# Forum Phycologicum



## Newsletter of the Phycological Society of Southern Africa

## Vol. 71 December 2009



## President

Eileen Campbell (<u>eileen.campbell@nmmu.ac.za</u>) Department of Botany Nelson Mandela Metropolitan University PO Box 77000 Port Elizabeth 6031 South Africa

## Secretary-Treasurer

Mark Rothman (<u>Mark.Rothman@uct.ac.za</u>) Seaweed Unit, Marine and Coastal Management Private Bag X2 Rogge Bay 8012 South Africa

## **Membership Secretary**

#### A.J. Smit (smitaj@ukzn.ac.za)

School of Biological and Conservation Sciences University of KwaZulu-Natal Westville Campus Private Bag X54001 Durban 4000 South Africa

## **Newsletter Editor**

Gavin W. Maneveldt (<u>gmaneveldt@uwc.ac.za</u>) Dept. of Biodiversity and Conservation Biology University of the Western Cape Private Bag X17 Bellville 7535 South Africa

## **Student Representative**

Nuette Gordon (<u>nuette.gordon@nmmu.ac.za</u>) Department of Botany Nelson Mandela Metropolitan University PO Box 77000 Port Elizabeth 6031 South Africa

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## From the Editor

Welcome to the 2009 December edition of Forum Phycologicum. You've all, no doubt been quite busy over the past year. Besides the various ongoing research initiatives, this is reflected in the numerous conferences and symposium (for which various PSSA members are reporting) that have taken place over the past few months as well as the forthcoming 25<sup>th</sup> meeting of our own society. As vou can well imagine, it has once again been challenging keeping abreast of all the exciting things occurring around us. This is particularly reflected in our featured article that showcases the large-scale movement toward molecular systematics and our understanding of the molecules, rather than the morphology as Lineekela states in his report on the IPC9.

It has been a while, but we managed a student submission in this issue. The article by Rosemary Eager highlights a facultative, non-trophic association between a winkle and a non-geniculate coralline red alga. Increasingly, ecological and habitat approaches to research (and also biodiversity conservation) are again being promoted and so it is encouraging that such research is still being pursued.

Despite your various administrative and teaching (and possibly even research) endeavors, I hope this past year has been a fruitful one for all of you. With this in mind, I wish you all happiness, lots of welldeserved rest and a safe return to work in the new year. For those celebrating *Christmas*, here's wishing you a blessed and safe festive season.

See you all next year!

Best wishes Sincerely



Gavin W. Maneveldt

### **News and Reviews**

## 1. First South African Southern Ocean Community

On 30 March 2009 a meeting was held between scientists having an interest in Southern Ocean research. The meeting was chaired by Dr Pedro Monteiro and its main aim was to establish an initiative that would facilitate effective planning between SANAP operations and the SANAP science community. The name of this embryonic group is SASOC (South African Southern Ocean Community) and William Froneman (Rhodes) and Howard Waldron (UCT) were asked to co-ordinate SASOC until it has been more formally established. We were acutely aware that those present at the meeting did not represent everyone with an interest in Southern Ocean science. The intention is to canvas more widely those scientists who wish to be part of SASOC.

Please contact Howard this is the case. You will be added to the mailing list and notified of the next meeting.

## Howard Waldron

Dept of Oceanography University of Cape Town Email: <u>howard.waldron@uct.ac.za</u> (Tel) +27 21 650 3284 (Fax) +27 21 6503979

## 2. Global Biodiversity Information Facility (GBIF) – key Informatics products

As planned in the GBIF Work Programme 2009-2010, the GBIF Secretariat has released a series of key Informatics products such as the Integrated Publishing Toolkit (IPT) and the Harvesting and Indexing Toolkit (HIT) (see apendices I & II). These products are the foundation of the data mobilisation activities. As an immediate response to community requests, they are aimed at simplifying the publishing process and reduce the latency between data publication and discoverability through the GBIF indexes.



The GBIF Integrated Publishing Toolkit (IPT) and the Harvesting and Indexing Toolkit (HIT) are open source software platforms developed by the Secretariat of the Global Biodiversity Information Facility. The IPT will facilitate efficient biodiversity data publishing to the Internet by all participants in the GBIF network. The HIT enables the data harvesting and the quick building of indexes of the harvested data.

An IPT training course was held in September in support of the establishment of a distributed helpdesk. More information about the IPT and HIT are provided in the form of a summary paper (see appendices I & II).

The Secretariat kindly requests that you publicise this information to the relevant data publishers and encourage them to download, make use of and provide feedback for improvement of the IPT and HIT, to the benefit of the wider GBIF community. As always, you are most welcome to contact the GBIF Help-Desk in case of any questions at: helpdesk@gbif.org

#### Samy Gaiji

Head of Informatics Global Biodiversity Information Facility (GBIF) Universitetsparken 15, 2100 Copenhagen Ø, Denmark (<u>http://www.gbif.org</u>) Email: <u>sgaiji@gbif.org</u> Phone: +45 35 32 14 85, +45 35 32 14 70 Fax: +45 35 32 14 80 Skype: sgaiji

## 3. The 9<sup>th</sup> International Phycological Congress (IPC9), Toykyo, Japan, 2-8 August 2009

The 9<sup>th</sup> International Phycological Congress was held under the auspices of the International Phycological Society (IPS) and the Japanese Society of Phycology. Tokyo, with a population of over 12 million people, is a very busy city and provides a balanced experience of both high-tech and historical sides of Japan. The congress venue, 'National Olympics Memorial Youth Center' located in Yoyogi, Tokyo, was on the other hand less busy. This year attracted over 500 participants from 44 countries. The conference proceedings comprised four full-day parallel sessions punctuated by a mid-conference excursion. It was comforting to see the many young phycologists, a very welcome scene indeed especially since many experts are on the verge of, or beyond retirement. This was notably the case with researchers such as Max Hommersand and especially Paul Silva who appeared very frail, but strong enough to travel all by himself from California; it was indeed a blessing to have them around.

As was expected, Japan had a very strong presence with 164 participants including many brave school-goers who presented posters on their experiences with seaweeds and the value of seaweeds in nature.

The PSSA contribution was comparatively poor with only one poster and two oral contributions. The low turnout was most probably due to the high cost of attendance. Looking at the PSSA membership though (which stands at about 50) one would have expected a few more members to have attended, even more so because we hold the Presidency of the IPS.

As is a culture with conferences of this magnitude, the proceedings were organized into plenary lectures, mini symposia, workshops and sessions of contributed papers (Oral and posters). The plenaries were very interesting and these world renowned phycologists showed indeed why they were invited to present such lectures. The presentations were as follows:

- 1. Taizo Motomura (Hokkaido University, Japan): Fertilization, development and cell division in brown algae.
- 2. Chuck Amsler (University of Alabama at Birmingham, U.S.A.): Macroalgal chemical ecology: microscopic spores to magnificent Antarctic forests.
- 3. Nils Kröger (Georgia Institute of Technology, U.S.A.): Molecular analysis of silica biomineralization in diatom silicification.



4. E. V. Armbrust (University of Washington, U.S.A.): Comparative genomics of marine phytoplankton.

Of the four plenaries, I enjoyed most the one by Chuck Amsler who reported on the chemical ecology of macroalgae from the Antarctic forests. had Ι always assumed that due to the harsh Antarctic environment, organisms there would be smaller. Amsler. however, reported that some the of Antarctic Desmarestiales can grow even larger than many of the temperate kelps due to the metabolites they produce to ward off grazers.

After the plenaries it was time for the mini-symposia, followed by the contributed papers and thereafter the workshops. The sessions that I found most interesting were:

- Alien algae and invasive species
- Frontiers of algal speciation research
- Biodiversity and ecological research
- Phylogeny new advances and insights

Perhaps one of the most

heated sessions at the conference was the *Frontiers* of algal speciation research and the debate mainly followed a presentation by Juliet A. Brodie entitled *Is morphology necessary for the taxonomy of* algae? As would be expected, the many traditional taxonomists felt that this was not even "in question" because for you to do molecular studies you needed to do morphological taxonomy because you must at least first have a sense of what it is that you are sequencing and not just put your samples in a black



Lineekela Kandjengo (top), John Bolton (middle) and Gavin Maneveldt (bottom) braving the misty slopes of Mt. Fuji.

box and see what comes out. On the other hand, the proponents of molecular systematics were of

the view that morphology has failed us dismally due to the fact that we have too many cryptic species and too many varieties and that it was high time we switched to the molecules as they are more robust.

With the respect to workshops, Ι failed to understand their meaning. I assumed that they would be more enlightening on how one can go about applying a technology, certain or analyzing specific data. The vast majority, however, were regular iust paper presentations not even followed by any discussion. I suppose the one big and unfortunate problem was the barrier. language which often manifested itself during discussion time.

The poster sessions (283 posters) were well organized and most were of exceptional quality and well presented. One can actually learn more from talking to the presenter on a one-to-one basis because it gives them time to think and to explain their work and findings. Many of the posters came

from the young Japanese delegates who were mainly in their first year of postgraduate studies.

For the mid congress tour, the PSSA crew (Myself, John Bolton and Gavin Maneveldt) coincidentally opted for the same Mt. Fuji – Lake Saiko tour. Upon arrival at the 5<sup>th</sup> station (2,305m above sea level) at around 11h30, we took a leisurely walk up to the 7<sup>th</sup> station (2,700m above sea level). While we thought we encountered



many hikers at the 5<sup>th</sup> station, we realized that, that was just the tip of the iceberg because many more people were still on their way down from the summit (some 3,700m above sea level). Many had even spent the night on Mt Fuji and only started

walking down after sunrise. Due to time constraints and very foggy weather (compared to humid Tokyo) we were never able to see the summit despite ascending for nearly an hour.

According to the tour guide, about 200,000 people climb Mt Fuji every climbing season (between 1<sup>st</sup> July - $26^{\text{th}}$ August) averaging about 3300 people per day. Climbers varied from school-goers to the very old, many seemingly in well organized groups, of which some comprised of pilgrims. Most people were very exhausted, probably drained by the change in altitude, temperature and humidity, and extreme cases were transported down the mountain-side on horse back and horse-drawn carts. A comment made by our tour guide, who indicated that she had no intention of

ever climbing Mt Fuji, was that "you would have to be crazy to climb Mt Fuji. Doing it a second time was just sheer stupidity". After descending back to the 5<sup>th</sup> station we had lunch; I must admit that this was the best meal I enjoyed during my entire stay in Japan.

After departing Mt Fuji we arrived at the Yamanashi Institute of Environmental Science (at around 14h00) where we were given a "short" lecture (actually turned out to be quite lengthy) on the activities of the centre and the other environmental issues concerning the Mt Fuji area. This leg of the trip did not go down very well since it was just after lunch and everyone was no doubt quite exhausted. We then departed for Lake Saiko, one of the big lakes at the foot of Mt Fuji. On this leg of the trip we were hoping to get another chance to view the summit of Mt Fuji, but



The summit of Mt. Fuji was not visible through the thick fog.



PSSA representatives enjoying a well-deserved cooler at the end of a most rewarding conference.

yet again the weather was not on our side. Those with a love of microalgae, however, still managed a go at collecting some water samples at the lake.

The social programme was very well organized, very punctual and created a much needed platform to engage other participants. Both the opening and closing ceremonies were held the at National **Olympics Memorial Youth** Center while the Banquet was held at the luxurious Keio Hotel in central Tokyo. In his speech, IPS president Prof John Bolton expressed his joy and honour at overseeing such a successful event and thanked both the IOC and the LOC for a job well done. He also thanked all those who traveled near and far to attend the conference and thereby making it such a success,

views shared by Prof Isao Inouye, co-convener of the IPC9 LOC. Prof Bolton took this opportunity of sharing his views on the issue of the IPS presidency. He commented that the IPC presidency only lasted two years. This meant that many presidents were and would never be able to host a conference.

IPC10 is to be held in Orlando, Florida, U.S.A in 2013. This gives us sufficient planning time and so I hope to see many more PSSA members at the next IPC.



## **PSSA presentations at IPC9**

- 1. John J. Bolton: The global biogeography of kelps (Laminariales, Phaeophyceae) with new insights from recent changes in family concepts.
- 2. Gavin W. Maneveldt, Martin Cocks and William J. Woelkerling: Phenetic analyses of the Corallinales (Rhodophyta) using an internet identification tool to elucidate their identity.
- 3. Lineekela Kandjengo, John J. Bolton and Terry A.J. Hedderson: Molecular systematics of *Ulva* in commercial aquaculture in South Africa (a poster)

Arigato (for those unfamiliar, this means "thank you" in Japanese)!

Lineekela Kandjengo Department of Fisheries and Aquatic Sciences University of Namibia Email: <u>lkandjengo@unam.na</u>

## 4. IX Conference of the Aquaculture Association of Southern Africa, Swakopmund, Namibia, 7-13 September 2009

The Conference of the Aquaculture Association of Southern Africa (AASA) is held every two years under the auspices of the Aquaculture Association of Southern Africa. This year marked the 9<sup>th</sup> running and the first time the conference had moved outside of the South African borders. Held at the Swakopmund Hotel and Conference Centre in Swakopmund, Namibia, the conference was jointly hosted by the AASA, the University of Namibia and the Namibian Department of Fisheries.

Besides being the foremost meeting on local aquaculture research and utilization (products, technologies and markets), the conference provides a platform for researchers to interact directly with aquaculture farmers. This meant several pleasant evenings where drinks and dinner were paid for by aquaculture farmers (depending on how much they valued your research). Lunch was outstanding! In particular the queue for the fresh oysters (obtained from Walvis Bay each morning) was longer than the



Just two of the many junior high school students who participated in the *Algae in Education Workshop*.



John Bolton, president of the IPS, presents awards of participation to high school students who attended the IPC9 *Algae in Education Workshop*.

queue at the bar! A word to the wise "stay away from the butter fish..."

This year attracted over 300 participants with a theme of *Africa in the Global village*. The conference kicked off with a tour of oyster cultivation facilities, followed by the Namibian fisheries research facilities at Hentjies Bay, a tour of a scallop hatchery, and finally a visit to the Swakopmund Aquarium and a demonstration of a recirculting aquaculture system.

The conference was opened with a talk by The Honorable Minister of Namibian Fisheries, Dr. Abraham Ivambo. I was impressed that all the dignitaries stayed for the entire day's proceedings. In particular, I was impressed that the minister wrote a personal note of gratitude to every presenter from his department, congratulating them on their presentations and the quality of their research. This personal touch was evident throughout the conference with the minister being presented with the "Aquaculturist of the year award" by the AASA. This was notably for his devotion over the past 10 years in developing a fisheries and aquaculture policy from scratch. Having read some of the supporting documentation and legislation it was hard to imagine that aquaculture research in Namibia had progressed so rapidly bearing in mind that there are only three qualified PhD's in the whole Namibian Fisheries department. The minister had just recently been awarded the "FOA responsible fisheries award for 2009", the first time the award has been given to an individual.

Conference topics ranged from country overviews, to design technology, genetics, aquaculture feeds and dietary matters, animal health, micro flora, biosecurity, oysters, scallops, abalone and abalone dietary matters, and seaweed aquaculture.

## Seaweed presentation by members of the PSSA:

- 1. John J. Bolton: Aquaculture and trophic levels, or why are the two most successful mariculture industries in south and east Africa a plant and an herbivore?
- 2. Mark Cyrus: Development of an artificial diet for the production of export quality gonads from the sea urchin *Tripneustes gratilla*.
- 3. Thembinkosi Steven Dlaza: *Porphyra* (Bangiales, Rhodophyta): A new species for aquaculture in South Africa.
- 4. Lineekela Kandjengo: Molecular Systematics of *Ulva* in commercial aquaculture in South Africa.
- 5. Deborah Robertson-Andersson: Integrated Seaweed/Abalone Multitrophic Recirculating Aquaculture (IMTA) In South Africa: Costs & Benefits.
- 6. Dina Shuuluka: Eco-physiological Studies of *Ulva* Species.

Aside from a name change from seaweed to sea vegetable, seaweeds literally stole the show! Mark Cyrus won best student oral presentation and I was awarded best overall oral presentation at the conference. Rather than being considered a smelly nuisance-growth that clogs aquaculture outlets and a necessary evil as a feed for herbivores, these presentations demonstrated that seaweed cultivation was profitable and accounted for the largest proportion of global aquaculture. In incorporation seaweeds addition. of into aquaculture systems notably made cultured herbivores even more valuable than single-species cultivation currently practiced in Southern Africa.

In addition I attended 2 workshops (Establishing of a WAS African Chapter, Taking Africa into the Global Aquaculture Village) and a 3-day training session on Recirculating Aquaculture Systems (RAS). From the information provided, I thought a RAS would be a completely man-made system with artificial means of nutrient removal, especially since the presenters did not approve of Integrated Multitrophic Recirculating Aquaculture (IMTA) systems. However, the RAS had autotrophic bacteria, heterotrophic bacteria and fish; this in the minds of the presenters was not an IMTA system. I found it particularly disturbing that the bacteria (which are often seen as being a bad thing especially when cultivating something for human consumption) are grown in systems in which the farmers know next to nothing about. Also, RAS are highly intensive systems with high stocking densities; the potential for problems is immense.

IMTA systems and RAS are to my mind the same thing. With an IMTA system that includes seaweeds you obtain secondary income steams from the seaweeds. Seaweeds are more visible than bacteria and you can see when your biofilter is in trouble. RAS are, however, more preferred than IMTA systems and this needs to be changed especially if we are to keep aquaculture sustainable.

> **Deborah V. Robertson-Andersson** Dept. Biodiversity & Conservation Biology University of the Western Cape, South Africa Email: <u>drobertson-andersson@uwc.ac.za</u>



### 5. Darwin 200 Symposium

Under the auspices of the International Union of Biological Sciences (IUBS) and the United Nations Educational Scientific and Organization Cultural (UNESCO), 'Darwin the 200' symposium was held to  $200^{\text{th}}$ celebrate the anniversarv of Charles Darwin's birthday in 2009. The aim of 'Darwin 200' was to celebrate the impact of Darwin's ideas on current scientific knowledge and comprised а series of scientific symposia and satellite meetings on five continents (see www.iubs.org for details), culminating in Evolution the Human Symposium held on the 12<sup>th</sup> October 2009 the at University of the Western Cape (UWC) in Bellville, South Africa.



While still a young man, Charles Robert Darwin joined the scientific elite (Image source: <u>http://en.wikipedia.org/</u>).

Pre-symposium satellite meetings included:

- *Biological Education* Christchurch, New Zealand 12-16 February 2009;
- Basic Issues in Evolution Venice, Italy 1-5 May 2009;
- *Biological Consequences of Global Change* Beijing, China – 8-10 July 2009;
- 150 Years of Darwin's Evolutionary Theory: a South American Celebration Punta del Este, Maldonado, Uruguay – 3-6 September 2009;
- *Marine Genomics* Okinawa, Japan October 2009; and
- *Biodiversity & Biological Resources* San José, Costa Rica – October 2009.

The symposium of the 12<sup>th</sup> October had a relatively broad focus on Human Evolution research and covered such topics as: the latest research on Human Genomics, Archaeology, Paleontology, Genetics and Genographic Research. The one-day symposium was flanked by a series of pre- and

post-symposium workshops and satellite meetings geared at placing human evolution research within the context of other global concerns.

These included:

- an *Integrated Climate Change* workshop, 7 October 2009;
- a Traditional Knowledge and Environmental Change (co-hosted by the South African National Biodiversity Institute [SANBI]), 9 October 2009;
- the 30<sup>th</sup> General Assembly of the International Union of Biological Sciences, 10-11, 13 October 2009; and
- a *Biology Education* (*BioEd*) workshop, 14 October 2009.

The entire programme of the 12<sup>th</sup> October was presented by various invited keynote

speakers, all world-leaders in their fields of specialization. I had found the following keynote addresses particularly interesting and thought provoking largely because they presented novel information on some very familiar subjects.

- 1. **Brian O'Connell**, Rector and Vice Chancellor of the University of the Western Cape, opened the symposium with a thought provoking introduction to "... making sense of it ." In his talk, Prof O'Connell emphasized the importance for mankind in making the right choices and decisions for a tomorrow that will need to accommodate a population growth of up to 50% within the next 40 years.
- 2. Giorgio Bernadi (Italy) explained that mutations, as previously thought, were NOT random events and that mostly negative natural selection (selective removal of alleles that are deleterious) are occurring. In his talk he commented that the transcription of  $GC \rightarrow AT$



occurred more frequently than  $AT \rightarrow GC$  and that warm-blooded organisms have high GC cores, which are lacking in cold-blooded organisms. Temperature was and is thus the main driving factor for natural selection, but other factors, particularly in the oceans (e.g. salinity) are also important.

- 3. **Mark Stoneking** (Germany) explained that humans, more so than any other species, are characterized by their reliance on social and cultural traditions and as a consequence, cultural differences often explain observed genetic differences. Similarly, genetic analyses can be used to provide new insights into particular cultural practices. By genetically analyzing body, head and pubic lice, it was found that loss of body hair occurred some 3 MYA and the origin of clothing some 72 000 YA.
- 4. **Himla Soodyall** (South Africa) reiterated that two types of DNA have been extremely useful in reconstructing our past: mitochondrial DNA (mtDNA), which is passed exclusively by females; and Y chromosome DNA, which is transmitted from father to son. Prof. Soodyall's work re-emphasized the origin of human existence from Africa, but proposed a southern African origin rather than an East African one.

This was argued because living San and Khoi people have retained some of the oldest mtDNA and Y chromosome lineages found today and thus possess the most ancestral lineage for human-kind.

5. Ronald Clark (South Africa) gave astounding news (perhaps not so astounding in the human evolution circles. but certainly to me) that the long accepted theory that humans have evolved from apes that walked on four limbs using their knuckles, was INCORRECT! New evidence from the Sterkfontein caves shows that Homo sapiens arose

from a pre-ape ancestor that never went through a knuckle walking stage, but climbed upright in trees and walked upright on the ground. It was argued that the appearance between humans and apes are partly due to convergent evolution.

6. **Yves Coppen** (France) has been researching WHY a pre-human became a MAN. His research has concluded that "... evolution is not blind chance and neither is it intelligent design, but a much more complex interaction ..." Throughout the recent history of the planet, a series of droughts had occurred and about 4 MYA opening of the tropical African landscape occurred resulting in a savanna-type landscape. By then, all pre-humans walked upright. Similarly as in pre-humans (that first evolved from around 10 MYA), it was concluded that *Homo* evolved because of the changing climate some 2-3 MYA.

At the start of the Darwin 200 Launch and Symposium Dinner on the evening of the 12<sup>th</sup> October, Professor Emeritus **Phillip Tobias** (South Africa) gave a most insightful account of the personal life of Charles Darwin. Darwin was



Charles Darwin seen in typical pose (Image source: <u>http://en.wikipedia.org/</u>).

indeed, for most of his adult life after the return to England of the HMS Beagle, a very, very sick Prof person. Tobias' research has shown that Darwin suffered from both Crohn's Disease (an inflammatory disease of the intestines that may affect of any part the gastrointestinal tract. causing a wide variety of symptoms) as well as Chagas' disease (a tropical parasitic disease caused by flagellate protozoan the Trypanosoma cruzi that is commonly transmitted to humans and other mammals by an insect vector, the blood-sucking assassin bugs of subfamily the



The voyage of the HMS Beagle. Of the 13 ports where the HMB Beagle called on its homeward voyage South America to England, it stayed longer at Simon's Town (Cape Town) than anywhere else except for the Galapogos Islands (Image source: <u>http://en.wikipedia.org/</u>).

Triatominae [family Reduviidae]). It is believed that Darwin probably inherited Crohn's disease because many members of his immediate family suffered similar symptoms. It is accepted know that Chagas' disease was probably acquired during his HMS Beagle travels to the east of the Andes where Darwin recorded "an attack (for it deserves no less a name) of the Benchuca, a species of Reduvius, the great black bug of the Pampas", which is associated with Chagas' disease. The combined effects of these diseases left Darwin so debilitated that often for months at a time he was bed-ridden. On a good day, Darwin was not able to work for more than three hours in total. Despite these afflictions, Darwin was still capable of making a significant impact on current scientific knowledge. Had he not been so ill, just how much more of an impact on our scientific existence would he have made?

This little exercise by Prof Tobias into the history of the later years of Darwin, and of biological science, has thrown new light on the wonderful works of Charles Darwin.

> Gavin W. Maneveldt Dept. Biodiversity & Conservation Biology University of the Western Cape, South Africa Email: gmaneveldt@uwc.ac.za

## **Featured Article**

## Modeling green algal macroevolution

Macroevolution is commonly defined as largescale change in the genetic material of a population of organisms from one generation to the next occurring over geological time. А number of questions are typically addressed by macroevolutionary scientists. How frequently do changes in a particular character happen over evolutionary time? When did key features evolve and how does this match up with earth history? Why are some groups of organisms more speciesrich than others? Is evolutionary success correlated with the origin of a particular character or certain genomic changes? More recently, the question as to whether speciation occurs more frequently in the tropics than in temperate and cold areas has become increasingly important to answer.

The most popular way of doing macroevolutionary research is to take a geologist's hammer and go hunting for fossils. By working with the fossil record, one can easily observe the chronology of when species come into being and when they went extinct, or when certain characters appeared and/or then disappeared. So, if you're fond of dinosaurs or hard-shelled mollusks, this is the way to go.



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**Figure 1.** Examples with illustrations of siphonous green algae. A. *Derbesia*, B. *Bryopsis*, C. *Codium*, D. *Udotea*, E. *Halimeda*, F. *Caulerpa*, G. *Batophora*, H. *Neomeris*, I. *Cymopolia*, J. *Acetabularia*. A-F represent the order Bryopsidales; G-J represent the order Dasycladales. Thallus architecture ranges from a simple collection of siphons (e.g. A) to more complex, corticated thalli as those of *Codium* (C), *Halimeda* (E) and *Cymopolia* (I).

However, if you happen to like seaweeds, this will only lead to frustration because they lack hard parts and are rarely preserved as fossils. Luckily, recent developments are starting to allow macroevolutionary inferences to be made in other ways, starting with species phylogenies and information about contemporary species. The advantage of this method is that the phylogenetic relationships among species become clear. However, unlike working with fossils, the chronology of appearance of characters and the patterns of speciation and extinction must now be inferred from information about contemporary species using statistical techniques.

Such inferences are made by modeling the evolution of traits, their rates or the associations between them in a phylogenetically explicit statistical framework. This no doubt depends on the type of questions being asked. Traits of interest could pertain to morphology, ecology or genetics, while rates can include molecular evolutionary rates, or speciation and extinction rates. One could also be interested in modeling associations between different traits or between traits and rates. Researchers at the Ghent phycology lab [1] have recently applied such methods to answer questions about when the siphonous green seaweeds originated and diversified, how certain genes were gained and lost from green algal genomes during the course of evolution, and how the macroecological niche of seaweeds have evolved.

Much of our research centers on siphonous green algae (Fig. 1). These organisms have the bizarre ability to form large, differentiated thalli from a single. giant tubular cell. Well-known representatives are Caulerpa and Codium, both of which are notorious invasive seaweeds. We were interested in knowing how old the siphonous green algae are, when certain key features like intercellular calcification evolved, and how old the genera that we use for our other macroevolutionary research are. The molecular clock, in combination with fossil observations can be used to calibrate phylogenetic trees in geological time and answer our questions. However, the molecular clock assumes that the





**Figure 2.** Illustration of the process of calibrating a phylogenetic tree in geological time by applying a relaxed molecular clock model. In the phylogram on the left, branch lengths are proportional to amounts of molecular change and it is obvious from the figure that some lineages have faster rates of molecular evolution because their species appear to be further from the root of the tree (especially lineages in lower half of tree). By modeling how the rate of evolution evolves along the phylogeny, we inferred the relaxed molecular clock tree on the right in which all species are equally distant from the root and branches are proportional to time. The origin of the siphonous green algae and of calcification in extant lineages of Bryopsidales are indicated with green arrows (modified from [2]).

rate of molecular evolution ticks at a constant rate, an assumption that has been desecrated in the majority of datasets, including ours. Luckily, it is possible to relax the molecular clock assumption and still infer divergence times from phylogenies by modeling how the rate of molecular evolution changes throughout the tree. An important observation in this regard is that rates of molecular evolution are hereditary because they depend on other hereditary features like generation times, DNA proofreading mechanisms, habitat preference, etc. This knowledge inspired the development of macroevolutionary models that allow for gradual changes of the rate of molecular evolution through the tree.

To answer questions about the timing of events in siphonous green algal evolution, we applied a relaxed molecular clock model to our dataset and calibrated it in geological time using knowledge from the fossil record [2]. This lead us to conclude that siphonous green algae evolved in the latest Proterozoic to early Cambrian (ca. 570 MY) periods, closely associated with the advent of complex animal life and the end of the global Proterozoic glaciations popularly known as Snowball Earth (Fig. 2). We were also able to show that the origin of calcification in the extant lineages of Bryopsidales was probably in the Permian (ca. 300-250 MY), a surprising finding given that other groups of fossils assigned to the Bryopsidales that are now extinct possessed

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**Figure 3.** Inferred probabilities for the presence of EF1 $\alpha$ , EFL, or both genes in the genomes of the ancestors of green algae. Probabilities are plotted on the reference phylogeny as colors. Red indicates that EF1 $\alpha$  is present with an inferred probability of 1, green means that EFL is inferred to be present with a probability of 1, and yellow stands for a probability of 1 that both genes are present simultaneously (see box in bottom right corner). Intermediate colors indicate uncertainty. Panel A is based on the first model run while panel B is based on the second model. The estimated rates of gene gain and loss for panel A are listed in the box in the bottom left corner (modified from [3]).

calcification only since the early Paleozoic (more than 200 million years earlier). Finally, we were able to close in on the age of *Halimeda* (see below) and *Codium*, two genera commonly used as models for studies of the evolution of ecological niches.

A second problem was the observation that two very different types of elongation factor genes were present in the green algae. Elongation factor 1 $\alpha$ (EF1 $\alpha$ ) genes commonly bind transfer RNAs charged with amino acids in the cytoplasm and deliver them to the ribosomes where the amino acids are integrated in proteins. In a large selection of green algae, another gene called elongation factor-like (EFL), performs this task instead. From their deviant structure and phylogenetic analyses, we know that EF1 $\alpha$  and EFL have a different origin that dates back to the early days of eukaryote evolution. In green plant genomes, one or the other gene is present, and the distribution of the two genes among the classes of green algae is not straightforward, suggesting that the genes must have been gained and/or lost from green plant genomes multiple times.

To gain insight in the gain-loss process, infer historical gains and losses of EF1a and EFL during green plant evolution, and determine which of the two genes was present in the ancestor of the green plant lineage, we modeled the process of gain and loss of these genes along a reference phylogeny [3]. A first run of the model indicated that gene gains occur at much lower rates than gene losses. This makes perfect sense considering that gains require horizontal transfer of the gene from other eukaryotes and that losses simply occur within a genome when both redundant genes are present. When we used the model to estimate the presence of the genes in ancestral genomes, ambiguous results were obtained. Nearly equal probabilities for the presence of EFL and the presence of both EFL and EF1 $\alpha$  in the ancestral

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**Figure 4.** Inferred evolutionary history of sea surface temperature (SST) affinities in *Halimeda*. Estimated ancestral values for SST affinity are plotted along the phylogeny. Numbers at nodes indicate the inferred ancestral values. Values are also drawn as colors along a gradient to allow rapid visual assessment of evolutionary patterns. Green indicates low values, red stands for high values, and yellowish colors indicate intermediate values. The four lineages that have invaded colder water are marked with green arrows behind the taxon name. The colors of the taxon names represent the geographic origin of the species (modified from [4]).

genomes were inferred (Fig. 3A). When confronted with such ambiguity, it is common practice to use external information to constrain some of the model parameters to attempt obtaining clearer results. Using information from phylogenetic analyses of EF1 $\alpha$  and EFL in a broader eukaryotic context to constrain the model parameters, a very different result was obtained. The new run of the model yielded the opposite effect i.e. nearly equal probabilities for the presence of EF1 $\alpha$  and the presence of both genes along the backbone of the phylogeny (Fig. 3B). We were thus no closer to knowing the ancestral situation. In the case of elongation factor genes therefore, it appears that macroevolutionary modeling cannot help us discern the ancestral genome features from information on contemporary species. This is still a meaningful result because it shows that previously published scenarios, which were based on ad-hoc interpretations of the distributions of genes in contemporary species, are not necessarily supported by the data and should therefore be interpreted with caution.

A third question is how ecological niches evolve through evolutionary time. More specifically, we

were interested in learning about niche dimensions relevant to global geographical distributions, rather than local distributional issues such as microhabitat preferences. Here we focused on the green algal genus Halimeda because it was likely to serve as a good model system for studying changes in niche preferences. Even though the genus is predominantly tropical. it has several representatives living in the more temperate waters of South Africa (2 species), Southwest Australia (1 species) and the Mediterranean Sea (1 species). This observation leads to several questions. Was the niche conserved through evolutionary time or did niche changes occur often. If niche changes had occurred, did the genus originate in the tropics or in more temperate waters and from where did the niche shift occur? Assuming niche shifts had occurred, could such niche shifts be related to global climate evolution?

To answer these questions, we identified and georeferenced 1080 specimens of Halimeda from around the world, matched the specimens to the macroecological conditions they were experiencing using global sea surface temperature (SST) satellite imagery, and modeled the evolution of SST preference along a reference phylogeny [4]. Results (Fig. 4) indicated that the genus originated in tropical waters, showing marked conservatism for nutrient-depleted, tropical habitats in four of the five sections of the genus (Rhipsalis, Micronesicae, Pseudo-opuntia and Opuntia). This conservatism for warm habitats was, however, lost in section Halimeda. In section Halimeda, four lineages had adapted to colder water (green arrows). These lineages are not closest relatives and show therefore that niche shifts from warmer to colder water had occurred four times independently. All niche shifts occurred relatively recently. For H. tuna.med it occurred at some point in the last 60 million years and for the other three shifts, within the last 25 million years. This period of earth history was marked by gradual lowering of global sea surface temperatures (ca. 8°C over the past 50 Ma) and a gradual narrowing of the tropical belt, making for less tropical and more warm-temperate habitats. This apparently selected for the survival of coldadapted Halimeda species and led to four independent invasions into warm-temperate waters.

In conclusion, the modeling of macroevolutionary processes has helped us understand several aspects of green algal evolution, but has also shown that in some cases information on contemporary species is simply insufficient to provide clear insights into the past. A next step in our research will be to study how evolutionary changes of the macroecological niche have shaped latitudinal diversity patterns and biogeography, and how niche evolution influences rates of diversification (speciation – extinction). Our initial results suggest that despite seaweeds having their center of diversity in warm-temperate ecosystems, rates diversification of are higher in tropical ecosystems. From such observations and the answers to countless questions relating to macroevolution and diversity of algae in general, we may find the complicated answer to the simple question of where, when and how did it all begin?

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## Heroen Verbruggen Phycology Research Group Ghent University, Belgium E-mail: <u>heroen.verbruggen@ugent.be</u>

**Popular Student Article** 

## Documenting the association between a non-geniculate coralline red alga and its molluscan host

Rosemary Eager

## Dept. of Biodiversity & Conservation Biology University of the Western Cape

Non-geniculate (encrusting) coralline red algae are widespread in shallow water in all of the world's oceans, where they often cover close to 100 % of rocky substrates (Adey and Macintyre 1973, Steneck 1986). While many molluscs include coralline algae in their diets (Steneck and Watling 1982, Steneck 1986, Maneveldt *et al.* 2006, Maneveldt and Keats 2008), some are known to form only passive, non-trophic associations with them without necessarily grazing them (Steneck and Paine 1986, Johnson *et al.* 1991, Daume *et al.* 1999). A facultative association between the encrusting coralline alga *Spongites discoideus* and

its winkle host Oxvstele had been sinensis observed at several sites within western False Bay. South Africa (Figure 1). Nearly all adult O. sinensis (98.6 ± 1.10 %) encountered had been observed to bear the coralline on their shells. This implied a strong positive relationship between the winkle and the coralline. The coralline was not found to occur on the morphologically similar winkle O. tigrina, despite the variable overlap in niches of the two winkle species.

To better understand the association, various natural data (e.g. invertebrate densities and

algal % cover, algal competitive biomass. interactions, coralline attachment strengths, % burrowing of the coralline, etc) were collected at Kalk Bay (34° 08'S, 18° 27'E) from all the habitats (mid-Eulittoral flats, mid-Eulittoral crevices, intertidal rockpools, shallow subtidal zone) occupied by the organisms. The results firstly show that S. discoideus was restricted to intertidal rockpools  $(34.8 \pm 7.14 \%)$  and the shallow subtidal zone  $(1.4 \pm 0.33 \%)$  where O. sinensis (rockpools  $-24.0 \pm 3.94$  number m<sup>-2</sup>, 12.2  $\pm$  2.84 g m<sup>-2</sup>; shallow subtidal - 34.4  $\pm$  2.25 number  $m^{-2}$ , 313.7 ± 20.49 g m<sup>-2</sup>) was the most abundant winkle. Despite the high overgrowth competitive ranking of S. discoideus, the coralline is extremely low in abundance in the shallow subtidal zone. Species that were typically at or near the bottom of the hierarchy in terms of overgrowth competition (interference) were the most abundant suggesting that exploitation competition was important in preventing competitive exclusion. The attachment strength of S. discoideus on boulders (8.4  $\pm$  0.77 kg) was greater than that on winkle shells  $(2.2 \pm 0.58 \text{ kg})$ 

> (p = 0.004). An inverse relationship with percentage burrowing was evident with the percentage burrowing of the coralline on the winkle shells (44 ± 3.32 %) being greater than that on boulders (25 ± 3.94 %) (p < 0.001).

> Preliminary data suggested that epilithic and epizoic forms of the coralline showed variably different stages in the life cycle of the coralline alga. To determine whether а difference in reproductive stages existed, frequency а measure was taken of the various reproductive stages occurring both epizoically and



**Figure 1.** The non-geniculate coralline red alga *Spongites discoideus* occurring epilithically (top) on an intertidal pebble (the typical habitat) and epizoically (bottom) on the shell of the winkle *Oxystele sinensis*.



epilithically (intertidally and subtidally); these data obtained were directly from prepared slides used to identify the coralline. Results showed that sporangial  $(54.4 \pm 16.98)$ %) and gametangial (45.6 16.98 %) plants ± contributed more or less equally to the alternating life cycle stages encountered epilithically in intertidal rockpools (p =0.821) (Figure 2). Α similar trend was observed for the shallow subtidal zone (sporangial  $-55.5 \pm$ 7.03 %; gametangial – 44.5  $\pm$  7.03 %; p = 0.494). In both of these habitats though, sporangial plants substantially occurred more frequently than either male or female plants. Furthermore, in both these habitats the ratios of male to female plants were (5.3:1), identical but reversed with more male plants occurring epilithically in intertidal rockpools and more female plants occurring epilithically in the shallow subtidal zone. In contrast intertidal rockpools, to occurring plants showed epizoically gametophyte (95.5  $\pm$  2.21 %) dominance over sporophytes  $(4.5 \pm 2.21 \%)$ (p = 0.003), with male plants occurring in far greater numbers (p = 0.008) (Figure 2).

To further investigate the strength of the association and the relative advantages



**Figure 2.** Frequency of gametangial versus sporangial material occurring epilithically in intertidal rockpools (top), occurring epilithically in the shallow subtidal zone (middle), and occurring epizoically on winkle shells in the shallow subtidal zone (the ratio in the gametangial bar represents the proportion of male to female plants encountered). Bars with the same letters are not statistically different at p > 0.05.



**Figure 3.** Stainless steel cages were mounted onto concrete slabs wherein the experiment was housed. Control winkles were caged in along with the mounted treatments.

of the association to both organisms, several manipulation experiments were set up. A cage experiment set up in the shallow subtidal zone (Figure 3) showed that the coralline survived equally well without the winkle and did therefore not require the winkle or its empty shell for survival. А second controlled laboratory aquarium experiment was designed under both fluorescent (rich in blue light) and incandescent light (rich in red light) to ascertain whether the coralline had preference for а 0 sinensis over the similar O. tigrina (Figure 4). This experiment was inconclusive as no recruitment was obtained under either of the light regimes. А third laboratory experiment designed to was determine whether the extra coralline weight had any possible advantage to the winkle, particularly against predation from the rock lobster Jasus lalandii. Results suggested that there were no apparent advantages to the winkle bearing the extra coralline load as adult O. sinensis bearing the coralline alga (3.7  $\pm$ 2.2 winkles  $24hr^{-1}$ ) were equally prone to predation than those lacking the coralline (2.3 ± 1.9  $24hr^{-1}$ ) (p winkles = 0.184). Observations suggested instead that the



convoluted nature of the coralline may indeed have promoted predation.

We ultimately deduced that the high occurrence of the coralline on the shells of O. sinensis was probably due to the substantial overlap in the niches of the two organisms. This conclusion was supported by the high densities of juvenile O. sinensis combined with the high percent cover abundance of the coralline intertidal rockpools. in sexual Understanding reproduction in coralline

algae (Figure 5) as well as the life cycle of the winkle, ultimately provided insight into the postulated life cycle of this coralline-winkle association (Figure 6). The interaction between *S. discoideus* and *O. sinensis* shows characteristics of a non-trophic, facultative association. The coralline benefits from the association by having an increased rate of fertilization, dispersal and recruitment, and possible refuge from interspecific competition. The benefit(s) to the winkle, if any, is unclear and all in all, the coralline alga appears advantaged at the

expense of the winkle. While we may never fully understand the association between this alga and its winkle host, this study has provided valuable insight into the ecology of both organisms and their association.

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**Figure 4.** Under both fluorescent and incandescent light, half the experimental aquaria were covered with a mesh frame that was larger than the aquarium, creating an artificial intertidal habitat and half the experimental aquaria (as seen in this image) bore a floating mesh frame, simulating a constant subtidal environment (bottom).

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Figure 6. Proposed life cycle of the association between the winkle O. sinensis and the coralline alga S. discoideus.

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## **PSSA Conference Countdown**

PSSA 2010 is being hosted by the Nelson Mandela Metropolitan University and is planned for their satellite campus in George, Western Cape Province, South Africa. By now those of you interested, should already have registered. If not, please find attached a copy of the registration form (see Appendix III).

## **Calendar of Events**

## **Upcoming Conferences**

- VI Southern Connection Congress, Bariloche, Argentina, 15-19 February 2010. <u>http://southernconnection2010.crub.uncoma.ed</u> <u>u.ar/php/index.php</u>
- 2. XX International Seaweed Symposium, Ensenada, Baja California, Mexico, 22-26 February 2010. <u>http://www.xxseaweedsymposium.org/</u>
- 8<sup>th</sup> International Conference on Recirculating Aquaculture, Roanoke, VA, USA, 20-22 August 2010. <u>http://www.recircaqua.com/abstract.html</u>



## GBIF Summary Paper: The GBIF Integrated Publishing Toolkit (IPT)

## DESCRIPTION

The GBIF Integrated Publishing Toolkit (IPT) is a software platform developed by the Global Biodiversity Information Facility (http://www.gbif.org/) to facilitate efficient biodiversity data publishing onto the Internet. This Java-based tool manages three types of data: taxon primary occurrence data, taxonomic checklists and resource metadata. Through the IPT, users will be able to publish data residing in local databases, upload existing files in comma-separated and tab-delimited formats, and access central services to make use of standardised controlled vocabularies and data quality reporting services. Extensions such as common names, species descriptive data or multiple identifications may be defined and shared amongst the IPT user community. The IPT also acts as a visualisation tool, as it includes a web application allowing for browsing and searching of published data, along with basic mapping services.



One of the main technical challenges of the GBIF decentralised architecture is to remove bottlenecks within data flow. The IPT offers interfaces to transfer complete resource archives efficiently in order to reduce the latency between data publication and discoverability through the GBIF indexes. Currently, much of the quality analysis is performed on the data after it is published onto the network. The IPT aims to provide data holders with the ability to easily run a growing number of quality checks against their data, before any data aggregators index the source. By decentralising the quality routines, it is expected that the data will become fit for a wider number of uses more quickly than possible with central quality analyses.

With an embedded database and web application, the IPT is an open platform to build upon, offering additional services and benefits both to the biodiversity data holders and users.

## **SPECIFICATIONS**

## GENERAL

- Open source (Apache 2.0 license) Java based customisable, multilingual web application.
- Connects and serves 3 types of data: taxon primary occurrence data, taxon checklists and general resource metadata. No manual data entry accepted (except for metadata).
- Manages multiple data sources (with individual metadata descriptions).
- Role-based user management, allowing for multiple data curators to share a common instance.
- Web interface with data browsing, full text search and individual pages for the three types of data, displaying features available for each type (i.e. density maps, charts, metadata).
- Several upload options: Relational Database Management System (RDBMS), tab files.
- Manages Universally Unique IDentifiers (UUID): recycles existing IDs or provides new ones, as appropriate.
- Manages technical metadata about the installation.
- Easy setup of Google Analytics<sup>™</sup> for usage statistics.

## TAXON PRIMARY OCCURRENCE DATA MANAGEMENT

- Data model with a core table using DarwinCore (DwC) terms and extension tables in a "star" schema.
- Data validation routines included via local files or central GBIF services for names, countries, basisof-record, etc.

• Interfaces: URL based resolution, Open Geospatial Consortium (OGC) Web Feature Service (WFS) and Web Map Service (WMS), TAPIR *intermediate* search and inventory, simple REST web services and complete resource available for download as a DwC based archive file.

## TAXONOMIC CHECKLIST

- Data model with a core table using DarwinCore (DwC) terms with extension tables in a "star" schema.
- Structure allows for modelling taxonomic hierarchy, synonymy and nomenclature notes, support for multi-lingual vernacular names and URLs associated with external sources for full taxonomic information.
- Interfaces: single TCS-RDF document, URL-based taxon resolution, complete resource available for download as a DwC based archive file.

### **RESOURCE METADATA**

- Manages metadata information for every resource connected to the IPT (taxon primary occurrence datasets and names checklists) and any other external resource defined by the user but not published through the IPT.
- Data model based on a profile of the Ecological Metadata Language (EML) allowing for definition of taxonomic, geospatial and temporal scope, along with rights and citation, contact information and keywords.
- Interfaces: EML data file. RSS feed for most recently changed/created resources.

## REQUIREMENTS

Pre-requisites for installing the software:

- Web server with a Servlet container (such as Tomcat or Jetty) connected to the Internet.
- Java version 5.

## SCHEDULE

- GBIF IPT public beta version release: 30 January 2009.
- GBIF IPT version 1.0 release: 31st March 2009.
- Software evaluation and bug-fixing May-October 2009
- New requirements gathering May-October 2009
- GBIF IPT version 1.1 release: October 2009.
- Review of new requirements October-November 2009
- GBIF IPT version 2.0 release: December 2009.

## RESOURCES

- 1. http://code.google.com/p/gbif-providertoolkit/ Project Home Site: documentation, downloads, source code, bug reporting, etc.
- http://www.gbif.org/ GBIF communications portal.
- 3. http://www2.gbif.org/WP2009-10.pdf GBIF Work Programme 2009-2010

## **GBIF CONTACTS**

Head of Informatics SAMY GAIJI sgaiji@gbif.org

Senior Developer MARKUS DÖRING mdoering@gbif.org Systems Architect TIM ROBERTSON trobertson@gbif.org

Training Officer ALBERTO GONZÁLEZ-TALAVÁN atalavan@gbif.org



## GBIF Summary Paper: The GBIF Harvesting and Indexing Toolkit (HIT)

## DESCRIPTION

The GBIF Harvesting and Indexing Toolkit (HIT) is a software platform developed by the Global Biodiversity Information Facility (http://www.gbif.org/) to manage biodiversity data harvesting and quickly build indexes of the harvested data.

This Java-based tool can harvest data from data publishers publishing their data through three protocols: DiGIR (<u>http://digir.net/</u>), BioCASe (<u>http://www.biocase.org/products/protocols/</u>), and TAPIR (<u>http://www.tdwg.org/activities/tapir/</u>). It can also harvest data directly from a single dump, created in accordance with the new Darwin Core Archive

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standard (<u>http://rs.tdwg.org/dwc/terms/guides/text/index.htm</u>). Built in such a way that it is fully extensible, the HIT allows support for additional protocols to be easily incorporated at a later time.

Because the various protocols differ from one another considerably, harvesting data from a heterogeneous set of data publishers can be quite complicated. The HIT's interface is effective at hiding these differences from the user, so that the same set of operations is presented to the user regardless of which underlying protocol is being used. By grouping data publishers together in one place, regardless of their protocol, the HIT provides a convenient mechanism whereby they can all be managed. Nodes needing/wanting to mobilise data from several data publishers, for example, will find this increasingly beneficial as their list of publishers continues to grow.

Another challenge encountered when harvesting is that it is extremely time-intensive for large datasets and that it requires uninterrupted communication with the provider. The HIT bypasses these problems by allowing harvesting operations to be automatically scheduled, and allowing them to restart from the point where they fail instead of beginning anew. Moreover, in most cases the HIT is capable of identifying the reason why an operation fails, responding with this information to the user. Whether it is a connectivity problem, or an issue with the way that the provider has structured their data, the user can quickly determine which course of action must be taken to enable harvesting to continue.

Once harvesting has been completed, the HIT displays relevant statistics such as the number of records successfully harvested and the number dropped. The user can then compare these numbers with the total number of records that were expected in order to determine which data publishers/datasets require more attention and which ones can continue to be harvested in an automated way. Ultimately the HIT aims to allow for a situation where all harvesting becomes a fully automated procedure, saving a great deal of time.

One of the main technical challenges of the GBIF decentralised architecture is to allow Nodes to aggregate data themselves which can then be made available back to GBIF. The HIT surmounts this challenge by allowing the harvested data to be synchronised with a relational database, and for an index of the data to be built. Once this has been done, it would be possible to build a regional or thematic portal on top of the database, providing the community with an additional means of accessing the data.

Entirely open source and extensible, the HIT is intended to grow as new protocols emerge. It is expected that the benefits to both the biodiversity data holders and users are significant, making the process of data mobilisation an easier one that people are keener to engage in.

## **SPECIFICATIONS**

GENERAL

- Open source (Apache 2.0 license) Java based, customisable multilingual web application
- Synchronisation with the GBIF UDDI registry
- Harvesting of 3 types of protocols: DiGIR, BioCASe, and TAPIR; extensible to others.
- Harvesting from the Darwin Core Archive format
- Internationalised output log messaging.
- Role-based user management, allowing for multiple data harvesters to share a common instance.
- An interface displaying the complete list of data publishers and their datasets, filterable by provider name, dataset name, and country name, displaying statistics, etc.
- An interface displaying the complete list of operations currently scheduled.
- An interface displaying the output log messages, filterable by provider or dataset.
- Allows the in-browser viewing of each individual xml request or response sent as part of the various operations.
- Automatic scheduling of operations.
- Synchronisation with one or more external databases.
- Generation of an index on the harvested data

## REQUIREMENTS

Pre-requisites for installing the software:

- Web server with a Servlet container (such as Tomcat or Jetty) connected to the Internet.
- Java version 5.

## SCHEDULE

- GBIF HIT internal alpha version release: 30 April 2009.
- GBIF HIT semi-public alpha release 31 May 2009.
- GBIF HIT public 1.0 beta release: 15 August 2009.
- Software evaluation and bug-fixing September-December 2009
- GBIF HIT version 1.1 release: December, 2009.

## RESOURCES

- 1. http://code.google.com/p/gbif-indexingtoolkit/ Project Home Site: documentation, downloads, source code, bug reporting, etc.
- 2. http://www.gbif.org/ GBIF communications portal.
- http://www2.gbif.org/WP2009-10.pdf
   GBIF Work Programme 2009-2010

## **GBIF CONTACTS**

Head of Informatics SAMY GAIJI sgaiji@gbif.org

**Developer** Kyle Braak kbraak@gbif.org Systems Architect TIM ROBERTSON trobertson@gbif.org

Training Officer ALBERTO GONZÁLEZ-TALAVÁN atalavan@gbif.org



25<sup>™</sup> congress of the Phycological Society of Southern Africa hosted by the Nelson Mandela Metropolitan University



## 12-15 January 2010 Saasveld Campus, George

## **CONFERENCE VENUE**

The Saasveld campus of the Nelson Mandela Metropolitan University lies amidst the tranquil indigenous forests of the Southern Cape just outside George. This campus offers all the modern facilities of a first choice technological university such as well equipped classrooms, laboratories, library, IT services, conference facilities, residences and sport facilities. The Campus consists of two schools namely the School of Natural Resource Management and the School of Business and Social Sciences. The spectacular landward and seaward vistas from Saasveld provide an inspiring backdrop for our 25<sup>th</sup> congress.

## PROGRAMME

Tuesday 12 January

Wednesday 13 January Thursday 14 January Friday 15 January Saturday 16 January Algal Biofuels workshop Arrival of delegates, registration, ice-breaker Full day conference Field trips, workshops Full day conference, Conference dinner and prize giving Delegates depart

## PRESENTATIONS

**Oral presentations** are 20 minutes (15 minutes presentation and 5 minutes question time). Data projectors are available for oral presentations. Should you require any other media for your presentation please inform the conference organisers at the time of submission of your abstract. Presentations on disk/flash must be submitted to the chairperson of the session well before the start of that session.

**Poster presentations** should be placed in the designated areas during registration time. They should remain on display for the duration of the conference. Poster dimensions should all be A0 size (120 cm tall x 84 cm wide). Please include a photograph of the presenting author. Ensure that poster text can be comfortably read from a distance of 2 m. Material for attaching posters will be provided.

## **DEADLINES**

## Return completed Registration Forms by 16 November 2009.

Completed registration forms should preferably be emailed (but may be faxed) to the conference administrator.

## Payment by 7 December 2009.

Late registration will be subject to a surcharge of R250.00.

## Abstracts due 4 January 2010.

The abstracts should be sent via e-mail as an attachment or in the body of the message, or faxed to the conference administrator. Please do not submit abstracts later than this userfriendly date as we will not have time to incorporate them into the programme.

## **REGISTRATION**

includes annual membership fees, the meet & greet function, the conference dinner, another dinner, lunches, tea & coffee, t-shirt, the field trip and registration.
excludes dinner on the free evening, accompanying persons.

## ACCOMMODATION

Accommodation on Saasveld Campus is available at R180 per person per night bed and breakfast. Each house has two single bedrooms and one sharing room. Please indicate if you wish to share with someone. The price includes bedding but NOT towels.

Off-campus accommodation is for your own arrangement. Links to some of the offcampus accommodation offered around George are as follows:

<u>General</u>: http://www.gardenrouteaccom.co.za/property.php?mode=accom\_home http://www.safarinow.com/destinations/george/hub.aspx

<u>Rooms for Africa</u>: http://www.roomsforafrica.com/dest/south-africa/westerncape/george.jsp?&page=2

<u>Acorn Guest House</u>: http://www.acornguesthouse.co.za/index.htm

<u>Pine Lodge Resort:</u> http://www.pinelodgegeorge.co.za

<u>Malvern Manor Guest House</u>: http://www.malvernmanor.co.za

## FIELD TRIP

The field trip will be an excursion to the rocky shores and sandy beaches of the Goukamma Nature Reserve, making use of the low tide in the morning. After lunch in the reserve, we will visit Lake Pleasant (Groenvlei) before returning to Saasveld.

## **WORKSHOPS**

The South African Algal Biofuels workshop will be held on 12 January.

If you are interested in, or wish to present another workshop, please indicate this with your registration response:

## **ACCOMPANYING PERSONS**

Please inform the Conference Secretariat if you will be bringing an accompanying person together with some indication as to which functions you wish to include for this person.

## **CONFERENCE ADMINISTRATOR**

Marilyn PhilanderE-mail:Marilyn.Philander@nmmu.ac.zaTel:041-5042397Fax:041-5832317Snail mail:Department of Botany, P O Box 77000, Nelson Mandela Metropolitan University, 6032

## <u>FEES</u>

Please mark the block for your choices:

Name:			
Address:			
Telephone:			
Email:			Amount due
Registration:	Ordinary Member	R1450.00	
	Life Member	R1400.00	
	Student Member	R1200.00	
	Late (add additional)	R250.00	
	Daily rate (registration pack & t-shirt included)	R500.00	
	Algal Biofuels workshop only (12 January)		
	Another day ( January)		
Campus	@ R180/night	nights	
accommodation	Sharing with:		
Tshirt size		S/M/L/XL/XXL	
Request information for accompanying person			Yes/No
Request transport from airport			Yes/No
Special dietary requirements		Vegetarian	
		Halaal	
		Other (spe	cify)
Banking details: AB	3SA Bank		

Account Holder's Name: Nelson Mandela Metropolitan University Branch: Port Elizabeth Account #: 1640000046 For the Reference please use: YOURSURNAME N033

## **ABSTRACTS**

Please submit your abstract in the box below in the format shown. Please underline the presenting author. (The box will be used in the final version)

## The title of the paper, which should be short and informative, and printed in Times New Roman, bold, 12 point, centred

First O. Author<sup>1</sup>, Second T.W.O. Author<sup>2</sup>, Third T. Author<sup>1,2</sup>

<sup>1</sup>The address of the first affiliation author(s); email address of presenting author <sup>2</sup>The addresses of other authors

The text of the abstract should be in Times New Roman, 12 point, single spaced, justified, single paragraph. Word limit is 300 words.