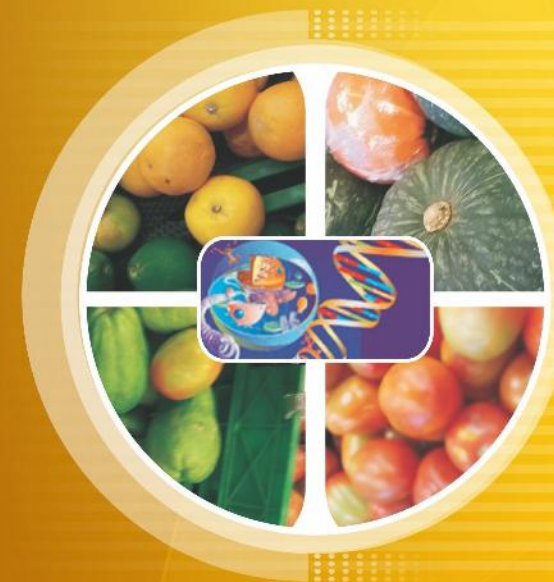




UNIVERSITAS
ATMA JAYA YOGYAKARTA
Fakultas Teknobiologi



PROCEEDING



1st International Seminar on
“Natural Resources Biotechnology:
From Local to Global”

September 8th – 9th 2015
Faculty of Biotechnology
Universitas Atma Jaya Yogyakarta

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ISSN: 2460-8238



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Welcome Speech Chair of the Seminar Committee

Distinguished Guests,
Honorable Speakers,
Ladies and Gentlemen,

It is a great pleasure to welcome all of you to the International Seminar "Natural Resources: From Local to Global". The Faculty of Biotechnology of Universitas Atma Jaya Yogyakarta runs this seminar to commemorate the 50th Anniversary of the Universitas Atma Jaya Anniversary and the 25th Anniversary of the Faculty of Biotechnology. Your presence is your present for the anniversary of our university and faculty as well.

The Anniversary is not the only reason to run this seminar. A greater reason is behind the seminar. Indonesia is rich in biodiversity. It is a challenge for us, as scientist, to maintain the biodiversity and to develop the potential of the biodiversity for the common good. Through this seminar, the scientific research on Indonesian biodiversity can be shared and probably the finding of the new research can inspire us for further exploration. Therefore, the seminars goal is to facilitate the spread of the research on local potential of biodiversity to the global level. Hopefully, it can attract more researchers to explore the wealth of local biodiversity.

The committee invites speakers who are expertise in the research concerning biodiversity. Our invited speakers are Assoc. Prof. Dr. Michael Murkovic from Graz University of Technology Austria (food scientist), Assoc. Prof. Worawidh Wajjwalku from Kasetsart University Bangkok Thailand (Veterinary disease biotechnology), Dr. Kathryn McMahon from Edith Cowan University Australia (Seagrass biotechnology), Prof. Marco Nemesio E. Montano, PhD from University of the Philippines (Seaweed biotechnology), Prof. Jun Kawabata from Hokkaido University Japan (food biochemist), Endang Semiarti, PhD from Universitas Gadjah Mada, Indonesia (Plant biotechnology), Ign. Pramana Yudha, PhD from Universitas Atma Jaya Yogyakarta (Conservation genetics), Dr Machmud Thohari from Technical Team for Environmental Biosafety, Ministry of Enviroment & Forestry Indonesia (Environmental Biosafety), Dr Harvey Glick from Asia Regulatory Policy & Scientific Affairs Monsanto Company (Regulatory Policy & Scientific Affairs Monsanto). It is a good opportunity to learn from the speakers to enhance and to update our knowledge. I hope this seminar is of benefit to all of us.

In conclusion, I wish you a successful seminar and a pleasant stay in Yogyakarta.

With kind regard
Coordinator of conference program

Dr. rer. nat. Yuliana Reni Swasti, S.TP., MP.

**WELCOME SPEECH
DEAN
FACULTY OF BIOTECHNOLOGY
UNIVERSITAS ATMA JAYA YOGYAKARTA**

Distinguished Guests,
Honorable Speakers,
Ladies and Gentlemen,

On behalf of the Faculty of Biotechnology, Universitas Atma Jaya Yogyakarta and the Committee of the International Seminar, I would like to first of all to extend our heart-felt thanks for your presence at this Seminar. This seminar is so significant in a sense that it focuses on natural resources with local content but by utilizing biotechnology they will become global and worldwide products and services as well.

Biotechnology has been developed very rapidly and it is believed to be "a new wave in the economic world". Biotechnology has contributed in all aspects of humans' life, such as food production, health, industry, environment, etc. The role of biotechnology for the betterment of human beings, however, is still need to be improved. Indonesia, with its huge biodiversity, has a potency to develop and applied biotechnology nationwide.

The role of biotechnology has increased rapidly. Many are believed that biotechnology has become an integral part of modern industries with high economic values. On the other hand, it needs to be closely managed in order to avoid its negative impacts. There are some examples of negative impacts with relate to biotechnology application, such as intellectual property rights, genetically modified organisms (GMOs), environmental degradations, biodiversity issues, indigenous people knowledge, biosafety, etc.

The Seminar covers topics such as: Functional Foods, Food Biotechnology, Biopharmacy, Health/Medical Biotechnology, Environmental Biotechnology, Legal Aspect of Biotechnology, Bioinformatics, and Social-Economic Aspects of Biotechnology. This Seminar will be presented by nine (9) invited speakers with different topics and expertise. There will be some papers and posters to be presented also in this Seminar from some participants from the Philippines and Indonesia.

Henceforth, in commemorating its 50th anniversary Universitas Atma Jaya Yogyakarta (UAJY) and 25th anniversary of Faculty of Biotechnology, Universitas Atma Jaya Yogyakarta (UAJY) on September 2015, it is worthy and appropriate to explore the newest innovations in the field of research and development of biotechnology to be applied in many aspects for the betterment of human beings. The Seminar takes this opportunity to discuss and hopefully find ways to solve problems faced by human beings in the world.

I would like to take this opportunity to express my sincere thanks and gratitude to the Committee and in particular to the honorable speakers. Before closing this remarks, allow me to ask the Rector of Universitas Atma Jaya Yogyakarta to open this Seminar officially.

Finally, this is an opportune time for me to wish you all in the two (2) fruitful days of interesting and beneficial programs and hope you have a pleasant stay in Yogyakarta.

Thank you very much and may God bless us all. Amen.

Yogyakarta, 8 September 2015

Dean

Drs. B. Boy Rahardjo Sidharta, M.Sc

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The Application of Molecular Techniques to The Conservation of Endangered Species in Indonesia

Ign. Pramana Yuda

How to conserve endangered species, the small and declining populations? Currently this question is receiving considerable attention, especially through the theoretical development of conservation biology and its application to endangered species conservation. In contrary is the fact that even basic information on the biology-ecology of most endangered species is extremely limited. Reviewing BirdLife International's database revealed that the availability and the quality of data currently being used to classify most endangered bird species was *poor*. Furthermore very little is known about the genetic consequences of population declines and fragmentation.

Theoretically, population declines increase extinction risk due to both the loss of genetic variation and associated increases in the level of inbreeding [1, 2]. For this reason, a common goal of many endangered species conservation programs is the maintenance of genetic variation. However, such goals are often set without a clear understanding of either the genetic/evolutionary history, or future potential trajectory of an endangered species.

Understanding how to manage the genetic resources of a species both within and among small fragmented populations is a complex task that requires the integration of a number of quite distinct but complementary data sets. Data are required on current demography and trends, contemporary connectivity as well as historical demographics, threats, behaviour, morphology, physiology, and biotic interaction. At present few comprehensive empirical data sets exist that can be used to develop and test either species-specific management options or general models of integrated management.

Interest in genetic variation and its relation to the environment is not new. In 1920s Turesson thoroughly investigated the correlation of habitat- genetic variation among plant species. Meanwhile the link between ecological and genetic variation in animal has been systematically studied in 1950s. These ecological genetics combined ecological fieldwork and laboratory genetics, which has made up the major ecological genetics and evolutionary biology.

The advance of molecular techniques have improved our ability to delineate relationship among individuals, populations and species and its environment. These techniques are being used to develop ecological genetics, much of which has now been encompassed by the phrase 'molecular ecology'.

The complexity of vast amount of empirical data have possible been analyzed as a result of methodological advances in the statistical analysis, low-cost computing power and the development of analysis software.

The greatest impact of new methods has been the development of protein and DNA markers for the analysis of genetic variation. For examples DNA sequencing, MHC (major histocompatibility complex), minisatellite, microsatellite, and RAPD (random amplified polymorphic DNA) have allowed to answer the difficult ecological genetics questions. These included identification of parentage, more distance relatives,

founders to new population, unidentified individuals or species, population structure, and effective population size. In addition molecular tools can be valuable as a means to plan for long-term genetic diversity and for clarifying demographic and ecological issues early in species recovery.

PCR (polymerase chain reaction) provides for more sophisticated analyses of endangered species. PCR allows amplification of DNA from minute amounts of fresh, alcohol-preserved, or even dry tissues. Non-invasive genetic sampling using blood samples, small biopsies, plucked hairs or feathers and even feces can provide a source of template DNA for PCR and for the genetic analyses.

The developments in molecular techniques have opened a new era on population biology, ecology and its applications on species conservation. Here I attempt to present a broad range of cases in which the molecular techniques have been used to provide insight into conservation of endangered fauna in Indonesia. The examples are on clarification of taxonomy, defining the extent of hybridization, understanding relative levels of within- and among-population differentiation and defining the structure of a population. These issues can call for greater or lesser consideration to a particular species and reprioritization of conservation efforts.

Defining species-subspecies

Based on morphological systematics, there were one species of orangutan with two subspecies: Bornean orangutan (*Pongo pygmaeus pygmaeus*) and Sumatran orangutan (*P. p. abelii*). The molecular relationship between the two orangutans has been studied using various molecular markers: allelic variation restriction mapping of mtDNA, nuclear DNA hybridization, protein electrophoresis and sequence comparisons of the mitochondrial COII gene. These studies have revealed similar, or somewhat greater, difference between the two orangutans compared to differences between the common chimpanzee (*Pan troglodytes*) and bonobo or pygmy chimpanzee (*Pan paniscus*). Further molecular comparison on the basis of complete mitochondrial DNA (mtDNA) confirmed that the two orangutans should be listed as different species, Bornean orangutan (*Pongo pygmaeus*), and Sumatran orangutan (*Pongo abelii*) [3].

Defining Hybridization

Hybridization among closely related species can have serious conservation implications. It can have both positive and negative consequences for population viability. In Indonesia most noteworthy issues associated with hybridization is the hybridization within the Sulawesi macaques. In Faruhumpenai Nature Reserve (South Sulawesi) a mix group of *Macaca tonkeana* and *M. ochreata* was reported. However no hybridization has been confirmed between the two species in the area and need further molecular analysis [4]. Meanwhile hybridization between *M. tonkeana* and *M. maura* has been confirmed based on molecular analysis using mtDNA, aDNA (microsatellite) and Y chromosome microsatellite [5].

Among Indonesian birds, five species have been naturally hybridized reported and two of them are endangered species. Hybridization between *Anas gracilis* and *A. gibberifrons* was reported in Papua. The other hybridization was reported between *Todiramphus lazudi* and *T. diops* [6].

Whitin and among-population genetic diversity

In addition to extensive field ecological data, genetic information of the taxa is required to evaluate population viability. Evaluation of diversity within and among populations, gene flow among populations provides an assessment of populations that are most genetically depauperate, most fragmented, and distance among others. The results can be used to identify populations in need of new individuals, populations that could safely donate individuals to more vulnerable populations, or populations in need of further demographic or environmental consideration. All of these factors are needed in assessment of recovery program of endangered species.

Few studies on describing population structure have been conducted for endangered fauna species in Indonesia. Primates, especially Orangutan, have been the most studied [3, 7-9]. Other studies included study in Sulawesi macaque monkeys [10], Silvery Gibbon [11]. Meanwhile study on bird is fewer, for example: Yuda [12], used mtDNA and microsatellite to assess the genetic diversity of Java sparrow.

Identification unknown individual

The relationship among individuals in the population is often not known. In small and/or captive populations knowledge of relatedness is essential. Each individual's contribution to past and future genetic diversity is critical. The management of a wild, translocated, reintroduced or captive population require identification of relatedness among founders. In some circumstances, identification of parentage or sex ratio will provide greater understanding of population structure.

Allozyme and mitochondrial data do not provide the detail necessary for parentage analyses. To date microsatellites provide the best resolution [13]. Some recovery population programs have been done for Indonesia fauna. But so far no molecular assessment have been applied prior to releasing the species of concern.

Estimation of population size

Direct count to estimate population of elusive species is not an easy work. Furthermore in most cases the field work are not able to determine the effective population size. Molecular technique provides an alternative tools for that purpose. Microsatellite analysis using fecal DNA has proven effective. In Indonesia the approach has been applied to estimate population size and distribution of Sumatra elephant [14].

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