
Plenary lecture

Role of high technology and citizen science in conservation biology of tropical ecosystems: The rocky path from Paine and Pimm to the terragreen Network (TGN)

Professor Monte Cassim

Professor (Health, Environment and Life Science), Ritsumeikan Center for Sustainability Science, Japan

Background: It is easy to fall into a utilitarian trap when science has to be mobilized for development. The agency for development, irrespective whether it is public or private, becomes the client of the scientist, whose independence can be compromised by virtue of this relationship. How can we escape from this trap as scientists and yet serve our country and its communities? Considering how expensive research has become in recent times in the natural, engineering and medical sciences, it is not easy to dismiss these external sources of research sponsorship either. I have found resolving this dilemma to be the most challenging of tasks in creating conducive research environments, where the joy of discovery can be coupled with the gratification of what it delivers to citizens. There is also another dilemma. Why have the natural sciences, especially the fundamental sciences, become so removed from the citizens at large? One does not have to be a writer to enjoy a book. Nor does one have to be a composer or accomplished pianist to appreciate good music. Why are the arts so intertwined with our lives while the sciences tend to stand aloof? This is the background to some of the thoughts I would like share with you today, viewed through the lens of a particular research endeavour in the field of conservation biology.

Beyond Paine and Pimm: The first part of this presentation relates to how a quarter century of field science led to a “eureka moment”. In the passage to discovery in the field of science we are trained to review the works of our peers and mentors. My work led me to two giants in the field of conservation biology. One of them was Robert Paine, who empirically indicated the significance of “keystone species” in conserving ecological habitats. Paine showed that removal of the keystone species caused ecosystem collapse, leading to mass mortality and even extinction of species in that particular habitat. The other was Stuart Pimm, whose work on food webs was also

inspirational. How did these two scientists influence my work? I asked myself if it would be possible to regenerate biodiversity and re-create an ecosystem by re-introducing keystone species into damaged habitats. In other words, could Paine's finding be stood on its head to achieve the reverse phenomenon? This led to many questions. Many different types of keystone species had been identified. Some created optimal physical environments for many other species to reproduce. Others disposed of detritus. Yet others provided food for many. I chose to focus on this last group. Influenced by Pimm's work, I felt that if biodiversity was to be restored, the starting point would be re-establishing the food chains and webs.

Field Science: This led to empirical work in the Malesian rainforests of Sabah in North Borneo. It appeared that the giant fig, a daily provider of sustenance to a host of birds and animals, including the endangered primate, the Orang Utan, was a good candidate for one of the keystone species. The second keystone species chosen was the giant dipterocarp. With its irregular mass synchronized flowering and subsequent seeding, which could occur at any time between two to ten years or so, the dipterocarpaceae occasionally provided an abundance of food, often helping to supplement depleting species counts due to a range of environmental hardships, such as drought. The giant fig, incidentally, has a symbiotic relationship in its early life with the dipterocarp. It was walking in the rainforest, observing different stages of this relationship until the fig completely subsumes its host when the "eureka moment" came.

The "Eureka Moment": The Danum Valley Field Centre, the Sabah Foundation's rainforest research organization located in the heart of 40,000 hectares of primary forest within the Foundation-managed 1 million hectares of timber lands, conducted a series of field experiments in resurrecting biodiversity in rainforests. One of the challenges was the high mortality rate of dipterocarp seeds in damaged habitats. Another was top soil runoff and the drying of soils. Several such hurdles had to be overcome, but progress was made and good practice guidelines for sustainable forest management evolved out of this. The forest workers who managed the Foundation's timber lands were mobilized to collect dipterocarp seeds and to care for them in nurseries until they were about 60 cm high, after which they were planted in the area to be regenerated. With time, increasing insect counts and diversity indicated that nature had taken over and biodiversity regeneration was under way. The steps of the process were the enlightened outcome of the "eureka moment", viz: First, find at least two keystone species which could contribute to the restoration of food webs, then nurture them in a certain

proximity to each other and finally, be patient...until nature takes over and biodiversity begins to reappear. There was only one snag. Insect count based calculations indicated that it would take 40-60 years for the original biodiversity to be restored. I was 56 years old at the time. It was very unlikely that I would see the results of this work in my lifetime. But scientists are strange animals. There is an irrepressible desire to see the outcomes of work one is engaged in. The answer was to see if the restoration principles would hold in other habitats.

From Rainforest to Coral Reefs: I stumbled upon Don Baker, who was restoring damaged coral reefs in the Tungku Abdul Rahman National (Marine) Park just offshore from Kota Kinabalu, the capital of the Malaysian State of Sabah. Working with a wealthy hotelier who had a vested interest in transforming the coral reef around his establishment he financed Baker's dream. Baker's findings were that if the giant clam was introduced strategically into damaged reefs, the zooxanthellae that grow in the conducive environment provided by this symbiotic host flourish. As their numbers increase they are released from the giant clam and if they land where coral spores exist, a new symbiotic relationship emerges. The zooxanthellae are micro-algae which can convert sunlight into energy. They provide the coral with nutrients and their carbon capture mechanism contributes to the calcium carbonate exoskeletons of corals, the building blocks of reefs. As the coral reefs flourish, nature takes over and marine biodiversity is restored. This time, however, the process occurs in 4-6 years....the scientist's prayers were answered!

From Setbacks to Saviour: Armed with nearly a decade of data, I was ready to do the analysis when disaster struck. A thief entered my flat, stole two computers (one of which had data backed up), my video and still cameras and the tapes and negatives in the camera box. Worst of all, at the base of the camera box lay the decade of handwritten data and field notes. While I still remembered much of it, I decided to impart as much of it as I could to my students. A research group called ATE (Action for Tropical Ecosystems) was formed in my lab (the Discovery Research Laboratory, or DRL), led by an extremely able doctoral student. She went on to perform brilliantly in the professional world, first working for UN FAO and later in the OECD's Environment Unit, writing the first chapter of the environmental outlook until 2025, when disaster struck again. At the age of 32, this promising early career researcher contracted cancer and passed away. This led to a Kafkaesque situation where even I began to think that this biodiversity restoration work was full of ill omens. This was amplified

because of an incident that had led me to suspend work in the rainforests of Sri Lanka in the late 1990s. The suspicion that a bioprospecting company had infiltrated one of my research team members led me to suspend operations in Sri Lanka for ethical reasons. This was what took me to Malaysia, where I was able to start anew with better checks on such incursions. I wished to take this work to other localities and had a very animated exchange with Professor Wangari Maathai at an international conference in Abu Dhabi. We decided that her “Billion Tree” campaign could use the principles of restoration unearthed in Malaysia. However, before these thoughts could proceed much further, the good lady passed away. In a moment of weakness, I aired my tale of woe to a fresh post-doctoral fellow, Dr. Park Jung-Hwan, who had joined my lab about three years ago. In any event, I concluded, what impact would a few doctoral research fellows trained in my lab have in the face of the enormity of the task of inventorizing biodiversity or in restoring it where damaged? He said “Give me a week to think about it”. Out of this modest moratorium he asked for, the TerraGreen Network (TGN) Project, subject of the second part in this presentation, was born.

Introducing TGN: This project attempts to create a plant census by integrating high technology with what is now beginning to be known as “citizen science”. As primary producers, vascular plants are stalwarts in capturing, storing and disseminating energy for sustaining terrestrial life on earth. A global inventory would benefit conservation biologists tremendously, particularly in tropical ecological habitats where levels of biodiversity are highest, but the million dollar question is “how do we achieve this?” There are differing views on how diverse tropical ecosystems are, with figures for biodiversity assessment ranging from 10 million to 30 million species. If it is the former we know a little over 20 percent of them and if the latter around 7 per cent. The dilemma is that in view of the magnitude of the task, the number of professionally trained scientists is way too small. What the TGN project does is to show a modality which: (1) Mobilizes advanced technologies; (2) Has platforms and modalities for scientists to collaborate with citizens; (3) Creates an open access bio-inventory archive; and (4) Includes an educational component to mobilize and nurture “citizen scientists”. A simplified image of the TGN components is indicated in figure 1 below:

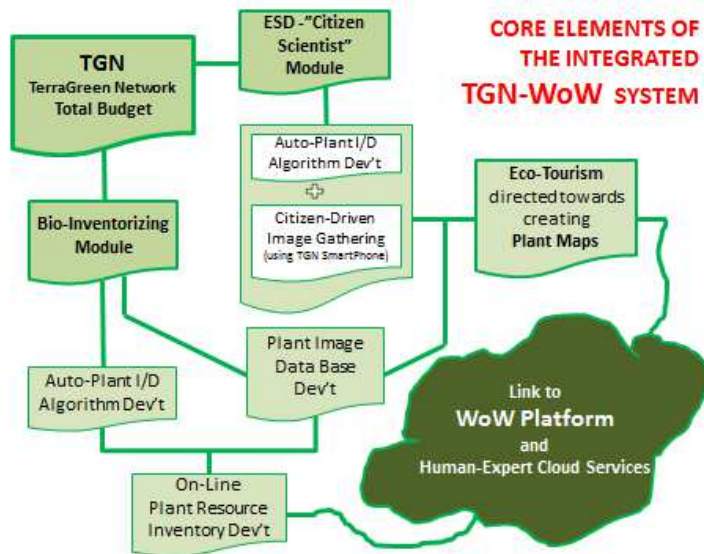


Figure 1: Core Elements of the TGN-WoW System
 (Source: Author, 2013)

The Primary Tasks: There are three fundamental tasks in establishing TGN, viz: (1) Image gathering for plant identification; (2) Algorithm development for auto-identification of plant image; and (3) Online plant resource inventory development. The sub-tasks among these three are grouped into the Bio-Inventorizing Module, which requires formal scientific expertise supported by “citizen scientist” image gathering from the Education for Sustainable Development (ESD) Module, which is also where the “citizen scientist” collaborates with scientists in creating pedagogic materials. The tasks and their outcomes are linked to a “Human Expert-Cloud” (HEC) service, based on an internet platform called WoW (Web of Wisdom), which provides: (1) Imaging protocols and help lines for both scientist and “citizen scientist”; (2) Domain expertise support in conservation biology and relevant ICT aspects; and (3) A cyber archive of educational materials regarding plant characteristics and plant locations coupled with an auto-plant identification function. Work on the Bio-Inventorizing Module, leading up to auto-identification algorithm development commenced in 2011 as a Japan-Korea collaborative in temperate ecosystems. The next step is to commence pilot experiments for creating plant inventories in tropical ecosystems where the biodiversity is much richer and the need for “citizen scientist” contributions more critical. Malaysia, possibly in the North

Bornean State of Sabah, and Sri Lanka, in and around its “Man and Biosphere” reserves, have been targeted for the next stage of the project.

Capturing Sri Lanka’s Biodiversity: Considering that Sri Lanka has one of the world’s richest biodiversity heritages but is also a biodiversity hotspot with endangered habitats, the TGN plant census will lay the foundations for conserving Sri Lanka’s forest biodiversity by training and mobilizing the “citizen scientist” to work in collaboration with scientific experts to create a plant census, where the forest habitat is seen as a living learning laboratory. Modalities employed in the pilot plant census building in Japan and Korea can be tried out in the buffer zone of the Sinharaja MAB reserve and the Knuckles Wilderness Area MAB reserve. It can be used for developing environmental educational materials around conservation zones as part of UNESCO’s Education for Sustainable Development (ESD) initiative. The use of “pervasive ubiquitous computing (PUC)” devices such as smartphones, “smart papers” and digital pens will result in the development of “smart” pedagogic applications, which can be widely applied in other learning environments. This can also help in the promotion of eco-tourism and getting user feedback from the tourist, trekkers and travelers.

In Conclusion: The ultimate aim of this presentation is to inspire early career researchers and those interested in conservation biology, be they scientific experts or ordinary citizens. A large number of people can, and indeed must contribute to biodiversity conservation because our genetic heritage is at risk in this “Anthropocene Age”, where Homo Sapiens appears to be a super dominant species. It is wise to remember what struck me as I walked through the Malesian and Amazonian rainforests. The species that outlasts all is not the strongest or the biggest...it is the most adaptable! Human beings must become wiser in the ways of the forests and coral reefs, which have been around for far longer on earth. I look forward to furthering the TGN project in Sri Lanka and would greatly welcome your support. I wish to thank the organizers of RISTCON 2015 for giving me the opportunity to share my thoughts with you. Young researchers, you can be sure that in a field like conservation biology there will be ups and downs in your professional career paths. Draw strength from the citizenry, like the arts have done from time immemorial, and remember Winston Churchill’s words in the darkest hours of World War II for the Allied Forces: “Success is not final, failure is not fatal; it is the courage to carry on that counts!”

Plenary lecture

The genetic control of rice yield using novel genes

Prof. Naoki Hirotsu

Faculty of Life Sciences, Toyo University, Japan

I appreciate organizers to giving me a great opportunity to have a chance to speak here. Today the talk will be about the genetic control of rice yield using novel genes.

As you all know, the population growing exponentially. To feed the ten-billion people in 2050, we should keep increasing cereals production constantly. Cereals production consists of “cultivated area” and “yield per area”. So, we should increase these parameters. Rice yield per area is determined by two component, Source and Sink size. Source can be consisted of “photosynthetic rate in leaves” and “carbohydrate translocation from leaf blade to leaf sheath or to sink”. Sink can be determined by the product of “tiller number”, “grain number per panicle” and “grain weight”. So, the yield is a product of total sink size and source ability. To increase rice yield, we should enhance both these components. If sink size was excessive, the source would limit the yield. If source was excessive, the sink would limit the yield. The balance of these two parameters is important to increasing rice yield.

In rice, the numbers of genes have been cloned by QTLs analysis. For sink development, some genes for regulating grain numbers and many genes for grain size have been cloned. While for source function, the reports was limited. Recently, Dr. Takai has reported that the amino acid substitutions in *NAL1* resulted in the increases in photosynthetic rate per leaf area (Takai et al 2013 Sci. Report 3, 2149). To increase rice yield, it is important to search and collect positive alleles to increase both source and sink.

In 2003, Dr. Ishimaru found QTLs for grain weight in chromosome no 6th (Ishimaru 2003 Plant Physiol. 133, 1083-1090). This QTL increases grain weight without decreasing the ratio of filled grain, and resulted in increasing grain yield. We first positional cloned the responsible gene for *qTGW6*. We

carried out high-resolution mapping with homozygous recombinant plants and delimited the *TGW6*-containing region to 4.9 kb between two markers. In this genomic region, there was only one ORF. This gene has only one exon.

The “Kasalath” allele contained six nucleotide substitutions and a 1-bp deletion at nucleotide 313 compared to the “Nipponbare” allele. The 1-bp deletion caused a frameshift and prevented the production of the mature protein. So, this 1-bp deletion might give functional loss of the Nipponbare-type *TGW6* protein. To show the complementation test, we transformed a RNAi construct for *TGW6* into “Nipponbare”. Grain length in the transformants was significantly increased. This increase in grain length was negatively correlated with *TGW6* gene expression. Thus, we could confirm that the loss of *TGW6* gives grain length up.

According to BLAST search, *TGW6* was similar to strictosidine synthase. It is a Key enzyme alkaloid biocynthesis. However, in rice grain, there would be no accumulation such alkaloids. Thus, *TGW6* should have another unknown functions. *TGW6* have a similarity with strictosidine synthase (STR1) and DFPase, these are structurally known proteins. These proteins have a large cavity, substrate binding sites. Then, we modeled *TGW6* protein structure from these known structures. This is a modeled *TGW6* structure, the calcium ion-binding residues of DFPase were conserved in *TGW6*. The spatial arrangement of His and Tyr on the surface of the large cavity of *TGW6* resembled the active site of the hydrolase. These results suggest that *TGW6* might have hydrolyzing activity.

Then, what is the substrate for *TGW6*? This is the structure of strictosidine. *TGW6* might hydrolyze the unknown substrate which size is similar to strictosidine molecules. Strictosidine consist of Tryptamine and Secologanin. Tryptamine partly have Indole-rings and Secologanin have glucose. We simulated some substrate docking with modeled *TGW6* structure, and tested whether it matches to the cavity or not. Then, one compound had a fine fitting with the cavity in *TGW6*. Blue compound is IAA-glucose, this is one of several Indole Acetic Acid (IAA) conjugate; it consists of Indole-rings and glucose. To confirm the hydrolyzing activity of IAA-glucose, we tested using synthesized IAA-glucose and recombinant protein of *TGW6*. “Nipponbare” type *TGW6* had hydrolyzing activities of IAA-glucose, while “Kasalath” type *TGW6* had no activity. So, we could confirm that *TGW6* has a hydrolyzing activity of IAA-glucose. In NIL(*TGW6*), the developing endosperm at 3 days after fertilization had lower contents of free IAA. These

results suggest that “Kasalath” type *TGW6* could not produce free IAA from IAA conjugate.

To show when *TGW6* gene expressed, we analyzed expression level of *TGW6* gene. *TGW6* expressed mainly in developing ovary, its level was peaked at 2 days after fertilization. By *in situ* hybridization experiment, this is longitudinal section of ovary, and *TGW6* transcript accumulated around the ovary. This pericarp is the site for cell division. In NIL(*TGW6*), carrying “Kasalath” chromosome region around *TGW6*, showed significant increase in grain length. Compared to “Nipponbare”, NIL(*TGW6*) had longer endosperm and greater dry weight throughout grain development. In the longitudinal section of Rice grain, the endosperm was composed by the layer of cells. So, we determined the numbers of cell layer and the length of individual cells. The number of endosperm cell layers in NIL(*TGW6*) was significantly higher than in “Nipponbare”, whereas endosperm cell lengths were identical. These results suggest that “Kasalath” type *TGW6* increases cell numbers in endosperm, and consequently increases in grain length.

Loss of function in the Kasalath allele had desirable effects on grain size. On the other hand, we analyzed the effect of loss of *TGW6* to source organ. Compared to “Nipponbare”, NIL(*TGW6*) accumulated more starch in the leaf sheaths just before heading. In grain developing, the growth rate of grain weight peaked at 15 d.a.f.; and the rate was higher in NIL(*TGW6*) than in “Nipponbare”. At the time of the greatest increase in grain weight, the expression of genes related to starch synthesis was stronger in NIL(*TGW6*) than “Nipponbare”. Thus, the accumulated starch in leaf sheath before heading might be a responsible source of developing grains after heading.

Here, we proposed the model of *TGW6* in grain developing. Native type *TGW6* has hydrolyzing activities of IAA-glucose, and it can release free IAA.

This IAA would limit the cell number in endosperm and grain length. Meanwhile, IAA might limit the starch synthesis and accumulation in source organ. Thus, grain weight is regulated to limited size. It might be a limiter (like a brake) to ensure to fill more numbers of grains. For reproductive strategy for plant, it will be more adaptive to develop more seeds than developing excessively larger seed. On the other hand, “Kasalath” allele can not produce mature *TGW6* protein, and can not hydrolyze IAA-glucose. Then, by the loss of limiter, cell numbers in endosperm and grain length increased. Further, starch synthesis and starch accumulation also increased,

and consequently grain weight is increased. This is a schematic model of yield development and known genes.

Numbers of gene had been cloned to regulate grain size, these genes involves in development of spikelet hull size. Then, the endosperm cell sizes were enlarged, and consequently increasing grain size. *TGW6* had a new point of action to grain development. It increases endosperm cell numbers, simultaneously *TGW6* increases starch accumulation and translocations. For further increase in grain weight, it seems to be desirable to collect the genes which have different types of point of action. This is a figure from Dr Zhang's works (Zhang et al. 2012 PNAS 109, 21534-21539). "N411" have an extra large grains. This cultivar have many positive alleles of known genes, *GS3*, *GW2*, *GW5*, *GS5* and *GL3*. This suggest that the pyramiding of known positive alleles for grain size could produce extra-large grains. Thus, to increase rice yield, we should glean superior genes to improving Source and Sink, and collect them.

Rice had been selected by human race and domesticated. In this process, superior and desirable alleles were selected and spread in modern cultivars. However, some desirable alleles might be left behind in domestication. Sometimes, such genes might be phenotypically invisible. To improve modern cultivars further, we should glean superior genes left behind in domestication, and introduce them into modern cultivars. This is a haplotypes of *TGW6* genes in world rice. We found 17 haplotypes of the *TGW6* from the core collection of cultivated rice and wild rice. We could find "Kasalath" type 1-bp deletion only in 4 rice including "Kasalath" and 1 *O. rufipogon*. These rice localized in indochina peninsula. "Kasalath" type 1-bp deletion was found to be desirable for grain yield, but it had not been spreaded in cultivated rice. To further improve modern cultivar, we made NILs in "Koshihikari" background. "Koshihikari" is a premier japonica cultivar in Japan. NIL in "Koshihikari" background also showed larger grain and weight than "Koshihikari". By field trial, we confirmed this NIL shows 15% higher grain yield than Koshihikari. Moreover, NIL showed higher content of perfect grain. Immature grain or chalky grain are caused by interruption of grain filling by limited source ability. The accumulated starch in leaf sheath might reduce immature grain and increased perfect grain. Thus, we conclude that *TGW6* can be used for further improvement of modern cultivars. Finally, I appreciate these collaborators and grant in aids to proceed this work. And thank you for your attention.

Plenary lecture

Recent Research Advances at ERL

Professor Upul Wijayantha

*Head of Energy Research Laboratory (ERL), Department of Chemistry,
Loughborough University, Loughborough, LE11 3TU, UK*

U.Wijayantha@lboro.ac.uk

Established in 2007, ERL is an advanced research facility involving a team of multi-disciplinary researchers (i.e. chemists, physicists, engineers, designers, economists and social scientists). It facilitates core research in energy harvesting, generation, conversion, conservation & storage. Research at ERL is funded by UK, EU and International funding agencies, charitable organisations and multi-national and UK industry.

Current research projects at ERL includes but not limited to novel photovoltaics, hydrogen generation (via chemical and solar-assisted routes), studies of CO tolerance levels in reformed H₂ for Fuel cell applications, CO₂ conversion for value added chemicals, N₂ fixation, biogas processing, advanced functional energy materials/coatings, smart windows, novel flexible stretchable and wearable supercapacitors.

In this presentation, we will report the recent advances made in some of these research projects.

Plenary lecture

Integration of natural resources in development through research: Biodiversity emphasis

Professor Sarath Wimalabandara Kotagama

Professor of Environment Science

Department of Zoology, Faculty of Science, University of Colombo, Sri Lanka

The world has seen the increasing impacts of human interventions and life styles on the components of the planet and the planet as a whole. We are today in the midst of probably the worst if not the ultimate “environmental issues” that mankind will have to face to avoid a catastrophic situation in the future. All previous “environmental issues” apart from the Nuclear issue, were issues that had limited impacts, often within contained local areas of the planet. Even some so called global issues such as “the brown haze” were primarily concerns of East Asia, while such phenomenons like “El-nino” and “La-nina” had their impacts in defined areas even though the events were the results of global dynamics. Climate Change on the other hand is “global in effect but local in impacts”. On the 16th of January 2015, it was announced that 2014 was the year with the highest ever recorded high temperatures, with out an El-nino effect. This is very significant and a clear eye opener to all climate change sceptics. The “Living Planet index” launched in November 2014 reiterated the disastrous state of the planet brought about since 1970. This is during the life time of the present rulers and decision makers. No element in nature is spared, no part of the globe is spared, and no organism is spared either. As such, it has become the concern of all disciplines and all people.

In the midst of these environmental issues and the “development” of Nations, we have seen the growth of information transfer. The world has become “small” and closely “connected”. We have come to recognize today as the “knowledge base” era. Actions for tomorrow must be based on “Knowledge” and this is the case for “Nature/ Biodiversity Conservation” too. The last

three decades have seen some major changes in the approach to conservation of nature and natural resources.

The evolution of conservation in general has evolved to become a complex but essentially a knowledge dependent activity. The presentation will attempt to clarify this trend, based on the major conceptual changes that have taken place during this era in

- Biodiversity emphasis, Change from “Game” to “wildlife” to “biodiversity”, Protection verses conservation, The Conservation Biology approach, Emergence of Sustainable Use, Adoption of MEAs – Conservation of Biological Diversity,
- Issues arising out of the CBD such as, Bio prospecting, Biopiracy, Technology transfer, Benefit sharing, Genetic resources, Taxonomy Research, PIC/MAT/MTA,
- Ecosystems Approach, Stakeholder Participation, Adaptive Management, Ecosystems Services, Economic Valuation of Nature, Significance of Monitoring and Evaluation, Technological revolutions such as GIS/GPS, Remote Sensing, computers and information transfer, Restoration, Invasives and Landscape Ecological approaches.

All of the aspects have profound impacts on the way we approach to manage the Biological Diversity. It affects the structures and mandates of institutional establishments that have been established to manage the “resource” in the past. Their continuation is largely dependent upon whether they recognize these changes and are willing to be part of the Knowledge Economy Development. The challenge for the future lies in this key element of knowledge, which effectively is a societal element and thus require “integration” at all institutional, social and political levels.

Conservation of the future is a matter of Societal choice, what ever the science may tell us. For it to be effective we need to recognize that it would be possible only on the basis of:

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1. A GOOD INFORMATION BASE (note not a COMPLETE information base as in the past)
 2. A well QUALIFIED and EXPERIENCED staff
 3. A well INFORMED PUBLIC, and
 4. A good INSTITUTION

The future challenge is based on achieving this end in each country. The generation of information is primarily based on RESEARCH. The approach to research in order to generate factual, scientific information cannot be compromised in any way to achieve conservation objectives. Thus the main hinge on which the above directions in conservation is dependent is scientific research. How much emphasis do we place on this information generation process and how much of such generated information do we incorporate in the conservation process as needed above. This has remained a major issue in Sri Lanka. The wildlife sector is yet to be able to differentiate clearly the needs of the sources of information for effective conservation. While some research is carried out by the sector itself, it is doubtful as to whether this research is “needs based”. The academic institutes and academics are indulging in research driven by their personnel interest and again it is a big question of whether the research is “needs based”. In summary the research is often not contributing to make conservation effective.

On the other hand, the finger is pointed at the conservation agencies for not even using the little information that is generated from research in the management to be effective. Attempts to bridge this was tried in 2013, but to this date beyond providing a group of distinguished select researchers with researched global literature on how research in the wildlife sector is “Best Practiced” globally, they have not met once to deliberate. Where is the fault, are the academics waiting to be summoned to formalize the process OR is the sector not interested to receive the directions to be more effective? While we wait to seek answers for this situation the future of biological diversity / wildlife/ natural resources is gently but surely slipping down the abyss – towards disaster.

Plenary lecture

Climate change threatens the human nutrition: Challenges and opportunities for increase food and nutrient security

Dr. Saman Seneweera

Discipline Leader, Senior Research Fellow, Centre for Crop Health, University of Southern Queensland, Toowoomba QLD 4350 Australia

saman.seneweera@usq.edu.au

The world's population is rapidly increasing and to match the global demand, food production needs to increase by 50% by 2050. Food security is largely determined by ten major crop species, of which, rice, wheat and maize contribute more than 70% of the food demand. Since the green revolution, crop productivity has increased significantly due to improved agronomy practices and adopting innovative breeding programs. Today, crop yield increases have plateaued but demand for food has increased substantially. On the other hand, global climate is rapidly changing as a consequence of burning fossil fuels and land clearance. Atmospheric [CO₂] concentration is expected to increase from 390 to 550 μmol^{-1} CO₂ mol⁻¹ by the middle of this century. Consequently, the atmospheric temperature is expected to increase by 1.4 to 4.5°C in 2100 which could lead to more extreme climatic events, such as high temperature, heat waves, and periodic drought, frequent and strong typhoons, prolonged wet and dry seasons, and increased incidence of disease outbreaks which affect the sustainability of agricultural production systems. Thus, understanding of how crops respond to such environmental stresses is essential to maintain food and nutrient security in the world. To address these concerns, (1) greater understanding of agronomic management of crops to avoid stress, (2) mechanistic understanding of stress regulation, (3) identifying new traits that avoid these stresses, (4) genetic engineering and/or breeding of crops to avoid such stresses are essential.

Many C₃ plants will respond positively to increased atmospheric CO₂ concentration under optimum growth conditions, but the beneficial effect of elevated CO₂ could be offset by other climatic stress factors, such as high temperatures and periodic drought. The primary mechanism that promotes plant growth at elevated [CO₂] is the increase in photosynthesis which could increase by up to 50%. Elevated [CO₂] also reduces photorespiration and is directly associated with decrease in O₂/CO₂ ratio at the site of CO₂ fixation. Elevated CO₂ also reduces stomatal conductance by 30-40% at double the CO₂ concentration, which leads to improved efficiency of plant water use. However, the positive effects of [CO₂] response cannot always be capitalized as high temperature and low soil water availability suppress photosynthesis and thus the growth response to elevated [CO₂]. In general, C₃ crops are likely to produce more harvestable products and that both C₃ and C₄ crops are likely to use less water with rising atmospheric [CO₂] under optimum conditions. Higher temperatures can adversely affect crop yield through two principal pathways, namely (i) high maximum temperatures that cause spikelet sterility and thus adversely affect grain quality and (ii) increased nighttime temperatures that may reduce assimilate accumulation that could lower the yield potential.

In the world, almost one billion people are undernourished and lack sufficient protein, fats and carbohydrates. An additional billion people are malnourished because their diets lack required micronutrients such as iron, zinc and vitamin A. These dietary deficiencies have an enormous negative impact on global health, resulting in increased susceptibility to infection and diseases, as well as increasing the risk of significant mental impairment. As with climate change scenarios, particularly under elevated [CO₂], the micronutrient such as Zn, Fe and Se concentrations are substantially decreased for many crops species including the C₄ biochemical type. In addition, the increased production of phenolics and tannins under elevated CO₂ in some species, as well as many alkaloids, may have potential consequences on the health of primary consumers. The decreased nutritional value in combination with increased tannin and phenolic production has been linked to decreased growth rate and conversion efficiency of some herbivores, as well as an increase in their relative demand and consumption

of plants. Furthermore, many “cyanogenic” species—plants which naturally produce cyanide, and which include 60% of all known plant species have been found to increase their cyanide production under elevated [CO₂]. This is detrimental to both animal and human food sources. Further, Zinc and iron deficiency has been recognized as one of lethal factors affecting human health and is very prominent in South Asia. Currently, breeding efforts are underway to increase the micronutrient density of cereals and legumes. Further, understanding of genotype and environment interaction on nutrient accumulation in grain and identification of new genetic materials are essential to improve global Zn and Fe malnutrition. The identification of genes that are involved in many agricultural traits has been identified by traditional molecular genetic and quantitative trait locus (QTL) mapping for complex traits. Further, these targets can be easily achieved through adopting a quantitative genetics approach together with “omics” technology such as genomics, proteomics, metabolomics and ionomics.

Plenary lecture

**Structural Biology: A Path to Understand Molecular
Machines**

Dr. Wimal Ubhayasekera

*Department of Molecular Biology, Swedish University of Agricultural Sciences,
Biomedical Center, Uppsala, Sweden*

wimal@xray.bmc.uu.se

Structural biology is one of the main contributors to understand the biochemical activities of living organisms. Protein structures provide the insights of the function describing the exact details of their activity. The structure determination of proteins is achieved using several techniques mainly protein crystallography. The information obtained from the protein structural studies helps finding ways to control different cellular processes, drug discovery and to enhance several biotechnological processes.