ideally, a formula should predict total CHLa without a non-zero intercept or correction value that would indicate an unknown source (+) or sink (-) of CHLa. Additionally, multipliers for photosynthetic accessory pigments should remain relatively constant, or change only in ways that are known, such that the formulae can be corrected. We choose to develop and adjust a formula for Florida Bay samples that did not contain a value for 'unaccounted' CHLa. Therefore, we were aiming at a formula that would give close to 100% estimated CHLa when compared to the sum of CHLa actually measured. Ideally, this should result regardless of the dominance or co-dominance of the contributory taxa (PFGs) present.

Photoprotectorant pigments (PPs: Hex and Zea) in the Gieskes et al.,^[34] report revealed a large decrease, relative to CHL*a*, in February of 1985, relative to August of 1984. Lowered photic flux, requiring less 'photoprotection', may be an explanation for the increased CHLa/PP ratios they reported. This point is especially noteworthy for the present Florida Bay study, as it is a high light $(2,000 + \mu \text{mol})$ phota m⁻² sec⁻¹ surface PAR irradiation) environment.

Various researchers have stressed the need to have pigment ratios reflect the known dominant species in any community and/or ecosystem under study.^[25–26,35] This point is easily extended to include the use of pigment ratios characteristic of what Paerl and others^[2] define as phytoplankton functional groups or PFGs.

The cyanobacterium *Synechococcus elongatus*, the diatom *Cyclotella choctawatcheeana*, and "a eukaryotic picosphere" have been the main species implicated in the "blue-green" or "blue-green/diatom/picosphere" blooms within Florida Bay.^[36] During a 1996 Florida Bay chlorophyll intercalibration study (US-EPA and Interagency Florida Bay Program, W. L. Kruczynski facilitator), we^[37,38] had the opportunity to analyze these 3 species as unialgal cultures provided by C. Tomas. Various *Synechococcus elongatus* samples gave CHL*a*/ZEA molar ratios of about 5:1. The 2 micron picosphere, originally reported as an eukaryote,^[36] was found to have CHLa/MYXO (myxoxanthophyll) of about 7.5:1 and ZEA equal to about 1.56 [MYXO], again all in molar ratios. The presence of myxoxanthophyll, found only in certain cyanobacterial lines, then identified the 2 micron 'picosphere' as a prokaryote. Subsequent electron microscopy and other criteria

reconfirmed this pigment based identity (W. Richardson, pers. commun. 1999). The diatom, *Cyclotella choctawatcheeana*, was found to have a CHLa to FUCO (fucoxanthin) molar ratio of 1.0:1.

Using our HPLC data on unialgal cultures, including the three species given above plus some 36 species covering 8 divisions, we formulated a preliminary chemotaxonomic Equation (1) for Florida Bay.^[39] The preliminary {molar} chemotaxonomic equation for the estimation of cyanobacteria, chlorophytes, diatoms, and dinoflagellates, respectively, took the form:

 $\Sigma CHLa = (7.5[MYXO] + 5.0[ZEA]) + 3.6[CHLb] + 1.1[FUCO] + 2.3[PERI]$ (1)

This Equation (1), when applied to phytoplankton (seston) field data, was found to overestimate cyanobacteria (ZEA) and to not account for the cryptophyte contribution of alloxanthin (ALLO). The overestimation of cyanobacteria stemmed from the fact that zeaxanthin is a photoprotectorant pigment (PP), rather than a photosynthetic accessory pigment (PAP) stoichiometrically related to the amount of CHLa. Thus, using the values from lab cultures, grown under limited photic flux conditions, led to higher CHLa/ZEA values $(\sim 5:1;$ lower amounts of ZEA) than we found in the bay. Natural Synechococ*cus* sp. blooms ([CHLa] > 10 μ g L⁻¹) from Whitewater Bay or the Snake-Rankin-North Whipray areas of Florida Bay were found to give CHLa/ZEA values of 2.5:1 or 1:1, respectively. The higher DOM loading (humics/brown water) in Whitewater Bay appears to have cut the 'felt' photic flux (e.g. $\sim 100 \,\mu$ mol phota m⁻² sec⁻¹ at 1.0 m), relative to Florida Bay (e.g., $\sim 100 \ \mu mol \ phota \ m^{-2} \ sec^{-1}$ at 3.0 m), and thereby lessened the requirement for the production of larger amounts of zeaxanthin. The values for photosynthetically active radiation (PAR; 400-700 nm) flux given are for periods with surface irradiation at about 2,000 to 2,500 μ mol phota m⁻² sec⁻¹. Again, attention to the photic field/history and the major species in the cyanobacterial 'functional group'^[2] is concluded as being quite important in the high light environment of southern Florida and similar sub-tropical/tropical settings.

Given the above and other input, we adjusted our molar based equation to the following (2):

$$\Sigma CHLa = (7.5[MYXO] + 1.1[ZEA^*]) + 2.4[CHLb] + 1.2[FUCO] + 1.5[PERI] + 3.8[ALLO]$$
(2)

or, on a weight basis (3):

$$\Sigma CHLa = (9.2[MYXO] + 1.72[ZEA^*]) + 2.45[CHLb] + 1.63[FUCO] + 2.13[PERI] + 6.0[ALLO]$$
(3)

In the above Equations (2, 3), the amount of ZEA is adjusted in order to account for ZEA also contributed by the MYXO containing population, if

present. Thus, $ZEA^* = ZEA - 1.56[MYXO]$, as derived from data on the 2 micron picosphere. It must be noted that, even though MYXO, and most likely the 2 micron picosphere, has been found^[40] in Florida Bay waters during 1994–1996, we did not find MYXO in any (seston) phytoplankton samples during 2000–2002.

Above, we described deriving an equation that included 2 main groups of cyanobacteria, one having only zeaxanthin as a biomarker and the second with myxoxanthophyll plus minor amounts of accompanying zeaxanthin. A zeaxanthin correction was therefore required. A third group of cyanobacteria to be considered contains many benthic forms that biosynthesize keto-carotenoids, echinenone and, to a lesser extent, canthaxanthin. A forth group may also be required in certain environments. That is, inclusion of aphanizophyll as an indicator of nitrogen fixing cyanobacteria should be considered when this pigment is detected.

Obviously, phytoplankton species containing highly specific biomarkers such as oscillaxanthin in *Oscillatoria rubescens*^[41] or gyroxanthin in *Karenia brevis*^[42] would require formula adjustment if and when present. The same holds for other taxa with specific biomarkers (19'-hexanoyl-or butanoyl-oxyfucoxanthins, prasinoxanthin, divinylchlorophylls, etc.). The reader is directed to the literature for extended discussion.^[22-26]

Chemotaxonomic Equation (#2) Testing

The HPLC pigment analyses of 266 seston samples from north-central and western Florida Bay were performed and chemotaxonomic estimates were made using Equation (2).

Figure 2 is a plot of CHLa estimated from biomarker pigments using Equation (2) versus the sum of CHLa species measured by HPLC. That



Figure 2. Plot of chlorophyll-*a* (CHL*a*) estimated from biomarker data using Equation (2) versus CHL*a* measured by HPLC. (y = 1.0056x, $R^2 = 0.9547$, mean = 105, Std. Dev. = 25).

is, measured CHLa (Σ CHLa) equals the sum of chlorophyll-a, chlorophyll*a*-epimer, chlorophyll-*a*-allomer, the epimer of CHL*a*-allo, chlorophyllide-*a* and pyrochlorophyllide-a. These pigments all have the chromophore and spectrum of CHLa per se. This also accounts for isomerizations and the action of chlorophyllase, especially active in diatoms.^[43] Good linearity of fit between estimated and measured CHLa is reflected by the regression of these data (Estimated = $1.0056 \times$ Measured) and a correlation coefficient (R²) of 0.9547. The mean and standard deviation for estimated CHLa from biomarker data are $105 \pm 25\%$. The confidence of the mean at the 95% interval is 2.968 and the data set yielded a coefficient of variation of 0.9784. Given a wide spread in the consistency and agreement between the microscopic exams, as covered in the next section, the $105 \pm 25\%$ chemotaxonomic estimations are concluded here as quite workable for rapid spatial and temporal community surveys/monitoring. Additionally, given in the next section, lessening the deviation is quite possible. Our goal of developing a protocol to come close to 100% estimated versus found CHLa without an adjustment for 'unaccounted for CHLa' was achieved.

Pheopigments

An examination of the pigment data for any underlying causal relationship that could contribute to the large standard deviation in the chemotaxonomic estimation of total CHLa was undertaken. Immediately obvious is the fact that large amounts of pheopigments (viz. pheophytin-a, pyropheophytin-a, pheophorbide-a, pyropheophorbide-a inter alia) were often present. Figure 3 (upper) is a plot of the percent estimated CHLa (=[estimated/ measured] \times 100) versus the molar percentage of pheopigments (where $\{[CHLs-a + pheopigments]/CHLs-a\} \times 100 = \%$ Pheopigments) and reveals a striking increase in the amount of estimated CHLa with increasing pheopigment content. Given that the overall data set yielded $105 \pm 25\%$ (Standard error of the mean $\{SEM\} = 1.58$) for estimated CHLa from biomarker data, we next constrained the data to include only those samples with <10% pheopigments. In this case (Figure 3 lower), the mean was 102 and the standard deviation dropped to $\pm 16\%$ (SEM = 1.81). If the percent pheopigments were further constrained to below 7.5% (not shown), the mean becomes 102 with a standard deviation of 13% (SEM = 1.76). A relationship between increased CHLa breakdown products and lowered chemotaxonomic efficiency has been reported for fresh water lentic microalgae.^[44] However, that study emphasized chlorophyllide-a as an indicator of "necromass". Chlorophyllide-a is quite often produced solely by induced decompartmentalization during extraction of living diatoms and is related to highly active chlorophyllase systems.^[43] Therefore, the presence of chlorophyllides-*a* does not necessarily indicate dead or even senescent microalgae, notably diatoms.^[35,41]



Figure 3. Percent estimated chlorophyll-*a* ([estimated CHLa/HPLC measured CHL*a*] × 100) versus molar percent pheopigments in the sample. (upper) all data (see Fig. 2), (lower) only samples with less than 10% pheopigments (mean = 102%, dotted line = Std. Dev. \pm 16%).

Herein, all CHLa chromophoric species are added into the 'total CHLa' pool and CHLa derivatives without chelated Mg are termed pheopigments (aka phaeopigments) by convention. As senescent and dead phytoplankton convert CHLa to a variety of pheopigments^[31,45] and both the flocs and surficial marl sediments of Florida Bay contain large amounts of pheopigments,^[21,39] sediment resuspension and resultant turbidity was suspected as a prime source for the pheopigment load.

A plot of turbidity versus percent pheopigments is given as Figure 4. The relationship between turbidity and pheopigments in the water column (seston) exists but is certainly not linear. A trend line plotted as a linear, logarithmic, or



Figure 4. Plot of percent pheopigments versus turbidity (NTU, nephlometric turbidity units). Regression lines are: Linear (dashed, $R^2 = 0.3146$), Logarithmic (solid black, $R^2 = 0.3218$), and 2nd order polynomial (solid gray, $R^2 = 0.3606$).

even as a second order polynomial function, all indicate that turbidity only explains for about 31-36% of the pheopigment presence.

Only very small amounts of pheopigments are reported in the upper layers of open oceans but these breakdown products do routinely increase with depth.^[46-49] In coastal, estuarine and lagoonal settings, the mixed layer extends to the benthos and, when enough wind/tidal energy is present, bottom sediments, detritus, and microphytobenthos are easily swept into the water column. The surficial floc and carbonate muds of Florida Bay are easily and routinely mixed into the water column increasing turbidity^[39] and, as shown herein, pheopigments. Pheopigment loading into the water column of estuaries and coastal areas has been reported previously,^[50-52] but accounting for linkages to lowered HPLC derived chemotaxonomy has been slow to emerge in these studies.

When pheopigments and other CHL*a* derivatives that are strongly linked to senescent and dead microalgae^[31,45,53,54] are present, then one must assume that preferential destruction/retention of the chemotaxonomic biomarkers has occurred.^[8,21,31,55] This would include a faster rate of chlorophyll-*b* (chlorophyte), fucoxanthin (diatom), and peridinin (dinoflagellate) destruction and relatively good retention of the carotenoid diols zeaxanthin (cyanobacteria) and alloxanthin (cryptophytes).^[21,31,56]

HPLC Pigment Based Chemotaxonomy and Microscopic Analyses

Given the need to 'ground truth' HPLC based chemotaxonomy versus conventional microscopic taxonomy, several samples were preserved in glutaraldehyde (0.25–0.50% final concentration) and refrigerated immediately

following collection. Samples were then sent on ice $(2-4^{\circ}C)$ to 2 individual microscopic service companies (Labs "A" and "B") for taxonomic evaluation. Ideally, it would be advantageous to have an expert algal microscopist familiar with each specific ecosystem in every lab but this is rarely possible.

It was decided to compare the results from different microscopy services prior to comparing microscopy based with pigment based taxonomy. Given that this is very expensive (\sim \$180.00 or \$275.00/ sample for genus or species level identifications with biovolume estimations) and time consuming ($\sim 1-2$ months turn around time), only a limited number (13) of samples could be contracted. Of these, four samples were sent to each of two separate labs in order to compare interlaboratory data. Table 2 contains the data obtained from these independent laboratories. The biovolume data on samples from sites 6 and 11 from March 2001 exhibited some differences but did agree on the divisional dominance order (Cyanobacteria > Diatoms). However, conflicting results were obtained for samples from sites 8 and 11 collected in June 2001. Here, lab "A" reported strong cyanobacterial dominance while lab "B" reported nearly 100% diatom presence. Following up on reasons behind this, it was found that lab "A" employed epifluorescence plus light methodologies, while lab "B" used only light microscopy. Lab "A" was then utilized for all samples to which HPLC comparisons were made. Exactly the same results, disagreement between labs, and a general noncorrelation of pigment data to biomass, have been reported using the CHEMTAX algorithm.^[57]

Comparing HPLC derived chemotaxonomic estimations with microscopic taxonomy (Table 3) we found the following R^2 values for individual CHLa/biomarker relations: cyanobacteria (ZEA: 0.49 {0.80}), diatoms (FUCO: 0.39 {0.56}), chlorophytes (CHLb: -0.44 {0.91}), dinoflagellates (PERI: 0.63{0.92}), and cryptophytes (ALLO: -0.94). The higher R^2 values within the inner brackets indicate data after discarding 1–3 major outliers. However, it must be noted that, without *a priori* knowledge of the full data set, an 'outlier' would not be identifiable as such. Additionally, negative correlations between CHLb/chlorophytes and alloxanthin/cryptophytes makes the microscopic data suspect, since there is no other explanation for these biomarker pigments other than the presence of their source organisms.

Adequate relationships between HPLC and microscopy for cyanobacteria, diatoms, and dinoflagellates were concluded. Chlorophytes and cryptophytes were shown to definitely be present as their corresponding taxon specific biomarkers, chlorophyll-*b* and alloxanthin, were conclusively identified. As given below, chlorophytes and cryptophytes appear also to be adequately estimated, but solely on the basis of overall community estimated versus measured CHL*a*. The lack of more direct relationships between HPLC and pigment data for the chlorophytes and cryptophytes is an enigma

			CIII a			T PERC	AXON ENTA	GE^c	
SITE #	mo/yr	TYPE ^a	ug/L	%Pheo ^b	CYANO	CHLRO	DIAT	DINO	CRYPT
1	03/01	No.	6.9	12	80.7	0.1	19.2	0	0.1
		Vol			0.4	0.1	99.4	0	0.1
		HPLC			0	0	87.4	0	12.6
6	03/01	No.	0.5	29	80.5	0.1	18.7	0.1	0.4
		Vol			0.4	0.1	98.5	0.1	0.2
		HPLC			0.0	0.0	100.0	0	0
11	03/01	No.	3.6	1.5	93.8	0.1	4.2	0.1	1.6
	,	Vol			0.4	0.1	99.0	0.1	0.4
		HPLC			0.0	19.0	64.0	0.0	17.0
11	04/01	No.	8.3	14	78.5	0.1	20.6	0.1	0.7
	,	Vol			0.2	0.1	99.4	0.1	0.1
		HPLC			1.5	7.7	77.0	0.0	13.8
12	06/01	No.	0.7	11	97.8	0.1	0.2	0.2	0.1
	,	Vol			53.0	3.2	5.6	9.3	0.7
		HPLC			33.2	12.5	36.5	7.9	9.9
8	06/01	No.	0.8	14	96.2	0.1	3.4	0.2	0.1
	,	Vol			2.5	1.8	93.2	0.5	0.1
		HPLC			7.3	0.0	42.3	20.0	29.9
1	07/01	No.	4.0	7.5	0.0	2.8	89.8	0.0	2.5
	,	Vol			0.0	0.4	98.9	0.0	0.1
		HPLC			11.7	3.0	66.0	1.7	17.3
5	07/01	No.	0.7	3.6	11.8	0.0	23.5	13.6	50.9
	,	Vol			23.4	0.0	51.1	19.8	5.7
		HPLC			6.5	0.0	27.9	34.4	31.2
10	07/01	No.	6.0	9.8	0.7	2.4	89.5	2.3	2.7
	/	Vol			0.1	6.5	93.1	0.2	0.1
		HPLC			2.5	4.0	80.3	4.3	9.2

Table 3. Comparison of microscopic cell counts and biovolume estimates with HPLC data

^{*a*}No. = cell number, Vol = Biovolume. Data from Laboratory "A", as given in text. ^{*b*}% PHEO = percent pheopigments ((PHEOs / [PHEOs + CHLa])100).

^cPercent taxon of 100% community. CYANO = cyanobacteria, CHLRO = chlorophytes DIAT = diatoms { \sim chrysopytes}, DINO = dinoflagellates, CRYPT = cryptophytyes.

at present. Fortunately, the major phytoplankton functional groups (PFGs) in this ecosystem^[58–60] are easily estimated. Additionally, it is reiterated here that the overall estimated (y) versus measured (x) CHL*a* for all samples studied had a mean of $105 \pm 25\%$, a regression of y = 1.0056x, and an R² of 0.9547 ($102 \pm 16\%$ at Σ Pheos < 10%). It therefore appears that, in spite

of perceived inadequacies to regress biomarker data to certain individual microscopic taxon estimates, chemotaxonomy is describing their presence within each community quite adequately.

A recent publication^[61] had the title "Routine quantification of phytoplankton groups-microscopy or pigment analyses?" Their conclusion was to use pigment analyses for monitoring purposes and to augment that with microscopy for screening of dominant species and flow cytometry for quantification of picocyanobacteria.^[61] As these and other authors ^[2,8,62,63] have concluded, there are indeed problems with all techniques.

It has been stated that microscopy is "a time consuming and costly procedure that requires a high level of expertise".^[2] Additionally, such variables as preservation^[64] and the "careful choice of appropriate volumetric shapes and taxa categories",^[65] in addition to the microscopist's expertise, can inflict bias into the results. One study questioned the marine ecology dogma of assumed or claimed 100% accuracy in microscopy and concluded by stating: "Trained personnel can be expected to achieve 67-83% self-consistency and 43% consensus between people in an expert taxonomic labeling task. Experts who are routinely engaged in particular discriminations can return accuracies in the range of 84-95%". [66] Failure of pigment based (chemo-) taxonomy to agree with microscopic analysis has also been attributed to 'subjectivity' during microscopic exams, especially "when small phytoplankton cells dominate".^[57] Biomass (~biovolume) estimations are reported to be prone to adverse effects due to preservation.^[64] As stated earlier, the present study utilized a final concentration of 0.25-0.50% glutaraldehyde for preservation. This routine method has been reported to decrease the biovolume of diatoms and athecate dinoflagellates, relative to living cells.^[64] An additional problem in the estimation of cell number and biovolume in the present case may derive from our need to ship samples. That is, turbulence during shipping, even though cells were preserved and shipped on ice, could have led to the disruption of certain fragile cells, such as the cryptophytes.^[67]

Advantages-Disadvantages of HPLC Derived Pigment Based Chemotaxonomy

The methodology of pigment based chemotaxonomy has several advantages as well as certain pitfalls. First, pigment data are derived from a much larger integrated sample than is microscopy. That is, all of the phytoplankton in a sample of from 50 to 10,000 mL, depending upon seston concentrations, is analyzed. Secondly, the technique itself, except for extraction differences^[29,30] that can be accounted for, is relatively unbiased (\sim objective) on the part of the operator. Data interpretation (formulae) forms the major part

of uncertainty in these studies. All in all, algal biomass^[55] and average cell volume^[68] are generally related to CHL*a* contents. Yet, the literature consensus is that much more is needed in these aspects as well. Again, it is the relation of biomarker pigments to taxon specific CHLa that presently forms the basis of chemotaxonomy.

Comparisons of microscopic and pigment based estimations of major taxa (aka PFGs^[2]) are well known.^[8,18,23,24,61-63] One of these studies found that CHL c_3 , peridinin, alloxanthin, and fucoxanthin gave good quantitative results for the biomass of Phaeocystis sp., dinoflagellates, cryptophytes, and the sum of brown algae (diatoms etc.), respectively. However, they also reported that CHLb had no relationship to chlorophytes and attributed this to uncertainties in the microscopic counts of small (<5 µm) cells and/or cells with low visibility membranes.^[62]

Effects of light on the C ('biomass') to CHL*a* ratios are known.^[69] Specifically, for diatoms and dinoflagellates in "high" (>100 μ mol phota m⁻² sec⁻¹) or "low" (<100 μ mol phota m⁻² sec⁻¹) light, it was reported that CHL*a*/C gave R² of 0.24 or 0.75 and 0.65 and 'not reported', respectively. Overall, for total phytoplankton, they obtained R² values of 0.48 and 0.8, respectively. This they correlated to low CHL*a*/C and high CHL*a*/C values, respectively.^[69] The effect of light on CHL*a* to non-stoichiometric biomarker (viz. PPs) ratios is also well known.^[70-72] As described earlier, light (low to high) was found to significantly change the CHL*a* to ZEA ratio (5–1 to 1–1, respectively) in *Synechococcus elongatus*. As these studies continue in Florida Bay, corrections for seasonal photic flux, at least summer versus winter for example, will likely evolve.

The microscopic estimation of biovolume is also reported to be exceedingly complex,^[73,74] especially when cells of less than 5 microns diameter are prevalent.^[75] It is given that phytoplankton cell volume ranges over 9 orders of magnitude.^[74] Additionally, it has been suggested that diatom cell volumes really need to be adjusted downward by the factor 0.54x in order to remove the volume of the siliceous frustules and intracellular vacuoles.^[76]

Potential and known problems with chlorophyte and cryptophyte estimations follow here. Chlorophytes, in this and other studies, are estimated from the CHL*a*/CHL*b* ratio. Lutein is also a 'marker' for green algae but recent evidences describe it as a photoprotectorant.^[72,77] We choose to use lutein as only a confirming or co-marker for chlorophytes, much as high levels of α -carotene are for cryptophytes. Therefore, CHL*b* is used and if present, then it must be concluded that chlorophytes are present.

The potential presence of prochlorophytes,^[78,79] having divinyl chlorophyll-*b*, in the present samples, was not overlooked. For all of the samples from Florida Bay studied, the position of the Soret (violet) band of CHL*b* exhibited no bathochromic (red) shift relative to monovinyl

('regular') CHL*b* ($\lambda_{\text{Soret}} = 458 \text{ nm}$, band I = 642 nm). DV-CHL*b* (DHI, Denmark) eluting from our C₈ system (Nova Pak-octyl, 3 µm, 3.9 × 150 nm) exhibits Soret and band-I absorptions at 464 and 648 nm, respectively. C₈ RP-HPLC, easily separating the mono-and divinylchlorophylls-*a*/-*b*, was therefore not required here. Additionally, chlorophytes (e.g., *Chlamydomonas*, several non-motile chlorococcales, *Oocystis*, and other chlorophytes) were identified (Lab "A") and are numerically included in the divisional microscopic data (Table 3). A lack of hard and fast correlation between CHL*b* and microscopically determined chlorophyte abundance has also been reported for the eastern English Channel.^[62] Chlorophytes in the nanoplankton (5–20 µm) size class have previously apparently led to deviations between CHL*b*/biomassbiovolume correlations.^[62]

Cryptophytes, in this and other studies,^[23,27,62] are estimated from the CHLa/alloxanthin (ALLO) ratio. As given above, we found and used a molar CHLa/ALLO ratio of 3.8:1 (6.0:1 by wt.) for the estimation of cryptophyte contributed CHLa and obtained a negative correlation of $R^2 = -0.94$ when related to the microscopic data. Given that ratios in the literature^[10,27] bracket (Table 2: 2.8-7.0) the value used here and since we are using a ratio obtained in our lab from the only genus (viz. Rhodomonas) reported by lab "A" from these samples, we can only conclude that HPLC is detecting more of the cryptophyte portion of these communities than is microscopy. This may derive from the fact that the cryptophytes (cryptomonads) are notoriously fragile,^[67] hence the Latin names equating to 'hidden plant' ('hidden single cells'), and that the requirement to ship these samples for microscopy may have exacerbated such destruction. A strong effect of light has also been reported for marine cryptophytes. That is, the ALLO/CHLa weight ratio was found to increase 1.3- to 9- fold going from the exponential to N-limited stationary phases of growth.^[80] Thus, as discussed for zeaxanthin, photic flux and history may need to be factored into cryptophyte estimation by alloxanthin abundance, especially in the high light $(1,000-2,500 + \mu mol phota$ m⁻² sec⁻¹) conditions of Florida Bay and other subtropical/tropical settings.

CONCLUSIONS

HPLC derived pigment based chemotaxonomy has been developed for use in the study and monitoring of phytoplankton community studies in Florida Bay. Florida Bay is a coastal ecosystem closely receiving input of fresh water and nutrients from the Everglades system and, as such, is intimately linked to the ongoing restoration efforts of the Comprehensive Everglades Restoration Plan (CERP). Analyses of 266 seston samples were collected monthly from northcentral and western Florida Bay between September 2000 and August 2002. Manipulation of a pigment based formula using empirically derived data gave excellent correlation ($R^2 = 0.9547$) and slope (estimated = $1.0056 \times$ measured) with a mean of 105.4% (Std. Dev. = 24.7) for total chlorophyll*a* (CHL*a*) estimated from individual divisional contributions when regressed against HPLC measured total CHL*a*. These data yielded a coefficient of variation of 0.9784 and a confidence on the estimated CHL*a* mean of 2.968 at the 95% interval.

It was found, that as the relative amounts of pheopigments increased so did the overestimation of CHL*a* from biomarker data. About 33% of the pheopigment load was found to be explainable by turbidity. The mean and standard deviation for estimated CHL*a* improved to $102 \pm 16\%$ when the data set was restricted to only those samples with less than 10% pheopigments (where Σ CHL*a* + Σ PHEOs = 100%). Phytoplankton communities varied from nearly total cyanobacteria to nearly total diatoms, with numerous samples also containing moderate amounts of chlorophytes, cryptophytes, and/or dinoflagellates.

While there was excellent correlation between estimated and total chlorophyll-*a*, estimation of individual taxa yielded correlations (\mathbb{R}^2) between -0.94 (cryptophytes) and 0.63. Significant increases in the correlation coefficients were found after the removal of 1-3 'outliers'. For example, \mathbb{R}^2 for chlorophytes went from -0.44 to 0.91 and for dinoflagellates it improved from 0.63 to 0.92. However, without coincident microscopic data, outliers would not be identifiable.

A strong effect of light was found for the biomarker of *Synechococcus* in the bay. That is, the CHL*a* to zeaxanthin ratio changes from 5 to 2.5 to 1:1 for samples from lab cultures, Whitewater Bay (dark humic stained waters) to the open bay, respectively. This directly paralleled the amount of photic (PAR) flux received by the cells. The effect of high photic flux (e.g., surface $>1,500 \mu$ mol phota m⁻² sec⁻¹) on other pigment ratios requires additional study. In the future, chemotaxonomic formulae may require seasonal (viz. light level) adjustments.

In conclusion, pigment based chemotaxonomy has been adequately developed for the study of Florida Bay phytoplankton and will become more robust in the future as light and pheopigment perturbations of the data are factored into chemotaxonomic formulae.

It may also be concluded that all studies using HPLC derived pigment based chemotaxonomy must not only consider the implications of pheopigments in their samples, but also list the percent pheopigments so that the reader may better understand each report. That is, pheopigments typically indicate senescent/dead/grazed/resuspended phytoplankton and, accompanying chlorophyll alteration, differential losses of biomarker pigments are known.

APPENDIX A: SELECTED PIGMENT BIOMARKER STRUCTURES



Gyroxanthin diester (Karenia brevis)

Abbreviation Identity CHL-a chlorophyll-a CHL-a' chlorophyll-a-epimer

APPENDIX B: ABBREVIATIONS

CHL-a-allo	chlorophyll-a-allomer
PHEOs	pheopigments (=pheophorbide-a, pyropheophorbide-a,
	pheophytin-a etc.
CHL-b	chlorophyll-b
CHLs-c	chlorophylls- $c_1/-c_2$
MYXO	myxoxanthphyll
ZEA	zeaxanthin
LUT	lutein
HEX	19'-hexanoyloxyfucoxanthin
BUT	19'-butanoyloxyfucoxanthin
FUCO	fucoxanthin
PERI	peridinin
ALLO	alloxanthin
PRAS	prasinoxanthin
PAP	photosynthetic Accessory Pigment
PP	photoprotectorant Pigment
CYANOS	cyanobacteria (aka 'cyanophytes')
GREENS	chlorophytes
CHRYS	chrysophytes
NANO	nonoflagellates
DIATS	diatoms
DINOS	dinoflagellates
CRYPTO	cryptophytes
PRASIN	prasinophytes
DOM	dissolved organic matter (~organic carbon)
HPLC	high-performance liquid-chromatography
RP	reversed phase
PDA	photodiode array (detection)
λ	wavelength (nm, nanometers)
IP	ion pairing (aka Ion Supression)
IS	internal standard
QA/QC	quality assurance/quality control
CERP-MAP	comprehensive everglades rrstoration plan-monitoring
	and assessment program

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