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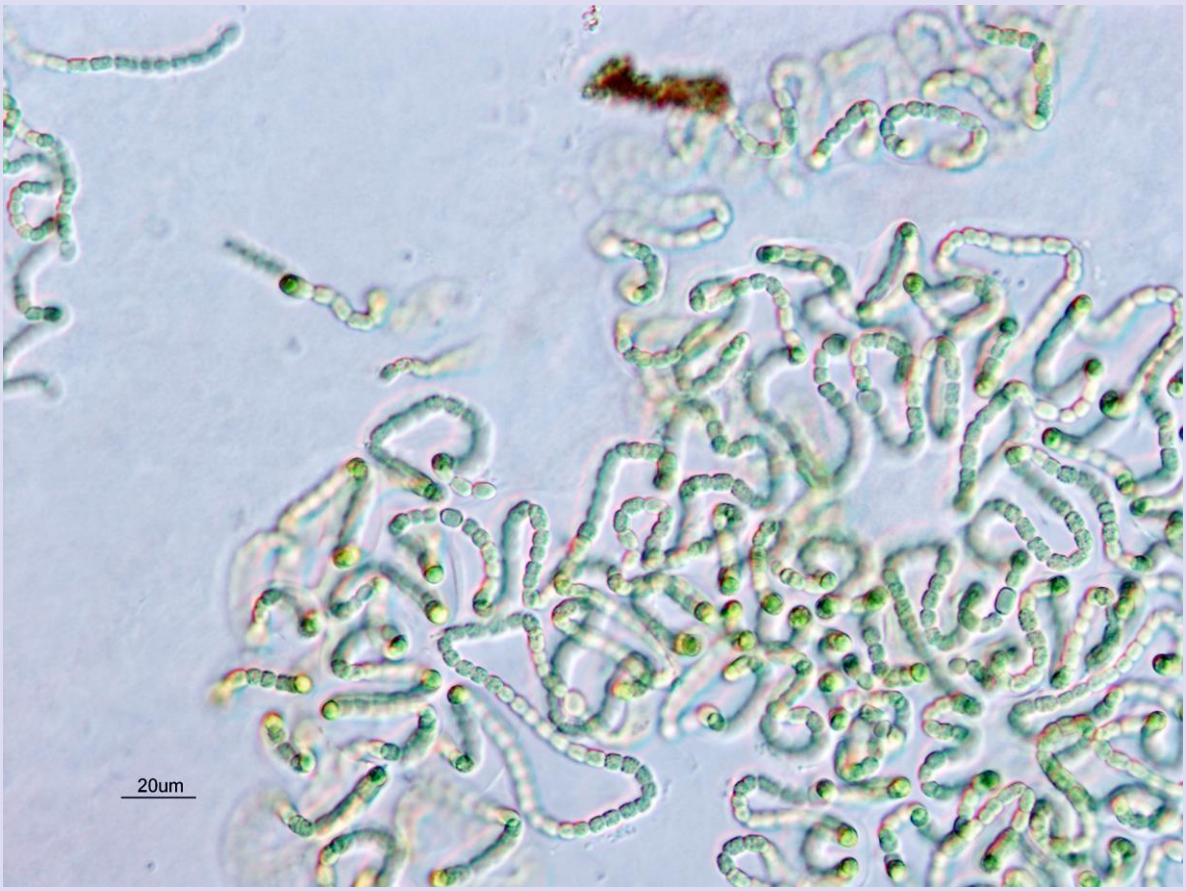
Para publicar en este Boletín, enviar sus propuestas a los editores. Políticas y normas en página 23.
Números anteriores en http://boletin-sociedad-mexicana-ficologia.meridion.mx/

MENSAJE DEL PRESIDENTE DE LA SOCIEDAD MEXICANA DE FICOLOGÍA Y DE LA SOCIEDAD FICOLÓGICA DE AMÉRICA LATINA Y EL CARIBE

Durante los próximos dos años (2014-2015) el presente boletín será el órgano informativo de dos Sociedades: la Sociedad Filológica de América Latina y el Caribe y la Sociedad Mexicana de Ficología. Precisamente, durante estos dos años las mesas directivas de ambas asociaciones trabajaremos conjuntamente para beneficio de ambas agrupaciones.

En los tiempos actuales todas las instituciones, con variaciones dependiendo del país que se trate por supuesto, están obligadas a buscar formas nuevas de lograr sus objetivos, con la visión de aprovechar mejor sus recursos y lograr resultados tangibles y concretos como efecto lógico de una planeación y del trabajo colaborativo entre los miembros de la agrupación.

Los problemas que enfrentamos de principio son complejos y deben de ser abordados en el concierto con otras disciplinas, para crear lenguajes comunes y de ahí la trascendencia de construir Sociedades que fomenten la transdisciplina.



En este sentido, un boletín informativo es crucial en la comunicación e intercambio de ideas, proyectos y logros. La construcción de conceptos ad hoc, de métodos pertinentes y apropiados, la discusión de resultados y la propuesta de alternativas, nacen precisamente de este diálogo entre pares, de distintos países y con formaciones diversas.

A la par con el boletín, publicación periódica, debemos construir páginas electrónicas actualizadas y que en tiempo real nos informen, por medio de directorios, perfiles de investigación, publicaciones, alumnos en formación, regiones geográficas en estudio, de las herramientas electrónicas que facilitan y hacen más expedita la realización de nuestro trabajo cotidiano.

Otros instrumentos de ayuda y que aprovecharemos, son las redes sociales. De estas, a la fecha contamos con una cuenta en Facebook y hemos alentado la inscripción de los agremiados a ResearchGate, una propuesta novedosa de cómo calificar el trabajo de investigación, pero sobre todo que permite la vinculación e intercambio entre profesionales que poseen intereses similares.

Todos estos instrumentos deberán estar enfocados a los problemas inmediatos de nuestras Sociedades como: la cooperación mexicana, latinoamericana e iberoamericana, como una prioridad importante para después o paralelamente, acrecentar los lazos con otras regiones del planeta con problemas similares; la actualización continua a niveles licenciatura y postgrado; la concreción de convenios con otras Sociedades, IES, ONG entre otras, para construir redes científicas que puedan, en el corto plazo, establecer estudios o investigaciones de largo aliento en regiones geográficas de interés común; la preparación de líderes de la ficología en cada región de los países miembros, por mencionar sólo algunos.

A nombre de las dos Sociedades agradezco el esfuerzo y dedicación, así como las ideas extraordinarias de nuestros editores, que hacen de este boletín un medio indispensable en la vida de nuestras asociaciones.

Francisco F. Pedroche
Presidente
Sociedad Ficológica de América Latina y el Caribe (2012-2015)
Sociedad Mexicana de Ficología (2014-2017)

EDITORIAL

Con el tercer número del Boletín de la Sociedad Mexicana de Ficología se inicia una etapa distinta para esta publicación. Por dos años será también el Boletín informativo de la Sociedad Ficológica de América Latina y el Caribe. Y es momento para rendir un homenaje a las editoras del primer Boletín Ficológico Latinoamericano: Dra. Marilza Cordeiro-Marino, Dra. Rosario de Almeida Braga y Dra. Maria Teresa de Paiva Azevedo, quienes mantuvieron durante el periodo 1987-1990 una publicación útil y de alta calidad. En 1993, coincidiendo con el 3er. Congreso Latinoamericano de Ficología y la Primera reunión Iberoamericana de Ficología en México, apareció el número 5 de ese Boletín en el que se incluyeron las direcciones de 1253 personas relacionadas con el estudio de las algas en esta gran región. Por su parte, la Sociedad Mexicana publicó Boletines informativos hasta 1998.

Así con este Boletín de las Sociedades Mexicana y Latinoamericana y del Caribe, sostenemos la idea de que las sociedades científicas requieren de un medio de comunicación con sus miembros. La publicación de una revista y de un boletín informativo fue planteada en varias ocasiones e incluso aparece como parte de los estatutos de la Sociedad Ficológica de América Latina y el Caribe pero no prosperó ninguna iniciativa al respecto. Las opciones editoriales han cambiado desde 1987 y por ello nuestra propuesta es un tanto intermedia, un boletín que ofrezca información calificada, comentarios y opiniones que puedan despertar el interés por las algas, además de información que no caduque o que sirva de referencia posterior. Un publicación tipo “newsletter” tiene la desventaja de parecer sobrepasado por la velocidad de difusión que se alcanza en internet. Una publicación científica requiere de un apoyo financiero y organizativo de tipo institucional o de la Sociedad que no tenemos por ahora. Una publicación que se mantenga en el intermedio es un reto y una oportunidad de probar nuestra capacidad de respuesta, de mantener la comunicación y de difundir la ficología al mismo tiempo.

En concordancia con lo anterior, en este número ofrecemos un artículo sobre metagenómica en el estudio de algas subaéreas que promueve la utilización de las técnicas moleculares para el estudio de la diversidad. Invitamos a los lectores a mandar su opinión y sobre todo sus resultados relacionados con estos temas. Las ilustraciones muestran varias facetas de especies de *Nostoc*, en cultivo y de muestras ambientales, una Cyanoprokaryota típicamente subaérea. También se incluye información del próximo Congreso Latinoamericano y nuestras secciones de Ficoweb y publicaciones recientes.

Los invitamos cordialmente a colaborar y apoyar en la difusión de la ficología en México y en Latinoamérica. Este Boletín aparecerá tres veces al año: abril, agosto y diciembre.

Atentamente,

Los editores

ARTÍCULO ORIGINAL

The use of metagenomics to infer algal diversity in a subaerial community from an African tropical rainforest, "Les Monts de Cristal" national park, Gabon.

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Abstract

The usefulness of metagenomics in assessing the biodiversity of "Les Monts de Cristal" National Park in Gabon, Africa was tested. This region was chosen in the basis of its botanical richness that makes it highly amenable for studies on the biodiversity of subaerial organisms and it is considered one of the richest in the country and in Central Africa. Trees were sampled for subaerial algae by scrapping where microorganisms' growth was evident. A portion of the large subunit of the ribosomal DNA (23S) gene was chosen as the molecular marker. This marker was successfully amplified from both prokaryotes (cyanobacteria) and eukaryotes (non-vascular plants). The resulting sequences were placed taxonomically by reconstructing a phylogeny using Maximum Likelihood (ML). The analysis consisted of 467 taxa including about 150 environmental 23S sequences from Africa and the following groups were represented within the "Monts de Cristal" forest: cyanobacteria, chlorophyte green algae including some trentepohlialean taxa, diatoms, mosses, and liverworts. This study showed the usefulness of this marker and also represents an inedited contribution in subaerial algal biodiversity because the terrestrial algal flora of Les Monts de Cristal has been overlooked and never assessed before.

Keywords: Subaerial, "Les Monts de Cristal", Metagenomics, 23S rDNA

Introduction

Since 1990's, microbial ecology has experienced major revolutions in part due to the constant developments of genomics and molecular biology. Initially, studies targeting the analysis of rDNA sequences obtained directly from the environment, coupled with traditional studies of microbiology, demonstrated that more than 98% microorganisms are not cultivable under laboratory conditions (Ward et al. 1990). Consequently, their morphological or physiological features cannot be characterized. A new field

emerged, metagenomics, which is the analysis of genomic DNA of assemblages of organisms from the environment (Handelsman 2004). Cloning environmental DNA (without any prior cultivation) is a relatively new method to unravel the diversity found in microalgal communities. Using such methods will help isolate phylotypes (a distinct, consistently found sequence that is classified by its phylogenetic relationship to other organisms) that are new to science (Gabor et al. 2003). Most studies of algal diversity relied on culture and morphological characters to separate different taxa. However, these studies were based on microscopical criteria that could not provide quantitative measures of genetic diversity, these methods rarely provided profiles of community structures (Edgcomb et al. 2002).

The power of molecular techniques makes it possible to understand the function and composition of terrestrial ecosystems. Giovanonni et al. (1990) study marked the advent of these techniques to solve purely oceanographical questions. By sequencing the 16S ribosomal RNA gene, these authors showed that there was an unexpected diversity of bacterial populations in oceanic ecosystems and none of these populations corresponded to populations established in culture at that time. Later, Urbach et al. (1992) showed that *Prochlorococcus marinus*, a cyanobacterium recently isolated in culture had in fact a 16S rRNA that was very close to certain unknown populations of the Pacific and Sargasso Sea. This study showed that metagenomic techniques could account for new taxa before they are ever accounted for in culture.

Following the footsteps of Urbach, the main part of the data gathered so far on diversity of eukaryotic communities (including heterotrophic, autotrophic organisms or mixotrophs) was related to oceanic, marine or coastal ecosystems (Moon-van der Staay et al. 2001a; Mann 2003). These studies have shown a high level of diversity as well as new evolutionary lineages in recent years (Díez et al. 2001; Guillou et al. 2002; Massana et al. 2002). Similarly, other metagenomics surveys of eukaryotic microbial diversity from marine environments have revealed higher diversity of eukaryotic algae (Lopez-Garcia et al. 2001; Fuller et al. 2006). The characterization of eukaryotic diversity in hydrothermal vents environments in the Guaymas basin in the Gulf of California has also revealed representatives of previously uncharacterized protists, including early branching eukaryotic lineages (Edgcomb et al. 2002).

The diversity of DNA recovered from environmental samples was distinctly higher than classical taxonomical methods as shown by denaturing gradient gel electrophoresis (Gabor et al. 2003). These metagenomic approaches have allowed the wealthy construction of environmental gene banks (Gabor et al. 2003). Environmental samples within algal organisms have shown the extent of taxonomic diversity in marine environments (Díez et al. 2001; Lopez-Garcia et al. 2001; Moon-van der Stay et al. 2001b), and from freshwater

environments (Sherwood et al. 2008). A study conducted by Lawley et al. (2004) demonstrated the usefulness of a metagenomic approach using samples from Antartic soils samples.

Sherwood and Presting (2007) have demonstrated the usefulness of a single pair of primers that can amplify the 23S plastid rDNA gene of eukaryotic algal and cyanobacterial groups. This molecular marker has been successfully used to identify algal groups from a stream in Hawaii (Sherwood et al. 2008). However, to our current knowledge, this is the first subaerial algal biodiversity study based on environmental sequences.

Our current research is focusing on the biodiversity of subaerial algae (Rindi et al. 2010). Subaerial algae are algae that live exposed on a variety of substrates above the soil surface (Graham et al. 2009). For an alga, this is an extremely harsh environment (terrestrial) where water plays a major role. As many other subaerial components, such as terrestrial mosses, liverworts, and hornworts, algae need water to complete sexual reproduction by allowing the motile sperm to fertilize the egg (Raven et al. 2005). Water is also essential, both as a substrate (in photosystem II) and as a medium (enzymatic reaction) to perform photosynthesis (Hoganson and Babcock 1997). Rainforests are among the wettest ecosystems where water reaches the habitat either as rainfall or as water vapor (due to high humidity) that is absorbed directly from the air. Thus, humid tropical rainforest are ideal habitats for subaerial algae. Tropical rain forests are housing a large proportion of the world's biological diversity. However, these forests are vanishing very rapidly compared with other biomes (Laurance 1999; Achard et al. 2002). In Africa, the tropical rainforests are restricted to the equatorial belt, with its largest block in the Congo Basin and the lower Guinean area. This central area is the second largest block in the world (Wilkie and Laporte 2001). Within Central Africa's tropical forest, lies the country of Gabon. With almost 80% of its surface area covered by the moist tropical forest, Gabon is one of the most biologically diverse countries in all Africa (Breteler 1996) and highly amenable for studies on the biodiversity of subaerial algae.

The African tropics were estimated to have 40,000 to 45,000 plant species (Beentje et al. 1994), among this diversity 6,000-10,000 plant species are found in Gabon (Letouzey 1968). In August 2002 a National Park System was created by a Presidential decree in order to protect the country's forest. This system has put 10.8% of the country's territory under full protection. One of these parks is situated in "les Monts de Cristal" (the Crystal Mountains). The region of "Les Monts de Cristal" is known for its botanical richness and is considered one of the richest in Gabon and probably in Central Africa (Wilks 1990).

Several biologists before have been interested in the flora and fauna of this region for decades (Reitsma 1988; Gentry 1993; Stévart 2003, 2004). However, the terrestrial algal flora has been overlooked and never assessed in this region. Considering the high

humidity and habitat diversity found in tropical rainforests (Neustupa 2005; Rindi et al. 2006), a Gabonese study is expected to yield a high diversity of subaerial algae.

Algae found in the tropical rainforest are assumed to belong to basically three different lineages: Cyanobacteria or Blue-green algae (Cyanophyta), Diatoms (Stramenopiles), and Green algae (Chlorophyta) (Rindi et al. 2010). About 200 subaerial genera found distributed among these three main lineages were implicated in previous floristic studies (Nienow 1996).

Metagenomic approaches to the study of subaerial algae have been absent from the literature. In this study, the subaerial algal community of "Les Monts de Cristal" National Park is evaluated using metagenomics. This study will provide evidence of the richness and the high biodiversity of the subaerial environment as well as test the presence of the three major groups of algae found in the subaerial habitat (diatoms, green, and blue-green algae) using environmental cloning.

Materials and methods

Epiphytic samples were collected at "Les Monts de Cristal" National Park, Gabon during the rainy season on May 20-24, 2008. Algae were scrapped off of their substrates using sterile blades form an area of 4 cm2. Substrates were chosen where evidence of algal growth was evident (red, green, yellow, or dark areas on different substrates). Samples were placed in sterile bags, desiccated using sterile silica gel and transferred to the laboratory at the University of Alabama for further analyses.

Collection and export permits were acquired from the "Agence National des Parcs Nationaux". Import permits were obtained from the United States Department of Agriculture.

DNA was extracted from field samples using a Qiagen DNeasy Plant Mini Kit (Qiagen, Valencia, CA USA) following the manufacturer's recommendations.

The PCR primer pair consisted of P23SrV_f1 and P23SrV_r1 (Sherwood and Presting 2007). These primers amplify the chloroplast-encoded 23S rDNA from prokaryotic and eukaryotic algae. To prevent the amplification of the bacterial DNA a touchdown PCR protocol was used as shown by Sherwood and Presting (2007).

The amplification of the PCR products was carried in a thermal cycler (Brand) and the PCR mix consisted of a total of 13 µL. The PCR reaction included: 4.4 µL of sterile distilled water water; 1.25 µL of 10x reaction buffer (Applied Biosystems California, USA); 1.25 µL of $MgCl_2$ (25 mM) (Applied Biosystems California, USA); 1.25 µL of dATP, dCTP, dGTP, dTTP cocktail (8 mM); 0.625 µL of each primer: P23SrV_f1 and P23SrV_r1 (10mM); 0.1 µL of Taq polymerase (New England Biolabs, Ipswich, MA). Additionally, we added 2.5 µL of 1% non-acetylated bovine serum albumin (BSA) as an additive. BSA has been used as an enhancer of PCR amplifications when humic substances are present. Finally, 1.0 µL of genomic DNA was added to the PCR reaction mix. PCR products were run on a 1% agarose gel with Ethidium Bromide to check the integrity, concentration and purity of the DNA. A fragment of about 450 base pairs was

cut from the gel and purified with a Qiagen Mini Elute Gel Extraction Kit (Qiagen) following the manufacturer's recommendations. The resulting DNA was then ligated into cloning vectors using ATOPO-TA Cloning Kit with the PCR 2.1-TOPO Vector (Invitrogen, California, USA) following their protocols. After the insertion, plasmids were transformed into *Escherichia coli* provided from the TOPO-TA Cloning Kit followed by a heat shock with the addition of S.O.C medium (Super Optimal broth with Catabolite repression). Bacteria were transferred to an incubator were they were shaken (200 rpm) at 37 °C for one hour. Bacterial cells were then plated on Luria agar plates with Xgal and ampicillin. Plates were incubated at 37 °C for 24 hours followed by a visual inspection to detect colonies with inserts (white colonies). These colonies were transferred into the aforementioned cocktail PCR and used as DNA template for the amplification. This time the PCR protocol included an initial denaturing phase of 5 minutes at 95°C, followed by 35 cycles of 94 °C for 30 seconds, 58 °C for 30 seconds and 72 °C for 30 seconds, with a final extension of 7 minutes at 72 °C. The resulting samples were run on a 1% agarose gel with Ethidium Bromide, excised from the gel with a sterile blade, and purified with a Qiagen Mini Elute Gel Extraction Kit (Qiagen). Resulting DNA was quantified via NanoDrop ND-1000 spectrophotometer (NanoDrop Technologies, Delaware, USA). DNA products were sequenced with the same primers in both directions using Big Dye version 3.1 sequence kit (Applied Biosystems California, USA). Following the cycle sequencing reaction DNA was sequenced using an ABI 3100 automated sequencer (Applied Biosystems). Sequences were captured as text as well as color-coded electropherograms using Sequencher 4.5 (Gene Codes Corporation, Michigan, USA).

DNA sequences were aligned in ARB (Ludwig et al. 2004) based on the secondary structure of the plastid ribosome (Cannone et al. 2002). For comparison, UPA (Universal Primer Amplicon) sequences for *Cephaleuros virescens* SAG 42.85, *Trentepohlia* sp. SAG 117.80, and *Printzina* sp. Panama [F223] were generated following the same protocols described. Phylogenetic analyses were carried out based on the cloned sequences. For comparison, UPA trentepohlialean sequences were added to the data matrix as well as other representatives of available algal UPA sequences reported previously (Sherwood et al. 2008) and deposited in GenBank.

The phylogenetic analysis was carried out using the Maximum Likelihood (ML) approach on the resulting dataset (Allali 2011) and the phylogeny was reconstructed using PAUP* 4.0b10 (Swofford 1998) using the general time reversible model with a portion of invariant sites and gamma distributed rate variation among sites (GTR+I+Γ) that was determined using Modeltest 3.07 (Posada and Crandall 1998). The resulting tree was processed using Adobe illustrator for printing and visualization purposes.

Results

The Maximum Likelihood tree (Figure 1) illustrates different photosynthetic eukaryotic and prokaryotic organisms as well as non-photosynthetic plastid-bearing Apicomplexans. The analysis consisted of 467 taxa including about 150 environmental 23S sequences from Africa. The dataset consisted of a total of 513 characters. There were 60 invariant characters. Among the 453 variable characters, 361 were parsimony informative.

The environmental sequences from Africa were inferred to four major lineages: the prokaryotic algae Cyanobacteria, and three other eukaryotic groups the Streptophytes, the Chlorophytes and the Stramenopiles. The different colors in the tree represent the different groups of algae. Subaerial environmental sequences (represented by the prefix GA MC ENV#) from Gabon are labeled with capital letters (see legend).

The tree was rooted through the mid-point rooting and the longest branch was that leading to the Apicomplexans depicted with the light blue color, following a counterclockwise direction of the Apicomplexans we have the Euglenoids (depicted in yellow color). Adjacent to the Euglenoids we observe the Rhodophytes with the red color, However the Rhodophytes shown here are non-monophyletic and are split by the Stramenopiles represented with the brown color. In the Stramenopiles we find some of the Gabonese subaerial environmental samples (sequences labeled S and T). These sequences were more related to the diatoms than the other Stramenopiles. Moving counterclockwise from the cluster of Rhodophytes and Stramenopiles we find the Cyanobacteria (blue-green algae) depicted in purple color. Sequences labeled P, Q, and R were inferred in the cyanobacteria. Cyanobacteria are a monophyletic group representing the only prokaryotic organisms in the phylogeny. Sequences labeled R were grouped with *Scytonema*, while sequences labeled P were grouped with *Phormidium* and *Microcoleus*. Finally colony 125 (labeled Q) forms a clade with *Anabaena* and *Nostoc*. Adjacent to the Cyanobacteria we have a cluster of Cryptophytes, Haptophytes, and Claucosystophytes depicted in orange. Moving counterclockwise from the cluster Cryptophytes, Haptophytes, and Claucosytophytes is the Streptophytes clade (the dark green color). In this clade we find land plants and photosynthetic green algae. Environmental sequences in this group were spread between Bryophytes commonly called mosses (sequences labeled O), the liverworts (sequences labeled H, K, and J), Angiosperms (sequences labeled N, M, L), and the Trentepohliales (sequences labeled I). Sister to the Streptophytes is the Chlorophytes clade depicted with the light green color. The Chlorophytes include the rest of the green algae. Sequences in this group were inferred to two major lineages the Chlorophyceae and the Trebouxiophyceae. Sequences labeled A and B were inferred as chlorophycean grouping with *Dunaliella, Chlamydomonas,* and *Chlorochoccum*. The other sequences (C, D, E, F, and G) were grouped with

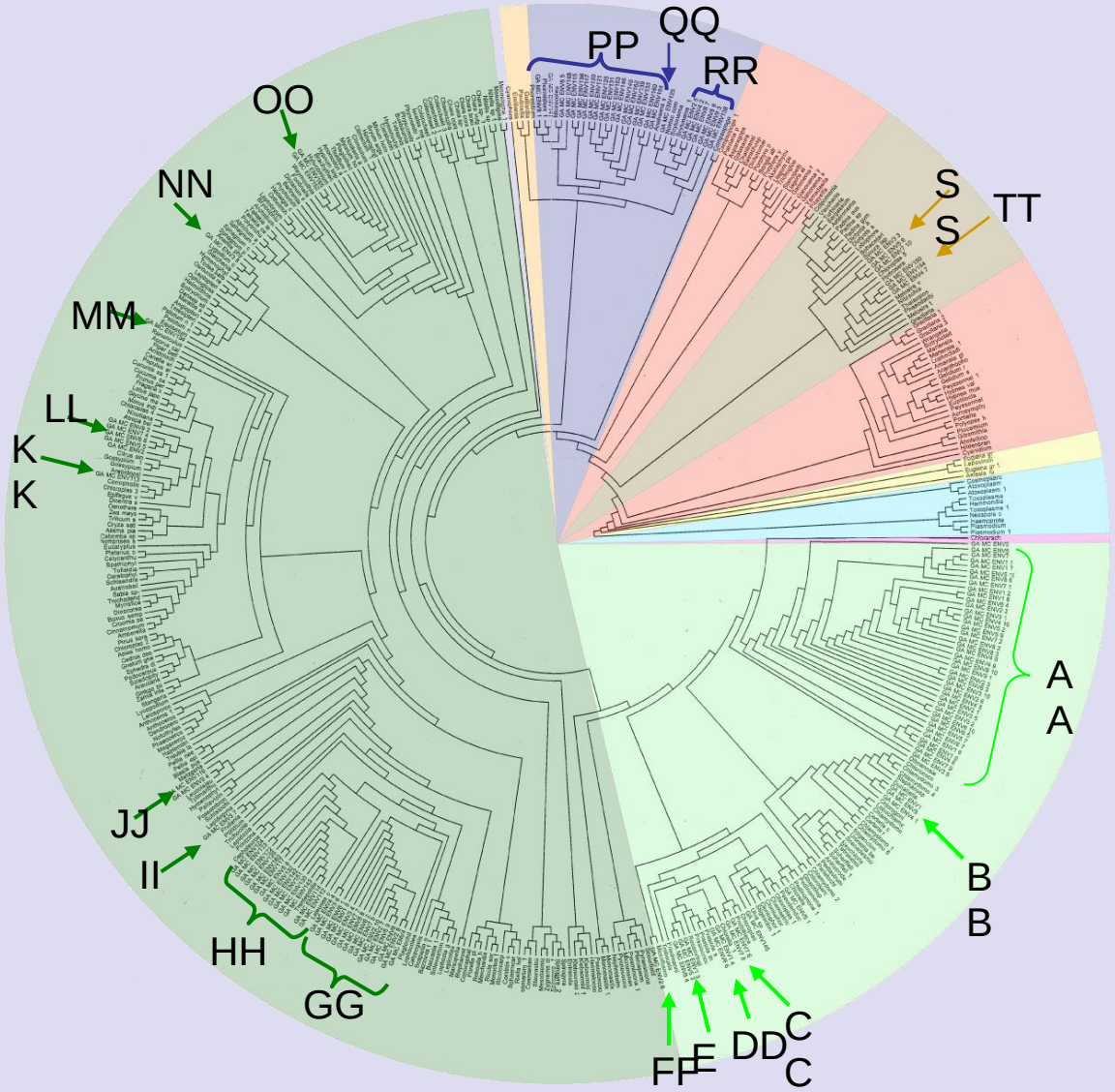

Figure 1. Maximum likelihood phylogeny of African subaerial epiphytes. The tree shows the major subaerial algal constituents (Cyanobacteria, diatoms, and green algae). The letters indicate phylotypes of subaerial algae found in "Les Monts de Cristal".

COLOR	TAXONOMIC GROUP	Gabonese environmental sequences
Light green	Chlorophyta	A,B,C, D, E, F and G
Dark green	Streptophyta	H,I,J,K,L,M,N,O
Orange	Cryptophyta Haptophyta Claucosytophyta	N/A
Purple	Cyanobacteria	P,Q, and R
Red	Rhodophyta (Group 1)	N/A
Brown	Stramenophiles	S and T
Red	Rhodophyta (Group 2)	N/A
Yellow	Euglenozoa	N/A
Light blue	Apicomplexa	N/A

the trebouxiophycean genera *Microthamnion*, *Rosenvingiella*, *Chlorella*, and *Prototheca*.

Discussion

Apicomplexans:

Depicted as the longest branch of the phylogeny, the Apicomplexans are unicellular parasitic organisms of animals and share a remnant chloroplast (the apicoplast) with other algae (Moore et al. 2008). These unicellular parasites acquired their apicoplast through secondary endosymbiosis of a red alga much like the same way the Dinoflagellates acquired their plastids (Moore et al. 2008). However, due to the parasitic nature of the Apicomplexans, their apicoplast is non-photosynthetic and is non-functional. The non-functionality of the remnant plastid may have lead to less selective pressure on its genome and may have led it to mutate rapidly (Wilson et al. 1996). This may explain why the Apicomplexans represented the longest branch in the ML phylogeny. Apicomplexan sequences were not found among the African environmental sequences.

Cyanobacteria

Cyanobacteria are photosynthetic prokaryotes that were among the first organisms to invade the terrestrial environment (Lopez-Bautista et al. 2007). Cyanobacteria share the same photosynthetic pathways as other algae, which lead to their classification with algae for a long time (blue-green algae); however, they were lately placed in the domain Bacteria based on 16S rRNA sequences (Woese et al. 1990). In the ML phylogeny (figure 1) Cyanobacteria were among the most diverse in the subaerial African environment based on environmental sequences. Particularly, African phylotypes were inferred to the order Nostocales with genera *Scytonema* and *Phormidium*. These genera are morphologically invested with firm mucilaginous sheaths and they all share a synapomorphy (the presence of a heterocyst) (Wilmotte 1994). Because the presence of the heterocyst in these cyanobacteria they are capable of fixing Nitrogen (N2) from the atmosphere. These sheathed genera are the second most successful group of subaerial algae after the algae that form symbiotic associations, and as a group they reach their maximum development in the tropics (Fritsch 1907). The Nostocalean cyanobacteria thrive in tropical regions mainly due to two major factors: first, the frequency and the abundance of rainfall in the tropics, and second, their ability to fix atmospheric nitrogen (Nienow 1996). A low concentration of nutrients, such as nitrogen (ammonium and nitrate) in the terrestrial environment might be the result of the extensive growth of these groups. The subaerial environment as opposed to aquatic environment is low in Nitrogen (N2), however, the air is composed of 78% N2. The ability of heterocystous cyanobacteria to fix atmospheric nitrogen may give them a selective advantage over other groups of algae.

A similar study using metagenomic approaches conducted by Lam (2010) in Suriname, South America has shown the presence of cyanobacteria in the

subaerial environment. Previous biodiversity studies using morphological observations have regularly found these genera in the African tropics (Frémy 1924, 1932; Duvigneaud and Symoens 1948).

Viridiplantae:

The Viridiplantae (Green plants) include all green algae and land plants, it is comprised of two sister lineages the Chlorophytan and the Charophytan (or Streptophytan) lineages. The Chlorophytan lineage comprises the Trebouxiophyceae, the Chlorophyceae, the Ulvophyceae and Prasinophytes (in part), while the Streptophytan (Charophytan) lineage comprises the Charophyceae, the Prasinophytes (in part), and land plants (Lewis and McCourt 2004). The "green plants" along with the Rhodophytes and the Glaucosystophytes share a close relationship with cyanobacteria. Chlorophytes, Rhodophytes and Glaucophytes evolved a plastidial condition by primary endosymbiosis. Endosymbiosis theory states that a photosynthetic cyanobacterium was engulfed (ingested and retained) by a heterotrophic protist (Delwiche 1999).

Our environmental sequences from Gabon, Africa inferred the following groups to be members of the subaerial community in "Les Monts de Cristal": the Chlorophyceae, the Trebouxiophyceae, the Ulvophyceae (represented by Trentepohlialean taxa), and some land plants. The presence of these groups in this environment was not surprising since previous biodiversity studies in the tropics of Africa have accounted for them (Rindi et al. 2006, 209; Printz 1921 and references therein). Chlorophyceae are third in importance when it comes to their abundance in the subaerial environment (Nienow 1996). Chlorophyceae have been reported previously by studies done by French naturalists in the 20th century from tropical Africa (Fremy 1924, 1932). The Trebouxiophyceae is a class of green algae with representatives usually integrated as phycobionts in associations forming lichens, and they are the most successful group of subaerial algae (Nienow 1996). Our third group of African algae found in the subaerial environment belongs to the class Ulvophyceae. The class is represented mainly by marine taxa (Rindi et al. 2006). However, some lineages from this group have been found living in terrestrial environments. One of these groups is the order Trentepohliales, an unusual group of ulvophyceaen algae, found exclusively in the subaerial environment and never associated with aquatic environments (freshwater or marine) (Lopez-Bautista et al. 2007). Trentepohlialean taxa are usually abundant in the tropics and found growing on different substrates where they compete with cyanobacterial and lichenic communities (Fritsch 1907).

This group was expected to be in the subaerial environment as it has been reported from the same environments in (Rindi et al. 2006; Hariot 1891, 1913; Gauthier-Lievre 1954; Joska and Bolton 1996). They were also reported in a similar study in the South American tropics (Lam 2010).

Stramenopiles:

Diatoms or Bacillariophyceae were the only organisms belonging to the Stramenopile group that were inferred from the subaerial environmental samples from "Les Monts de Cristal", Gabon (sequences labeled S and T). Phylogenetic analyses show that the plastids of the heterokonts are likely derived from members of the Order Cyanidiales (Muller et al. 2001) from the Rhodophytes. The placement of the Stramenopiles in the ML phylogeny between the two groups of Rhodophytes further provides evidence to the red algal origin of the Stramenopile plastid.

Diatoms are a major group of eukaryotic algae, and they are perhaps the most widespread group of aquatic algae on the earth (Norton et al. 1996). Diatoms are organisms that are encased in cell walls made of silica called frustules. They occur in soils, on rocks and on plants (Round et al. 1990). They contribute to about 20-25% of all organic carbon fixations in the world (Round et al. 1990). However, diatoms are a minor contributor to the epiphytic community and are usually confined to wet surfaces (Van de Vijver et al. 2004). The presence of diatoms was not surprising, as these organisms have been found in the subaerial environment previously. Lam (2010) conducting a similar study in South America reported the presence of environment sequences that were inferred to diatoms. Traditional studies have also reported the presence of subaerial species of diatoms (Round et al. 1990; Taylor et al. 2010; Van de Vijver et al. 2004).

Conclusions

Our metagenomic study on the algal subaerial communities from an African tropical rainforest has resulted on a new approach to understand and appreciate the biodiversity.

Biodiversity studies of this kind are of great importance in discovering different algal taxa before they are extinct. They are in need and fast especially in the tropics because of the faster rate at which tropical rainforest are disappearing.

Problems with traditional methods of assessing biodiversity made necessary to undertake cloning and sequencing methods. These methods have proven useful at estimating algal diversity in the subaerial environment. However, the time and cost that are required to make clone libraries for an environment are the main drawback. This will limit the number of libraries created which may lead to an underestimation of important species that are rare in the environment.

This study revealed the presence of prokaryotic (Cyanobacteria) and Eukaryotic (Chlorophyta and diatoms) algae from "les Monts de Cristal", Gabon. The higher number of sequences corresponded to cyanobacteria followed by green algae. These results support the hypothesis that the subaerial environment is home to cyanobacteria, diatoms, and green algae as well as mosses and liverworts. This study also shows the tremendous potential of these UPA primers to be used as DNA barcode material for further studies. The amplification of a wide range of photosynthetic (and even

non photosynthetic such as the apicomplexans) provide a strong base for the support of UPA as a universal marker for DNA barcoding plant material. Further studies are needed to evaluate UPA and its utility in DNA barcoding DNA, the use of metagenomics and the spatial and temporal variations of subaerial algal communities in tropical rainforests.

Metagenomic studies are providing fast and accurate results on the biodiversity of algal communities in the tropical rainforest in Africa. This study can be developed as a model system and can be further used to promote and protect national parks not only in Gabon but also other neighboring areas.

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NOTICIAS

X Congreso de Ficología de Latinoamérica y el Caribe
VIII Reunión Iberoamericana de Ficología
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Página web del Congreso: http://www.sofilac.com
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Segunda circular: http://congreso.sofilac.com/2daCircular.pdf

Fechas importantes:
Límite para inscripción de resúmenes: 15 de mayo de 2014
Cuotas de inscripción reducidas: 01 de junio de 2014

FICOWEB

Compilación de Claudia Pedraza.
Una sección sobre páginas web de interés para ficólogos. Bases de datos sobre biodiversidad de algas:

A Database of Plant Biodiversity of West Bengal
http://bioinfo-presiuniv.edu.in/wbpbdivdb_genera_algae.php

Catalogue of Diatom Names
http://researcharchive.calacademy.org/research/diatoms/names/index.asp

Hawaiian Freshwater Algal Database
http://algae.manoa.hawaii.edu/hfwadb/

A collection of freshwater algae (and protozoans) from the Keweenaw Peninsula, MI
http://www.keweenawalgae.mtu.edu/genera_index.htm

Portuguese Seaweeds Website MACOI
http://macoi.ci.uc.pt/macoi_list.php

Checklist of phytoplankton in the Skagerrak-Kattegat
http://www.smhi.se/oceanografi/oce_info_data/plankton_checklist/ssshome.htm

Aussie Algae
http://www.aussiealgae.org/

Swedish taxonomic database
http://www.slu.se/sv/centrumbildningar-och-projekt/dyntaxa/search/

Herbario Nacional MEXU (UNIBIO)
http://unibio.unam.mx/

CAUP Culture Collection of Algae
http://botany.natur.cuni.cz/algo/caup.html

Marine Plants of Western Australia (FloraBase)
https://florabase.dpaw.wa.gov.au/marineplants/

Centre of Excellence for Dinophyte Taxonomy (CEDiT)
http://www.dinophyta.org/index.php?option=com_frontpage&Itemid=1

Centro de documentación de Biodiversidad Vegetal (CeDocBiV)
http://herbaribcn.ub.es/query.php?db=algas

BDB
http://biodiver.bio.ub.es/biocat/#pas4

A flora of the benthic marine algae of Alaska
http://herbarium.botany.ubc.ca/herbarium_data/algaltypes_web/search.htm

Fresh Algae
http://plantnet.rbgsyd.nsw.gov.au/PlantNet/fwalgae/index.htm

Phytoplancton de Méditerranée
http://www.com.univ-mrs.fr/PHYTOCOM/rechabond.php

Phycologigal Checklists
http://www.phycology.net/

Sinice a řasy.cz – gallery
http://galerie.sinicearasy.cz/galerie

PUBLICACIONES RECIENTES

LIBROS

Manuel Bonilla ha traducido del alemán el libro de Rieth, A. 1980. Xanthophyceae. Teil 2. Vaucheriaceae. Sußwasserflora von Mitteleuropa. El texto puede solicitarse al email: werbiovau@comunidad.unam.mx. Manuel Bonilla es coautor de una nueva especie de *Vaucheria* descrita para México.

REVISTAS

Recientemente se han publicado artículos sobre algas mexicanas en las siguientes revistas:

Phycologia:
http://www.phycologia.org/

Journal of Applied Phycology:
http://link.springer.com/journal/volumesAndIssues/10811

AUTORES

El Dr. Gustavo Hernández ha publicado recientemente los siguientes trabajos:

Cruz, I, Y. Bashan, .G Hernández-Carmona, L.E. de-Bashan. 2013. Biological deterioration of alginate beads containing immobilized microalgae and bacteria during tertiary wastewater treatment. *Applied Microbiology and Biotechnology* 97 (3): 9847-9858

Rodríguez-Montesinos, Y.E., D.L. Arvizu-Higuera, G. Hernández-Carmona, M. Muñoz-Ochoa, J.I. Murillo-Álvarez. 2013. Seasonal variation of the agar quality and chemical composition of *Gracilaria veleroae* and *Gracilaria vermiculophylla* (Rhodophyceae, Gracilariaceae) from Baja California Sur, Mexico. *Phycological Research* 61: 116–123.

Hernández-Herrera, R.M., F. Santacruz-Ruvalcaba, M.A. Ruiz-López, J. Norrie, G. Hernández-Carmona. 2014. Effect of liquid seaweed extracts on growth of tomato seedlings (*Solanum lycopersicum* L.). *Journal of Applied Phycology* 26: 619-628.

Rosas-Alquicira, EF, R. Riosmena-Rodríguez, G. Hernández-Carmona, A.I. Neto. 2013. Development of conceptacles in *Amphiroa* (Corallinales, Rhodophyta). *Acta Botanica Brasilica* 27(4): 698-708.

Briceño-Domínguez, D., G. Hernández-Carmona, M. Moyo, W. Stirk, J. van Staden. 2014. Plant growth promoting of seaweeds liquid extract produced from *Macrocystis pyrifera* under different pH and temperature conditions. *Journal of Applied Phycology*. DOI 10.1007/s10811-014-0237-2.

Suarez-Castillo, A.N., R. Riosmena-Rodríguez, G. Hernández-Carmona, M.M. Mendez-Trejo, J.M. López-Vivas, C. Sánchez-Ortiz, M.M. Lara Uc, J. Torre-Cosio. 2013. Biodiversity associated to *Sargassum* forest at the Gulf of California. En: Riosmena-Rodríguez, R. Ed.*: Invertebrates classification, Evolution and biodiversity*. New York, Nova Science Publishers, Inc. p: 205-223

Hernández-Carmona, G., Y. Freile-Pelegrin, E. Hernández-Garibay. 2013. Conventional and alternative technologies for the extraction of algal polysaccharides. En: Dominguez, H. Ed.: *Functional ingredients from algae for foods and neutraceuticals*. Sawston, Woodhead Publishing Limited. pp. 473-516 pp. DOI 10.1533/9780857098689.3.475

Estas y otras publicaciones del Dr. Hernández pueden descargarse de su página en ResearchGate:
https://www.researchgate.net/profile/Gustavo_Hernandez-Carmona

Para anunciar publicaciones recientes, enviar la información (referencia y acceso electrónico) a los editores.

IMÁGENES

Página 1: *Nostoc* sp. y *Trentepohlia* sp. Bonampak, Chiapas (por E. Novelo).
Página 5: *Nostoc sphaericum*, El Edén, Q.R. (por R. Tavera).
Página 23: *Nostoc microscopicum*, Cantera Oriente, CU, D.F. (por E. Novelo).

Política editorial y normas editoriales para el Boletín de la Sociedad Mexicana de Ficología

El Boletín de la Sociedad Mexicana de Ficología tiene la finalidad de dar a conocer información sobre las algas mexicanas en un formato múltiple (vía la página web y en formato digital imprimible – pdf, disponible en http://boletin-sociedad-mexicana-ficologia.meridion.mx). Se estructura en secciones permanentes o temporales, dependiendo de las actividades de la Sociedad y de la oferta de documentos por los socios.

1. Se publicarán textos de difusión, presentación de proyectos y resultados de investigaciones. Los textos podrán ser artículos originales, artículos de revisión, artículos de opinión, reseñas bibliográficas, resúmenes de tesis, datos complementarios a publicaciones formales, etc. Estos materiales serán evaluados por los editores y en su caso por árbitros *ad hoc*.
2. La extensión del texto deberá ser de cerca de 2,500 palabras con un 40 % para ilustraciones originales, incluyendo gráficas; invitamos a los autores a enviar imágenes extras para ilustrar todo el Boletín.
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