

ASIAN BIG CAT'S CONSERVATION GENETICS WORKSHOP



The first regional hand-on training workshop on the conservation genetic techniques for the conservation and management of Asian big cats' populations (March 21-23, 2018)

ORGANIZED BY

Seoul National University College of Veterinary Medicine, Seoul, Republic of Korea
Amity Institute of Forestry & Wildlife, Amity University, Noida, Uttar Pradesh, India

SUPPORTED BY

Ministry Of Environment, Republic of Korea
Secretariat of the Convention on the Biological Diversity, Montreal, Canada

VENUE

Amity University Uttar Pradesh (AUUP) Campus, Sector 125, Noida – 201313, Uttar Pradesh

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Contents

Sr.No.	Content	Page number
	Summary	1
1.	Introduction	2
2.	Organizers	2
3.	Special invitees and keynote speakers	3
4.	Resource persons	3
5.	Workshop proceedings	4
6.	Conclusion	33
7.	Annexure	34

SUMMARY

The Seoul National University College of Veterinary Medicine (Seoul, Republic of Korea) and Amity Institute of Forestry and Wildlife, Amity University (Noida, India) jointly organized the Asian big cats' conservation genetics workshop from March 21-23, 2018 at Amity University Uttar Pradesh (AUUP) campus in Noida (India). The organized workshop was a part of ongoing India-Korea cooperative research project titled, "Asian Big Cats' Conservation Through Technology Sharing and the Use of Unified DNA Typing Methodology" supported by the Secretariat of the Convention on Biological Diversity (CBD, Montreal Canada) and Ministry of Environment (MOE, Republic of Korea) under the Bio-bridge Initiative.

The aim of the hands-on training workshop was to enhance the capacity and expertise at regional wildlife research institutions in India and Nepal on the aspects of the use of DNA based tools for the conservation of Asian big cats. Forty participants attended the training workshop from regional wildlife research institutions, universities, NGO from India and Nepal. It was a nice mixture of senior and junior scientists/faculties, researchers, and students representing ecologist, taxonomist, and molecular biologists. The training, which consisted of lectures, case reports and practical session, focused on the understanding the need of the use of molecular tools for the conservation of Asian big cat species such as tiger, leopard, lion, snow leopard, and clouded leopard. The resource persons shared the updated information about the use of genetic tools in wildlife management, especially big cat species. During the practical sessions, participants were introduced to fecal samples DNA extraction, agarose gel electrophoresis, polymerase chain reaction and DNA fingerprinting. In addition, the sample collection and storage protocols were discussed.

Overall, participants provided positive feedback on the workshop, which they considered met its objectives. Participants also expressed that the schedule and administrative arrangements were well organized.

1. Introduction

The Seoul National University College of Veterinary Medicine (Seoul, Republic of Korea) and Amity Institute of Forestry and Wildlife (AIFW), Amity University (Noida, India) jointly organized three days Asian big cats' conservation genetics workshop from March 21-23, 2018 at Amity University Uttar Pradesh (AUUP) campus in India. The organized workshop was apart of ongoing India-Korea cooperative research project titled, "Asian Big Cats' Conservation Through Technology Sharing and the Use of Unified DNA Typing Methodology" supported by the Secretariat of the Convention on Biological Diversity (CBD, Montreal Canada) and Ministry of Environment (MOE, Republic of Korea) under the Bio-bridge Initiative.

The three days training workshop included plenary talk, scientific presentations, laboratory and technical sessions, and group discussions. Forty participants (Annexure C) attended the training workshop from regional wildlife research institutions, universities, NGO from Indian and Nepal. It was a nice mixture of senior and junior scientists/faculties, researchers, and students representing ecologist, taxonomist, and molecular biologists. The objectives of the organized workshop were:

- a. Development of the capacities of scientists, faculties, and researchers of the regional wildlife institutions in India and Nepal on the use of genetic tools for the population monitoring of Asian Big Cats.
- b. Hands on training on laboratory techniques – DNA extraction, PCR, gel electrophoresis, and fragment analysis
- c. Exposure to phylogenetics and population genetics data analysis
- d. Familiarization with the concept of PanPlex and its utility in obtaining scientific synergism for wildlife conservation.

2. Organizers



Prof. Hang Lee, B. Vet. Med., Ph.D

Seoul National University College of Veterinary Medicine, Bldg. # 85-812, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Prof. Lee is the principal investigator and overall coordinator Korea-India cooperative research project titled, "Asian Big Cats' Conservation Through Technology Sharing and the Use of Unified DNA Typing Methodology". He has done extensive genetic and genomic research on big cat species and other endangered species of Asia.



Prof. Puneet Pandey, M.Sc., Ph.D*

Amity Institute of Forestry and Wildlife, D-Block, Amity University, Sector 125, Noida, Uttar Pradesh, India

Prof. Pandey is the Indian principal investigator of Korea-India cooperative research project titled, “Asian Big Cats’ Conservation Through Technology Sharing and the Use of Unified DNA Typing Methodology”. He along with Prof. Lee and other collaborators and has developed PanPlex, a simple and efficient way of genetic monitoring of all big cat species.

3. Special invitees and key note speaker



Dr. Anmol Kumar, M.Sc., Ph.D

IFS retd. and former Director General, Forest Survey of India, Dehradun

Dr. Kumar has worked for more than three decades with Ministry of Environment, India. During his tenure, he contributed in finalizing the Wildlife Action Plan and prepared recovery plans for many threatened species.



Dr. S.P. Goyal, M.Sc., Ph.D

Emeritus Scientist, Wildlife Institute of India, Dehradun, India

Dr. Goyal is renowned wildlife biologist, geneticist, and forensic expert from India. In past, he established and headed the wildlife forensic cell at Wildlife Institute of India with the support of US Fish and Wildlife Services. He has undertaken genetic studies on tigers and other endangered species in India.

4. Resource Persons

Ms. Jeeyun Hyun

Research Scholar, Seoul National University College of Veterinary Medicine

Ms. Kyungeun Lee

Research Scholar, Seoul National University College of Veterinary Medicine

Ms. Daechol Jeong

Research Scholar, Seoul National University College of Veterinary Medicine

Dr. Mukesh Thakur

Scientist C, Zoological Survey of India, Kolkata, India

Dr. Sujeet Kumar Singh

Post-doctoral fellow, Wildlife Institute of India

Dr. Randeep Singh

Assistant Professor, Amity Institute of Forestry and Wildlife, Amity University, Noida, India

Dr. N.P.S. Chauhan

Director, Amity Institute of Forestry and Wildlife, Amity University, Noida, India

5. Workshop Proceedings

Inaugural session (Day 1: March 21, 2018)

The two and half hour inaugural session included welcome address, opening remarks, workshop overview, and a keynote lecture.



Welcome speech by Dr. NPS Chauhan during inaugural session

Dr. N.P.S. Chauhan, the director of Amity Institute of Forestry and Wildlife (AIFW), facilitated the introductory session. He welcomed the Chief Guest, Dr. Anmol Kumar (Former Director General, Forest Survey of India) and Guest of Honors, Dr. S.P. Goyal (Emeritus Scientist, Wildlife Institute of India) and Dr. Mukesh Thakur (Scientist, Zoological Survey of India). The session started with a word of thanks and appreciation for Prof. Hang

Lee, the Principal Investigator Asian big cats' conservation genetics project, for his generous support and guidance in developing workshop modules. The lighting of the lamp and Saraswati Vandana followed this.



Lightening the lamp and SaraswatiVandana during inaugural session



Dr. Anmol Kumar (Chief Guest) sharing his thoughts on need to international technical and scientific cooperation with the workshop participants during inaugural session



Prof. Hang Lee presented a brief appraisal of the workshop program and BBI program of CBD



Prof. (Dr.) Balvinder Shukla, Vice Chancellor, Amity University sharing her experience and Amity University's contribution to biodiversity conservation



Vote of thanks and felicitation of guest by Puneet Pandey

Following the introductory remarks, Puneet Pandey, Assistant Professor, AIFW, briefly introduced the participants about the Amity University's academic presence, research accomplishments and contribution towards biodiversity conservation. Later, Prof. Hang Lee presented a brief appraisal of the workshop program and explained the need for such a capacity-building program and its basic objectives. According to Prof. Lee, the main aim of the training workshop was to bring awareness among young wildlife biologist about recent technological advancements in the field of conservation genetics and how best these can be exploited through technical and scientific cooperation for the effective species conservation, with Asian big cats' as example species. In his presentation, he also discussed about the Convention on Biological Diversity (CBD) and its Bio-bridge Initiative program. CBD is a multilateral treaty, which came into force on December 29, 1993, has 193 parties. CBD has three main goals including the conservation of biological diversity; the sustainable use of its components; and the fair and equitable sharing of benefits arising from genetic resources. CBD promotes transference of the biodiversity conservation techniques and to promote such technology transfer CBD launched the Bio-bridge Initiative (BBI) program in the year 2014 with the support and assistance from Ministry of Environment (MOE), Republic of Korea. BBI is a catalytic program intended to inspire long-term technical and scientific cooperation among Parties and is focused on developing countries and countries with economies in transition. Prof. Lee shared with participants that the organized workshop is also a part of

BBI supported India-Korea scientific cooperation project titled, “Asian Big Cats’ Conservation through technology sharing and the use of unified DNA typing methodology”. Prof. Lee encouraged the trainees to make the utmost of the training program and sought active participation from the participants.

During the inaugural session, Dr. Balvinder Shukla, the Vice Chancellor, Amity University also highlighted the importance of technical and scientific cooperation in present scenario citing some recent examples from Amity University. Speaking on occasion, Dr. Anmol Kumar shared his experiences while working with the government of India to promote technical and scientific cooperation for biodiversity conservation in India. He mentioned about the role of US Fish and Wildlife Services (USFWS) in establishing wildlife forensic facility at Wildlife Institute of India. Dr. Goyal also supported Dr. Kumar’s thoughts and stressed the need for more such initiative for wildlife protection and conservation. Dr. Mukesh Thakur thanked organizers for inviting him and Dr. Kailash Chandra, the Director of Zoological Survey of India. He also read the message of Dr. Chandra for the participant who was unable to attend workshop due to some urgent meeting.

The inaugural session ended with the felicitation of guest and vote of thanks by Puneet Pandey.

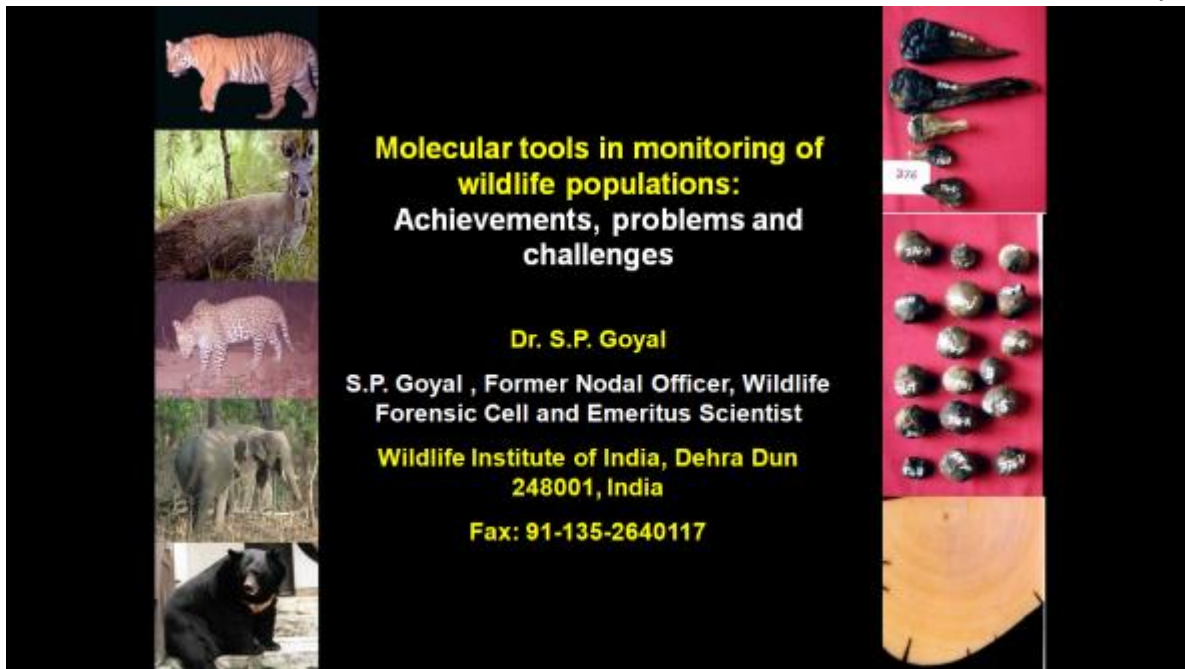


Participants at inaugural session

Plenary lecture

Molecular tools in monitoring of wildlife populations: Achievements, problems and challenges

Dr. Surendra P. Goyal



In his talk, Dr. Goyal discussed the work accomplished in his long-term project titled, “*Pantheratigris* genome – Implications in forensics.” Wildlife Institute of India (WII) initiated the project in the year 2005 with the aim to develop the genetic database (nuclear as well as mitochondrial) of all tiger populations in India and identifying the source of origin of tiger seizures using the genetic information. According to Dr. Goyal, the major hurdle faced during the project was to optimize the protocol for the DNA extraction from noninvasive samples such as scats and selection of microsatellite markers to balance amplification success, errors, and polymorphism. In the mentioned project, the research team lead by Dr. Goyal successfully developed population genetic database of northern, western, sunderbans, and central India tiger population using nine microsatellite markers and four mitochondrial genes. Dr. Goyal told the audiences that the genetic characterization of the tiger populations of northeast and southern India was not completed during the project tenure due to limitations of time and resources. According to Dr. Goyal, the work of genetic characterization of all tiger populations would have completed timely if all scientific institutions in India have worked in cooperation. Nevertheless, despite limitations, the project data was found to be of great importance for tiger conservation and management.

The findings of the tiger genome project were helpful in selecting the candidate population for tiger reintroduction in Sariska Tiger Reserve. At the beginning of 21st century, the tiger went extinct from Sariska due to extensive poaching. Based on the presence of TIG10 haplotype in the tigers of Ranthambhore and Sariska and absence of it remnant tiger populations of northern and peninsular India, tigers from Ranthambhore were used to constitute reintroduced Sariska tiger population. In addition, the project findings were used to infer the source of origin of tiger seizure received by WII forensic facility. In the pilot study, thirty-four tiger seizures were tested for the geographic assignment using population-level data of nine microsatellites. The fourteen (41%) were successfully assigned to the population level following the Bayesian approach. According to Dr. Goyal, the lack of genetic data for all tiger populations (especially northeast and southern India) and low genetic resolution (only nine microsatellites) hinders the assignment of all tiger seizures.



Plenary lecture by Dr. Goyal

After the plenary, one participant asked Dr. Goyal about the biggest challenge he faced while working in the field of wildlife genetics. Responding to the question, Dr. Goyal said that he finds representative sample collection of endangered wild species as the biggest

challenge. Over the years, he has developed wildlife biological sample repository with the assistance of zoo veterinarians, forest staff, and museum donors.



Workshop participants during plenary session

Presentations by organizers and resource persons

Day 1 (March 21, 2018)

Presentation 1: Introduction to Phylogenetics and Population genetics

Dr. Mukesh Thakur, Zoological Survey of India

The first technical presentation of the workshop was on the basic terminology and concepts of phylogenetics and population genetics to aware workshop participants about the scope of genetics in wildlife conservation and management. In his presentation, Dr. Thakur discussed the biological species concept with the participants. As defined by Ernst Mayr, “species are groups of interbreeding natural populations that are reproductively isolated from other such groups.” The biological species concept explains why the members of a species resemble one another, i.e., form phenetic clusters, and differ from other species. When two organisms breed within a species, their genes pass into their combined offspring. As this

process is repeated, the genes of different individuals are constantly shuffled around the species gene pool. The shared gene pool gives the species its identity. By contrast, genes are not (by definition) transferred to other species, and different species, therefore, take on a different appearance.

Introduction to Phylogenetics and Population Genetics

DR. MUKESH THAKUR
SCIENTIST- C
CENTRE FOR DNA TAXONOMY
ZOOLOGICAL SURVEY OF INDIA, KOLKATA



He further continued his talk discussing the importance of phylogenetics in basic research on ecology and evolution, identifying the conservation units, i.e., MU and ESU. Phylogenetics is a branch of science to study evolutionary relationship between organisms. Phylogenies are based on the assumption that more closely related species will be more similar to one another, and they are commonly built using genetic sequences or physical characters. They are often visually represented as trees: the tips of the ever-branching tree representing species, and the branches representing 'evolutionary distance' (e.g., length of time) from the ancestors from which they evolved. In molecular phylogeny, the relationship between an ancestral sequence and its descendants is studied to estimate time of divergence between groups of organisms that share a common ancestor. When two sequences found in two organisms similar, we assume that they have derived from one ancestor. The sequence alignment reveals which positions are conserved from the ancestor sequence. Further, he explained the phylogenetic trees types and the basic nomenclature, i.e., nodes, branches, leaves, etc. He also explained participa

nts how phylogenetics trees are constructed using DNA sequences and the importance of bootstrap analysis.



Presentation on phylogenetics and population genetics by Dr. Thakur

According to Dr. Thakur, apart from evolutionary relationship, understanding of the level of genetic vigor at a population level is also important for the endangered species management. The branch of science, which deals with such type of studies, called population genetics. The higher the population's genetic diversity, more vibrant future. The knowledge of the population level genetic statistics is vital in formulating the remedial action plan for the genetic rescues of species/populations suffering from low genetic diversity or inbreeding. Dr. Thakur also shared the research finding of his past and ongoing research on wild and captive animals to support his statements.

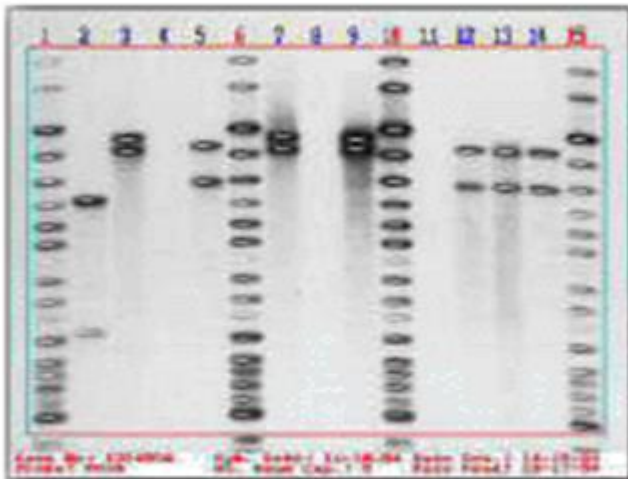
Presentation 2: Introduction to DNA fingerprinting

Puneet Pandey, Amity University

Prof. Pandey started his presentation with a word of appreciation for Dr. Thakur for familiarizing the participants with the basics of conservation genetics. He told participants that DNA or deoxyribonucleic acid is the hereditary material of almost all living creatures

and nearly every cell of the individual's body contain same DNA. In an animal cell, based on the location, DNA is of broadly two types, the cytoplasmic or mitochondrial DNA and nuclear DNA. In a sexually reproducing organism, cytoplasmic DNA is maternally inherited as cytoplasm is contributed by ovum. In contrast, the nuclear DNA is bi-parentally inherited as each of the parents (father and mother) contributes the equal proportion of nuclear genetic material to the offspring. Thus, an offspring's cytoplasmic DNA is almost 100% similar to that of a mother; but the nuclear DNA has 50% similarity to that of each of the parent. According to Mendelian genetics, during gamete formation, the alleles for each gene segregate from each other so that gamete carries only one allele for each gene and genes for different traits segregate independently during the formation of alleles. Thus in every generation or every individual (except the identical twins or clones), we expect differences in the nuclear DNA. This is the basis of DNA fingerprinting. DNA fingerprinting is a process of determining individual-specific DNA signature. The concept is similar to that of fingerprints analysis wherein individual identity is established based on fingerprint pattern.

Introduction to DNA fingerprinting



Puneet Pandey,
 Assistant Professor, Amity Institute of Forestry & Wildlife,
 Amity University

DNA is composed of four different nitrogenous bases namely adenine, guanine, cytosine, and thiamine, and the arrangement of these bases codes for amino acids, the

building blocks of proteins. The proteins are the phenotypic expression of genes. In nuclear DNA, there exist certain regions that have a repetitive arrangement of nitrogenous bases or nucleotides (the building blocks of the DNA). The repetitive unit may be of two nitrogenous bases (e.g. $(AT)_n$, $(GC)_n$, $(CT)_n$, etc.), or three nitrogenous bases (e.g. $(ATC)_n$, $(GCT)_n$, $(CTA)_n$, etc.), or many. These are called microsatellites, and they are the part of noncoding DNA, i.e., they do not store information for the synthesis of proteins or do not have any function in the body. Being noncoding repetitive DNA sequence, microsatellites are hypervariable. Microsatellites are widely distributed in the genome. In DNA fingerprinting, the polymorphism in microsatellites is analyzed to establish individual level identity.



Presentation on DNA fingerprinting by Prof. Pandey

According to Prof. Pandey, DNA fingerprinting has many applications in wildlife research such as paternity testing, selection of candidates for reintroduction or conservation breeding programs, establishing an identity of conflicting individuals (human-wildlife conflict), and forensic examination of wildlife seizures. Most of the wildlife genetic studies employ noninvasive samples such as feces, urine, shed hair, etc. as these are easy to obtain from wild without disturbing or harming animals. Before initiation of any genetic study using noninvasive samples, it is necessary to establish an individual level identity of each of the

collected sample to exclude repetitive samples of an individual which if incorporated may severely affect the genetic findings or conclusions. Thus, DNA fingerprinting is used to establish individual level identity to select unique genotypes from the samples for the genetic studies. For DNA fingerprinting, a panel or groups of microsatellites are amplified using PCR using fluorescently labeled primers. The amplified products are then subjected to capillary electrophoresis to record the size of microsatellites in an individual.

According to Prof. Pandey, there exists no universal panel of microsatellites for the DNA fingerprinting of Asian big cat species due to lack of scientific cooperation and synergism among different researcher groups globally. The different set of microsatellite markers are used by different research groups globally. The genetic information thus generated is not compatible and has no utility for developing species conservation strategies at global scale. Understanding the need of unified marker system for big cat species, PanPlex was designed by researchers of Seoul National University (Republic of Korea), Ulsan National Institute of Science and Technology (Republic of Korea), Wildlife Institute of India (India), and Amity Institute of Forestry and Wildlife (India). PanPlex consists of 32 polymorphic microsatellite markers that are designed by analyzing the whole genome DNA of four big cat species namely tiger, lion, leopard, and snow leopard. These markers are uniformly distributed in the genome and have same annealing temperature. The PanPlex has already tested on several wild and captive populations of big cat species and the initial results have shown the high amplification success and uniform polymorphism across the species. Being simple, convenient (multiplex PCR), and cost-effective, PanPlex can be easily adopted for routine population monitoring of Asian big cat species.

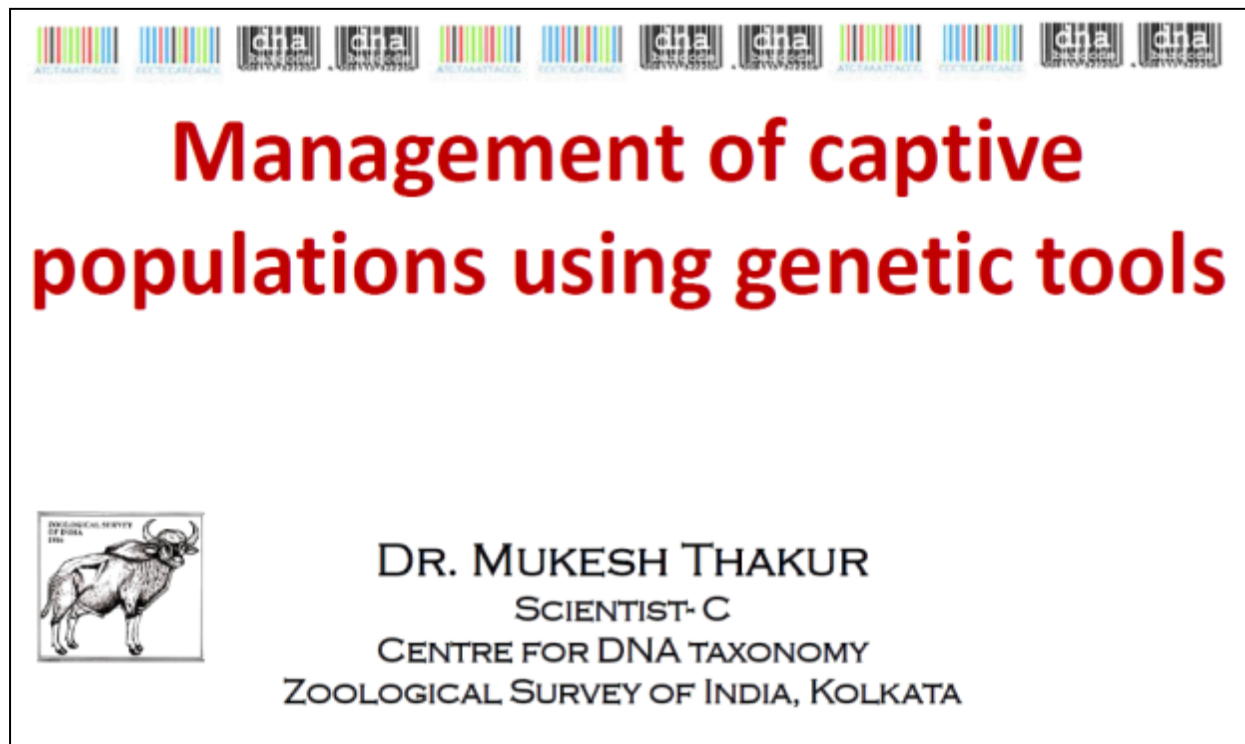
Day 2 (March 22, 2018)

Presentation 3: Management of captive population using genetic tools

Mukesh Thakur, Zoological Survey of India

In the era of Anthropocene, the species extinction rates have increased tremendously. We have lost many species from the earth, and many more are on the verge of extinction due to habitat loss, hunting, and climate change. The captive populations of wild animals support in-situ conservation in many ways – conservation education, fundraising, and supplementation or restoration of wild populations. They also serve as the ultimate insurance against the final loss of a species as in case of Hawaiian crow, Pere David's deer,

Przewalski's horse, and several other species. The relative emphasis on these various roles for captive populations has been evolving, and there has been a debate about how well and in what circumstances captive populations can serve these roles. Importantly, however, proper genetic management is a prerequisite for any of these conservation goals of captive populations to be achieved.



Dr. Mukesh Thakur has worked on the genetic assessment of captive populations of red jungle fowl, cheer pheasant and western tragopan in India, and he shared some of his research findings with the participants. According to Dr. Thakur, the use of genetic tools in captive population management is necessary, especially in case of Asian big cat species, as previous studies have reported errors in studbook records of these species. Studbook records are used for the selection of candidates for breeding programs and thus can significantly affect the success of the planned breeding program. Only with the use of genetic tools, studbook records can be rectified. Candidates with high genetic diversity and pure genetic lineage are preferred for conservation breeding. Under the project titled, “Conservation of Red Jungle Fowl in India”, Dr. Thakur sampled four zoos (Kufri, Gopalpur, Morni, and Delhi) populations of red jungle fowl in India and assessed their genetic diversity using microsatellite markers to identify most potential individuals for future conservation breeding programs. Based on his research, he identified and recommended ten red jungle fowl individual to zoo authorities. Similarly, he studied the genetic diversity of the captive population of cheer pheasant and western tragopan in

Himachal Pradesh, India. There was a paucity of information regarding the origin of the founder individuals, their genetic composition and the extent of inbreeding, which often constraints conservation breeding in achieving the goals of ex-situ conservation programs. Based on microsatellite data analysis, the managerial queries were addressed and studbook data on genetic diversity indices were corrected.

Presentation 3: Geographic assignment of Bengal tiger seizures using genetic tools

Sujeet Kumar Singh. Wildlife Institute of India



Tigers are endangered in the wild and face increasing threats from habitat loss and fragmentation. The majority of their range occurs in the Indian subcontinent, which is, therefore, a critical area for tiger conservation. Bengal tigers are distributed across many small-protected areas in India. Dr. Singh studied two important Bengal tiger landscapes - Terai Arc Landscape (TAL) and Sundarbans in India and shared some of his research findings with the participants. He studied the genetic vigor of TAL and Sundarbans tiger population to address the impact of anthropogenic pressure and climate change on the genetic makeup to identify conservation units. He employed nuclear and mitochondrial genetic markers on TAL and Sundarbans ti

ger individuals. Thirty-nine heterologous microsatellite loci were screened on Bengal tigers, and thirteen of these loci were selected to genotype Bengal tiger samples from western TAL (WTAL) and Sundarbans. He genotyped seventy-one Bengal tiger individuals from WTAL and found the cryptic population genetic structure, moderate gene flow and asymmetric migration among the subpopulation. Genetic diversity was found moderate, and there were no signs of population bottlenecks.



Dr. Singh sharing his research findings with the workshop participants

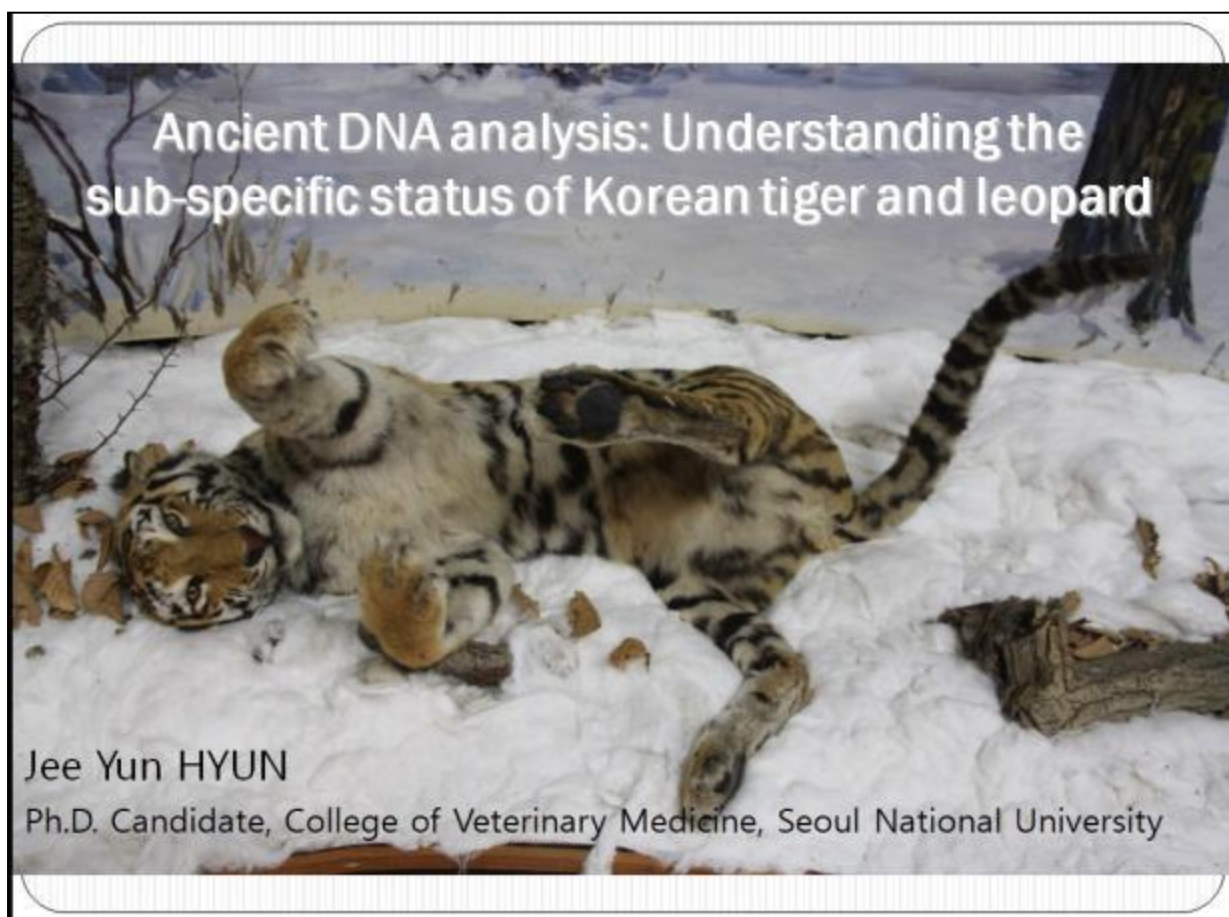
According to Dr. Singh, relocation of villages is necessary to maintain the connectivity of subpopulations and to avoid human-wildlife conflict. Preventive measures against habitat encroachment and a ban on sand and boulder mining in the corridor area should also be implemented.

Sunderbans is a unique tiger landscape, i.e., mangrove forest and the tigers of Sunderbans are considered genetically distinct from mainland Bengal tigers due to body size differences. Dr. Singh analyzed noninvasively collected tiger samples from Sunderbans for mitochondrial and microsatellite markers and compared with the mainland (northern and peninsular) Bengal tiger populations in India. The findings of Dr. Singh's research suggested that the tigers of Sunderbans are genetically distinct and had lower genetic variation in

comparison to other mainland tiger populations. The demographic analysis indicated that the tigers of Sunderbans isolated from the mainland in recent history (600-800 years ago). According to Dr. Singh, genetic isolation from the mainland tiger population and adaptation to the mangrove ecosystem might have jointly shaped the genetic architecture of the Sunderbans tiger. Hence, the Sunderbans tiger needs special conservation attention for the preservation of its unique ability to adapt and for its genetic individuality. In the article published in 2015 in PLoS ONE, he suggested the Sunderbans tiger population should be managed as an evolutionary significant unit (ESU) under the adaptive evolutionary conservation (AEC) criteria.

Presentation: 4 Ancient DNA analysis: Understanding the sub-specific status of Korean tiger and leopard

JeeyunHyun, Seoul National University



In her presentation, Ms. Hyeun shared her experiences of working with the ancient DNA. Ancient DNA is DNA from old samples and includes museum specimens such as skull, bone, and leather. The museum samples are good to study the historical populations of a species to understand past and extant genetic diversity and divergence. However, working

with museum samples is a tedious task as these samples yield poor quality and fragmented DNA due to the application of the preservatives. In addition, these samples suffer from potential contamination of human DNA, as many people could have handled them without wearing the gloves.



Ms. Hyun sharing her tiger ancient DNA genetic research finding with audience

According to Ms. Hyun, the tigers and leopards have once lived throughout the Korean peninsula, but are now extinct. In Korea, the tiger and the leopard are not distinguished from each other, and they are called as 'Bum.' Even though the biological entities of tiger disappeared in Korea, the symbolic tiger remains, influencing the lives and spirit of Koreans, both consciously and unconsciously. There has been a debate about whether Korean tiger is an independent subspecies (*Pantheratigriscoreensis*) or not, because of morphological character. Similarly, some researchers in the past have argued the taxonomic status of Korean leopards suggesting it as a distinct subspecies. Ms. Hyun collected the museum samples of known Korean tigers and leopards from USA, Japan, and Korea. She successfully extracted DNA and amplified the mitochondrial genes to understand their

phylogeny. Her findings suggested that Korean tigers are the same subspecies as Amur tiger and Korean leopard are similar to Amur leopard. The findings of her research has raised the hope of tiger and leopard restoration in Korean Peninsula through facilitated movement of Amur tigers and leopards from Russia Far East.

Presentation 5: Participation in Asian Big Cats' Conservation Genetic Project – Scope and extend of collaboration

Hang Lee, Professor, Seoul National University



Prof. Lee begins his presentation with a word of appreciation to all the resource persons and organizers. He also thanked the participants for attending the workshop. In his presentation, Prof. Lee briefly explained about the “conservation genetics”. According to him, the term conservation genetics is composed of two words, i.e., conservation biology and genetics. Conservation biology is the branch of biology that deals with the threats to biodiversity and when genetic tools are used to assess and address such threats, the discipline is called conservation genetics. Conservation genetics is a linking field between field biology and laboratory work and is helpful in solving population problems that could not be solved by

the traditional ecological research such as effective population size, population size structure, population history, gene flow, etc. Understanding of these parameters is crucial in formulating an effective population management strategy.



Prof. Lee interacting with workshop participants during the workshop

He further explained to participants that the field of conservation genetics has two main branches - phylogenetics (a study of evolutionary relationship) and population genetics (a study of population genetic parameters). For population genetics research, scientist mostly uses microsatellite markers as they are co-dominantly inherited, polymorphic, hypervariable, and are easy to apply. Microsatellites are used to develop genetic fingerprint of an individual, or a population. There exist many microsatellite regions in the genome of species. According to Prof. Lee, for big cat's genetics, different research groups are using different sets of markers. This has led to development of incompatible genetic datasets for a species across the range. If pooled, such data has no or minimal utility in assessing the species conservation status or planning conservation policy at a landscape level.

Further, he introduced the participants to his ongoing India – Korea cooperative research project titled, “Asian Big Cats’ Conservation through Technology Sharing and Use

of Unified DNA typing methodology.” This project is supported by Ministry of Environment, Republic of Korea and the Secretariat of the Convention on the Biological Diversity (CBD) under the Bio-bridge Initiative. The project was conceived to share the unified DNA typing methodology developed for Asian big cat species by researchers of India and Korea. He invited all participants to join the project and assuring that the project will provide necessary resource and expertise to adapt to unified DNA typing methodology. At the end of the presentation, many participants asked questions regarding participation in the project and Prof. Lee address all queries efficiently.

Laboratory sessions (Day 1 and 2 i.e. March 21-22, 2018)

The three days workshop included the laboratory sessions to familiarize and train workshop participants on different aspects of conservation genetics tools and techniques. Five laboratory exercises were planned during the workshop to cover DNA extraction from fecal samples, PCR (polymerase chain reaction), gel electrophoresis to evaluate the quality and quantity of extracted DNA and PCR products, and sample preparation for the microsatellite or fragment analysis. A team of technical experts from India and Republic of Korea coordinated these sessions. Before every laboratory exercise, the resource person in charge of the session made a small presentation so that the participants can understand the techniques’ concept and principal.



Prof. Pandey explaining the process of extracting DNA to participants



Participants processing scat samples for DNA extraction – scrapping the outer layer of faecal samples to collect intestinal epithelial cells



Resource persons assisting the participants in scat sample processing



DNA extraction exercise (cont.)



Prof. Pandey discussing the basics of PCR with participants



Participants during lecture session before laboratory experiments

The first laboratory session was on the DNA extraction from noninvasive samples. Ms. Kyungen Lee from Seoul National University explained to the participants that the noninvasive sampling techniques are mostly employed to study the genetics of Asian big cat species, as they are endangered, elusive, nocturnal, and ferocious. Scat or a feces is most commonly used noninvasive sample type. The outer surface of the scat sample contains intestinal epithelial cells of the species. During the workshop, the participants were trained to extract DNA from scat samples. Participants were provided with scat samples and they scrapped the outer layer of scat sample to extract DNA. Resource persons supervised the whole exercise.

The second laboratory session was planned on day 2 and was on agarose gel electrophoresis. Before the start of the laboratory, Mr. Daecheol Jong, a researcher from Seoul National University made a small presentation about agarose gel electrophoresis. In the presentation, he explained the basic concept and principal of agarose gel electrophoresis. According to him, in electrophoresis, the separation of DNA is by charge and pore size. DNA being negatively charge move from cathode to the anode. The small DNA molecule moves faster compare to large molecules as they can pass quickly through gel mesh. He also discussed the safety measures and troubleshooting exercise during the presentation. Post

presentation, participants did agarose gel electrophoresis to check the quantity and quality of DNA extracted by them from scat samples.



Mr. Jeol explaining the participant about electrophoresis



Agarose gel electrophoresis – evaluating the quality of scat DNA

After agarose gel electrophoresis, Prof. Pandey briefly introduced the basic concepts, components and applications of polymerase chain reaction (PCR). During the session, the participants were provided PCR reagents, and they set PCR reaction for microsatellite markers using extracted scat DNA. Dr. Singh and Dr. Thakur assisted the participants during PCR exercise. After PCR, the participants checked the PCR products using agarose gel electrophoresis to verify PCR amplification success.

In the last laboratory session, Dr. Singh and Dr. Thakur discussed the concept and process of fragment analysis. They explained the difference between DNA sequencing and fragment analysis. In fragment analysis, the researchers look for base pair change in different sample and not the composition of DNA like in DNA sequencing. In the past, fragment analysis was undertaken using polyacrylamide gel electrophoresis (PAGE). Now days automated capillary electrophoresis instruments are used for the separation of fragments as they can provide resolution up to 0.5 DNA base. During fragment analysis, the amplified PCR products are first denatured and are then resolved using the capillary electrophoresis based automated genetic analyzers. During the laboratory session, the participants were demonstrated the process of denaturation. The resource persons also explained the role of different reagents used during fragment analysis such as Hi-D-Formamide and size marker (LIZ).

Technical session (Day 3)

Introduction to microsatellite data analysis and hands on training on genetic software

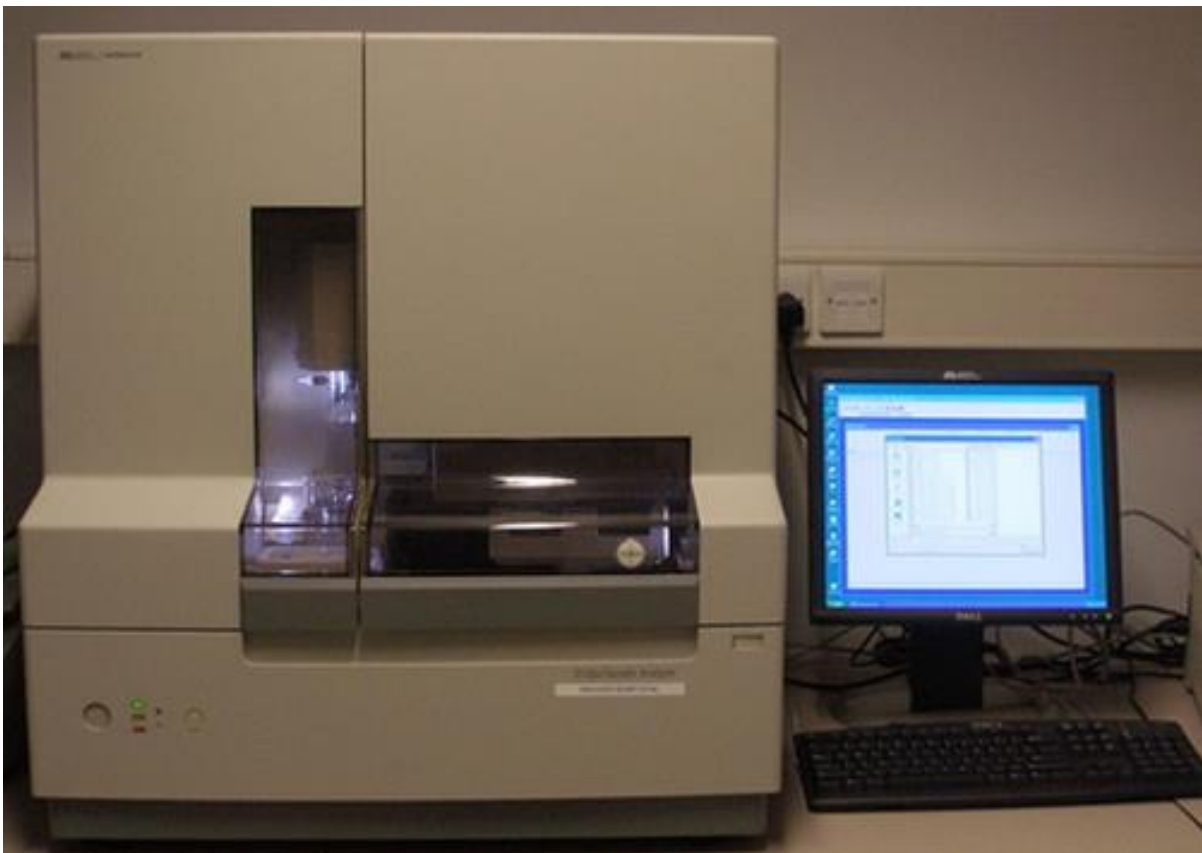
Dr. Mukesh Thakur and Dr. Sujeet Kumar Singh

Microsatellites have been popular molecular markers ever since their advent in the late eighties. Despite growing competition from new genotyping and sequencing techniques, the use of these versatile and cost-effective markers continues to increase, boosted by successive technical advances. In wildlife sciences, microsatellite markers are used for DNA fingerprinting (individual identification), population estimation, and for the assessment of genetic diversity and gene flow.

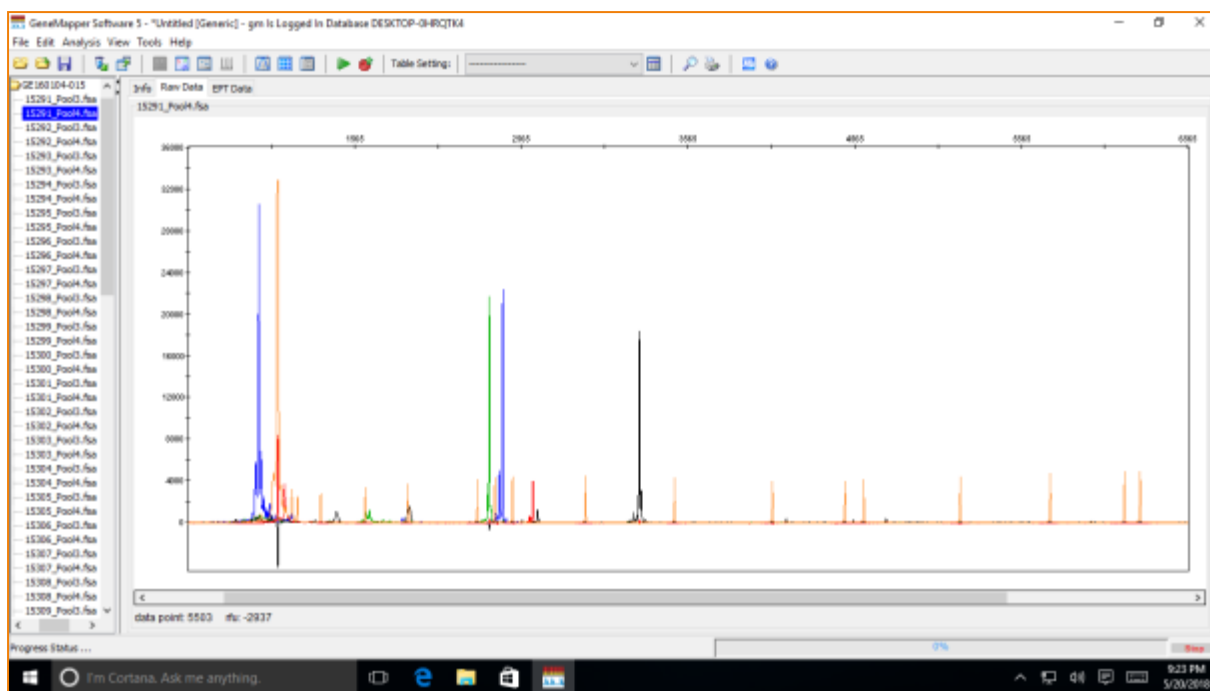
During the session, Dr. Thakur and Dr. Singh discussed the technical aspects of microsatellite data. According to them, in past microsatellite polymorphism was evaluated using polyacrylamide gel electrophoresis (PAGE). However, the PAGE is now replaced with more technically advanced capillary electrophoresis based genetic analyzers as the later has better resolution and reproducibility.



Dr. Thakur explaining participants about microsatellite data analysis



Genetic analyzer (ABI 3130, Applied Biosystems) used to check the polymorphism of microsatellite markers (source: internet)



Analysis of genetic data (microsatellites) out using GENEMAPPER software

Further explaining to participants, the resource persons informed that the microsatellite primers are required to be fluorescently labeled (forward primer) for the detection using automated genetic analyzers. The most common dye matrix used is G5, which offers labeling of primers with four colors, i.e., 6-FAM (blue), VIC (green), NED (yellow), and PET (red). For the analysis of the output of genetic analyzer requires specialized software such as GENEMAPPER or GENEMARKER. These software's help in the scoring of product size and the numerical values once scored are subsequently exported to excel file for further genetic analysis.

During the session, participants were introduced to different genetic analysis software used to estimate genetic indexes such as the number of alleles, heterozygosity, gene flow (F_{ST}) and inbreeding coefficient (F_{IS}), etc. Some of the participants requested the session organizers to brief about phylogenetic analysis. Dr. Thakur and Dr. Singh then explained about DNA sequencing, NCBI, and construction of phylogenetic trees. At the end of the session, the participants were provided with e-copy of the resource material.

Session on biological sample preservation and storage

Dr. Mukesh Thakur and Dr. Sujeet Kumar Singh

One of the biggest challenges faced by wildlife geneticist is the access of biological samples from wild populations of endangered species. Several speakers repeatedly mentioned the same during the workshop. Noninvasive samples such as scats (or feces), hairs, etc. are most commonly used in wildlife genetic studies. However, the PCR amplification success

with these sample types is not efficient as the samples yield very small quantity of target species DNA and DNA extracted is mostly degraded with many PCR inhibitors, especially with scat or feces samples.

During the session, Dr. Thakur and Dr. Singh explained participants about the need of proper sample storage as improper sample storage might further degrade the DNA, affecting the PCR success. It was told to participants that the fecal samples are broadly stored in two ways – dry storage and wet storage. In the dry storage, the field collected scat samples are dried (if wet or fresh) either in the sun or hot air oven and then stored in plastic bag or container containing silica gel. Silica gel removes moisture from the storage container. Wet storage protocol is followed for fresh samples as they contain much moisture, which can contribute to further degradation of DNA due to microbial action. In wet storage, samples are stored in ethanol in a sealed plastic container. Though DNA preservation is better with wet storage, researchers still prefer dry storage as it is more convenient considering the field conditions. Further, the session coordinators informed the participants that the remotely collected hair samples can be stored in plastic bags or tubes but must be stored at a cool temperature as the root portion of the hair samples contains some tissue which could get easily degraded if not preserved well.

Concluding session (Day 3: March 23, 2018)

The three day long CBD sponsored Asian big cat's conservation genetics workshop concluded on the evening of March 23, 2018. The concluding session was chaired by eminent forest officer Dr. Anmol Kumar (former Director General of Forest Survey of India) and was facilitated by Prof. Pandey. The session began with a word of thanks and appreciation for distinguished guests, resource persons, volunteers, and participants by Prof. Pandey for their guidance, support, and active participation. Prof. Pandey also thanked the funding agencies and management of Seoul National University and Amity University. Prof. Lee told participants that he hoped the customized training modules must have helped the workshop participants in understanding the concept and application of genetics in conservation. Speaking on occasion, Dr. Kumar asked participants whether they have now recognized the importance of molecular tools in wildlife conservation. Dr. Kumar thanked the organizers for organizing such customized training workshops, and he hoped that such activities would

continue in future. Dr. Kumar also advised the participants to make maximum use of techniques they learned during the workshop.

During the concluding session, Dr. Kumar gave the souvenirs and certificate to resource persons and participants.

6. Conclusion

This workshop was organized with an aim to develop the capacities of scientists, faculties, and researchers of the regional wildlife institutions in India and Nepal on the use of genetic tools for the population monitoring of Asian Big Cats. During the workshop, the scientific presentations from subject experts, technical sessions, and practical exercises were organized to achieve the goals. The scientific presentations from subject experts covered the most of the topics related to conservation genetics ranging from DNA fingerprinting, captive population management, ancient DNA analysis, ongoing genetic research on tigers in India and extant technological challenges faced, etc. The technical sessions were designed considering the background and needs of the participants. During the technical session, all aspects of sample preservation and data analysis were discussed. The five practical or laboratory sessions organized during the workshop equipped the participants to undertake genetic research independently in future.

During the concluding session, the participants were provided with the feedback form to understand how well the workshop was organized and whether the workshop format was better to meet the participants' expectations. In the feedback form, the participants were asked a total of fourteen questions (Annexure D) ranging from overall arrangement of the workshop, module content, and training/teaching techniques, and knowledge of the resource person.

The participants were positive in their feedback (Annexure E); the workshop met its objectives. About 96% of the participants considered overall arrangement of the workshop were good to excellent and the content of the workshop appropriate. The workshop venue was rated excellent by 59% participants whereas 33% considered it good considering the infrastructure and logistic arrangements. The participants were found fully satisfied with the hands-on practical sessions as most of them (89%) rated it as good and excellent. Similarly, 96% considered teaching/training techniques were appropriate. All the participants considered resource persons knowledgeable and rated them from good (11.54%) to excellent (88.46%). When asked whether the knowledge gained in the workshop will be useful in their future work, 92% responded positively (good to excellent).

7. Annexure

- A. Workshop flyer
- B. Workshop schedule
- C. List of workshop participants.
- D. Participants feed-back form and analysis
- E. Participants feedback analysis



Asian Big Cats' Conservation Genetics Workshop

Organized by:

Seoul National University College of Veterinary Medicine, Seoul, Republic of Korea
Amity Institute of Forestry and Wildlife, Amity University, India

Supported by:

Secretariat of the Convention on Biological Diversity (CBD), Montreal, Canada
Ministry of Environment, Republic of Korea
Tiger and Leopard Conservation Fund in Korea, Republic of Korea

Venue and dates: Amity Institute of Forestry and Wildlife, Amity University Uttar Pradesh Campus,
Sector 125, Noida, Uttar Pradesh, India **(March 21-23, 2018)**

Workshop topics:

- ❖ Basics of DNA extraction from blood, tissue, scat, hair, and bone samples.
- ❖ Basics of PCR and electrophoresis.
- ❖ Basics of DNA sequencing and fragment analysis.
- ❖ Introduction to phylogenetics.
- ❖ Introduction to the microsatellite markers and their applications in wildlife conservation.
- ❖ Introduction to microsatellite data analysis
- ❖ Hands on training on basic genetic software.
- ❖ Introduction to sampling design and hands on training on GIS software.

Target group:

Researchers from scientific institutions, universities, and NGO engaged in Asian big cats' conservation programs

Application deadline: March 19, 2018

For further correspondence:

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Amity Institute of Forestry and Wildlife, Amity University,
Sector 125, Noida, Uttar Pradesh – 201013
Email: ppandey3@amity.edu
Ph: +91-7838293037

Provisional Agenda

Asian Big Cats' Conservation Genetics Workshop
Amity University (Noida, Uttar Pradesh)
21st to 23rd March 2018

Wednesday, 21 March 2018 (Venue: C-Block Auditorium)	
10:30 AM – 11:00 AM	Registration and Networking/Tea
Inaugural session	
11:00 AM – 11:10 AM	Invocation and welcome address by <i>Dr. NPS Chauhan, Amity Institute of Forestry and Wildlife (AIFW), Amity University</i>
11:10 AM – 11:20 AM	Presentation on Amity
11:20 AM – 11:35 AM	Theme of the workshop by <i>Dr. Hang Lee, Professor, Seoul National University</i>
11:35 AM – 11:40 AM	Address by <i>Dr. Balvinder Shukla, Vice Chancellor, Amity University Uttar Pradesh</i>
11:40 AM – 11:50 AM	Few thoughts by <i>Dr. Ashok K. Chauhan, Founder President, Ritnand Balved Education Foundation</i>
11:50 AM – 11:55 AM	Address by Guest of Honour <i>Dr. S.P. Goyal, Emeritus Scientist, Wildlife Institute of India</i>
11:55 AM – 12:05 PM	Inaugural Address by Chief Guest <i>Dr. Anmol Kumar, Former Director General, Forest Survey of India</i>
12:05 PM – 12:10 PM	Vote of Thanks by <i>Puneet Pandey, Amity Institute of Forestry and Wildlife (AIFW), Amity University</i>
12:10 PM – 12:40 PM	Group Photo and Hi Tea
12:40 PM – 01:20 PM	Plenary Talk by <i>Dr. S.P. Goyal, Emeritus Scientist, Wildlife Institute of India</i>
01:20 PM – 01:35 PM	Discussion
01:35 – 02:30 PM	Lunch
<u>Technical session I</u>	
02:30 PM – 03:00 PM	Introduction to phylogenetics and population genetics by <i>Dr. Mukesh Thakur, Zoological Survey of India</i>

03:00 PM – 03:30 PM	Introduction to DNA fingerprinting by <i>Puneet Pandey, Amity Institute of Forestry and Wildlife</i>
03:30 PM – 03:40 PM	Discussion
03:40 PM – 03:50 PM	Tea/Coffee break
<u>Laboratory session I</u>	
03:50 PM – 04:10 PM	Basics of DNA extraction by <i>Kyueneun Lee, Seoul National University</i>
04:10 PM – 05:20 PM	Experimental exercise I: DNA extraction from feces
05:20 PM – 05:30 PM	Discussion
End of the day 1	
Thursday, 22 March 2018 (Venue F3 Room No 101)	
<u>Laboratory session II</u>	
09:00 AM – 10:00 AM	Experimental exercise I : DNA extraction from feces (cont.)
10:00 AM – 10:20 AM	Basics of Agarose gel electrophoresis by <i>Daecheol Jeong, Seoul National University</i>
10:20 AM – 10:45 AM	Experimental exercise II: Agarose gel electrophoresis (visualization of fecal DNA)
10:45 – 11:00 AM	Discussion
11:00 AM – 11:15 AM	Tea/Coffee break
11:15 AM – 11:35 AM	Basics of PCR by <i>Puneet Pandey, Amity Institute of Forestry and Wildlife</i>
11:35 AM – 12:35 PM	Experimental exercise III: Polymerase Chain Reaction (Microsatellites)
12:35 PM – 12:50 PM	Discussion
12:50 PM – 01:50 PM	Lunch
<u>Technical session II</u>	
01:50 PM – 02:20 AM	Management of captive populations using genetic tools by <i>Dr. Mukesh Thakur, Zoological Survey of India</i>
02:20 PM – 02:50 PM	Geographic assignment of Bengal tiger seizures using genetic tools by <i>Dr. Sujeet Kumar Singh, Wildlife Institute of India</i>
02:50 PM – 03:20 PM	Ancient DNA analysis: Understanding the sub-specific status of Korean tiger and leopard by <i>Jeeyun Hyun, Seoul National University</i>
03:20 PM – 03:40 PM	Participation in Asian Big Cats' Conservation Genetic Project – Scope

	and extend of collaboration by <i>Prof. Hang Lee, Professor, Seoul National University</i>
03:40 PM – 03:55 PM	Discussion
03:55 PM – 04:10 PM	Tea/Coffee break
04:10 PM – 04:45 PM	Laboratory exercise IV – Evaluation of PCR product using agarose gel electrophoresis
04:45 PM – 05:00 PM	Basics of fragment analysis by <i>Dr. Sujeet Kumar Singh, Wildlife Institute of India</i>
05:00 PM – 05:20 PM	Laboratory exercise V – Sample preparation for fragment analysis
05:20 PM – 5:30 PM	Discussion
Friday, 23 March 2018 (Venue: C Block Auditorium)	
09:00 AM – 10:30 AM	Introduction to Microsatellite data Analysis by <i>Dr. Mukesh Thakur (Zoological Survey of India) and Dr. Sujeet Kumar Singh (Wildlife Institute of India)</i>
10:30 AM – 10:45 AM	Tea/Coffee break
10:45 AM – 11:30 AM	Hands on training on basic genetic softwares by <i>Dr. Sujeet Kumar Singh (Wildlife Institute of India) and Dr. Mukesh Thakur (Zoological Survey of India)</i>
13:30 PM – 14:30 PM	Lunch Break
14:30 PM – 14:50 PM	Session on biological sample preservation and storage by <i>Dr. Sujeet Kumar Singh (Wildlife Institute of India) and Dr. Mukesh Thakur (Zoological Survey of India)</i>
14:50 PM – 15:20 PM	Participants feedback
15:20 PM – 15:30 PM	Tea/Coffee break
15:30 PM – 17:00 PM	Valedictory function and distribution of certificates
17:00 PM	Hi-Tea

List of participants

S. No.	Name	Address	Participating as
1.	Prof. Hang Lee	Professor, College of Veterinary Medicine, Seoul National University, Republic of Korea	Organizer
2.	Puneet Pandey	Assistant Professor, Amity Institute of Forestry and Wildlife, Amity University, Noida, Uttar Pradesh, India	Organizer
3.	Dr. Anmol Kumar (IFS Retd.)	Former Director General, Forest Survey of India, Dehradun, Uttarakhand, India	Guest
4.	Dr. S.P. Goyal	Emeritus Scientist, Wildlife Institute of India, Dehradun, Uttarakhand, India	Guest
5.	Dr. Kailash Chandra*	Scientist G and Director, Zoological Survey of India, Kolkata, India	Guest
6.	Dr. D.N. Singh*	Member Secretary, Central Zoo Authority, New Delhi	Guest
7.	Dr. Mukesh Thakur	Scientist C, Zoological Survey of India, Kolkata, India	Resource Person
8.	Dr. Sujeet Kumar Singh	Research Biologist, Wildlife Institute of India, Dehradun, Uttarakhand, India	Resource Person
9.	JeeyunHyun	Research Scholar, College of Veterinary Medicine, Seoul National University, Republic of Korea	Resource Person
10.	DaeCheol	Research Scholar, College of Veterinary Medicine, Seoul National University, Republic of Korea	Resource Person
11.	Kyung Eun	Research Scholar, College of Veterinary Medicine, Seoul National University, Republic of Korea	Resource Person
12.	Bidyut Sarania	Research Scholar, Tezpur Central University, Assam, India	Participant
13.	Dr. Ved Prakash Kumar	DST-Young Scientist, Wildlife Institute of India, Dehradun, Uttarakhand, India	Participant
14.	Malay Shukla	Senior Research Fellow, Institute of Forensic Science, Gujarat Forensic Sciences University, Gujarat, India	Participant
15.	Dr. Kuladip Sarma	Post doctoral fellow, Department of Zoology, Guwahati University, Assam,	Participant

		India	
16.	Dr. Deepak Rai	Asst. Professor Department of Zoology, Kurukshetra University, Haryana, India	Participant
17.	DrSumitDookia	Assistant Professor, University School of Environmental Management, Indraprastha University, New Delhi, India	Participant
18.	Dr. Hemant Kumar Sahu	Professor, Department of Zoology, North Orissa University, Orissa, India	Participant
19.	Dr. Hemant Joshi	Assistant Professor, College of Veterinary & Animal Sciences, Navania, Vallabh Nagar, Udaipur, Rajasthan, India	Participant
20.	Dr. HemsinghGehlot	Assistant Professor, Department of Zoology, JN Vyas University, Jodhpur, Rajasthan, India	Participant
21.	Dr Rishi Sharma	Landscape Coordinator, WWF- India, New Delhi	Participant
22.	Lakshit Sharma	IMS University Campus College, Ghaziabad, Uttar Pradesh, India	Participant
23.	Dr. VipinTyagi	University College of Medical Sciences, University of Delhi, New Delhi, India	Participant
24.	Tanya Ambadkar	Research Intern, Wildlife Trust of India, Noida, Uttar Pradesh, India	Participant
25.	Arzan Ali	Research Scholar, Department of Wildlife Sciences, Aligarh Muslim University, Uttar Pradesh, India	Participant
26.	RohitChoudhary	Research Scholar, Department of Wildlife Sciences, Aligarh Muslim University, Uttar Pradesh, India	Participant
27.	S. BalajiNaik	M.Sc. Student, Dr. Y.S. Panwar University of Horticulture & Forestry, Nauni-173230, Solan, Himachal Pradesh, India	Participant
28.	Deepa M.S.	M.Sc. Student, Dr. Y.S. Panwar University of Horticulture & Forestry, Nauni-173230, Solan, Himachal Pradesh, India	Participant
29.	Sheetal Rana	M.Sc. Student, Dr. Y.S. Panwar University of Horticulture & Forestry, Nauni-173230, Solan, Himachal Pradesh, India	Participant
30.	ShudhantaSood	Assistant Program Coordinator, Wildlife Trust of India, Noida, Uttar Pradesh, India	Participant
31.	Rohit Sharma	M.Sc. Student, Dr. Y.S. Panwar University of Horticulture & Forestry, Nauni-173230, Solan, Himachal Pradesh, India	Participant
32.	AkshayPingale	M.Sc. Student,	Participant

		Dr. Y.S. Panwar University of Horticulture & Forestry, Nauni-173230, Solan, Himachal Pradesh, India	
33.	Tahim Ali	Research Scholar, Department of Wildlife Sciences, Aligarh Muslim University, Uttar Pradesh, India	Participant
34.	BalramAwasthi	Lecturer, TribhuvanUnivesity, Siddhanath Science Campus, Nepal	Participant
35.	Subham	M.Sc. Student, Amity Institute of Forensic Science, Amity University, Noida, Uttar Pradesh, India	Participant
36.	AkangkshyaPriya Gogoi	M.Sc. Student, Amity Institute of Forestry and Wildlife, Amity University, Noida, Uttar Pradesh, India	Participant
37.	JatinMathur	M.Sc. Student, Amity Institute of Forestry and Wildlife, Amity University, Noida, Uttar Pradesh, India	Participant
38.	Ridhima Sharma	M.Sc. Student, Amity Institute of Forestry and Wildlife, Amity University, Noida, Uttar Pradesh, India	Participant
39.	Ananta Ana Tigga	M.Sc. Student, Amity Institute of Forestry and Wildlife, Amity University, Noida, Uttar Pradesh, India	Participant
40.	GujjaHarshavardhan	M.Sc. Student, Amity Institute of Forestry and Wildlife, Amity University, Noida, Uttar Pradesh, India	Participant
41.	Fatima Jabeen	M.Sc. Student, Amity Institute of Forestry and Wildlife, Amity University, Noida, Uttar Pradesh, India	Participant
42.	Saurav Chaudhary	M.Sc. Student, Amity Institute of Forestry and Wildlife, Amity University, Noida, Uttar Pradesh, India	Participant
43.	Pal MamtaRamshankar	M.Sc. Student, Amity Institute of Forestry and Wildlife, Amity University, Noida, Uttar Pradesh, India	Participant
44.	M. Baskaran	M.Sc. Student, Amity Institute of Forestry and Wildlife, Amity University, Noida, Uttar Pradesh, India	Participant
45.	Mansi Gaur	M.Sc. Student, Amity Institute of Forestry and Wildlife,	Participant

		Amity University, Noida, Uttar Pradesh, India	
46.	AyushSharan	M.Sc. Student, Amity Institute of Forestry and Wildlife, Amity University, Noida, Uttar Pradesh, India	Participant
47.	Kunal Chauhan	Amity Institute of Virology, Amity University, Noida, Uttar Pradesh, India	Participant
48.	Puneet Singh	Amity Institute of Virology, Amity University, Noida, Uttar Pradesh, India	Participant
49.	Deepak Sahani	Amity Institute of Virology, Amity University, Noida, Uttar Pradesh, India	Participant
50.	Gurpreet Kaur	Amity Institute of Environmental Science, Amity University, Noida, Uttar Pradesh, India	Participant
51.	Vimarsh Sharma	Research Officer, SVSJS Trust, New Delhi	Participant

***not attended**

Asian Big Cats' Conservation Genetics Workshop
Jointly organized by
Amity University (Noida, Uttar Pradesh) and
Seoul National University, Seoul, Republic of Korea

21st to 23rd March 2018

Feedback Form

Your feedback is critical for us to ensure we are meeting your educational needs. We would appreciate if you could take a few minutes to share your opinions with us so we can serve you better.

Please return this form to the instructor or organizer at the end of the workshop. Thank you.

Name of the participant: _____

Institute: _____

Date: _____ **Email Id:** _____

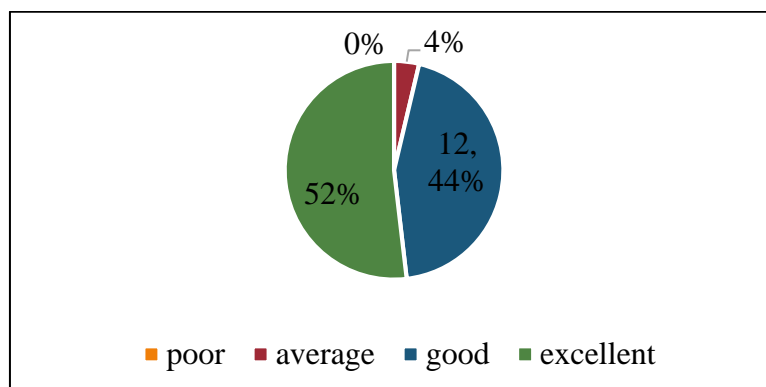
Sr. No.	Remarks	Evaluate us based on your experience: Please tick the appropriate box			
		Poor	Average	Good	Excellent
1.	What is your overall assessment of the event?				
2.	Was the content of workshop appropriate?				
3.	Were you satisfied with hands-on practicals?				
4.	Teaching /training techniques were appropriate?				
5.	Did instructors answer your questions in appropriate way?				
6.	How do you rate knowledge of resource person (s)?				
7.	Knowledge gained in the workshop will be useful to you in future works?				
8.	To what extent were concepts clear after attending the workshop?				
9.	Rate Instructors presentation style				
10.	How do you rate useful visual aids and hand-outs?				
11.	Instructor facilitated interactions among participants well, rate them.				
12.	How do you rate the venue for the workshop?				

13.	How can we improve the existing skills/content of workshop	
14.	Any other comments or suggestions?	

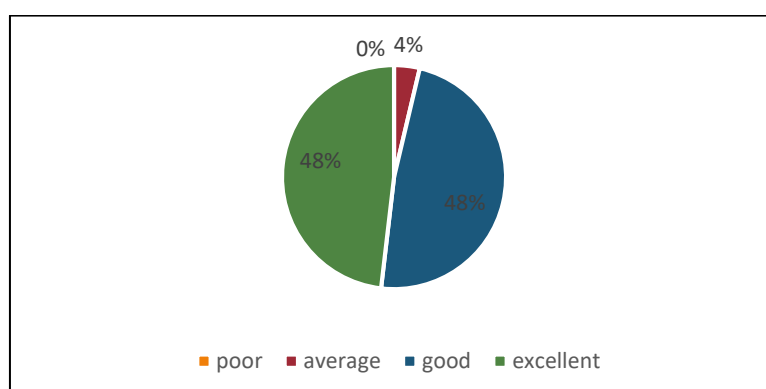
Participants Name/Signature

Participants Feedback Analysis (Total number of responses: 27)

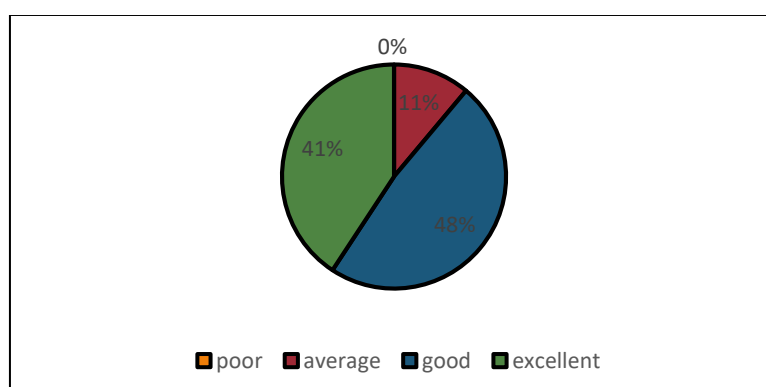
Question 1: What is your overall assessment of the event?



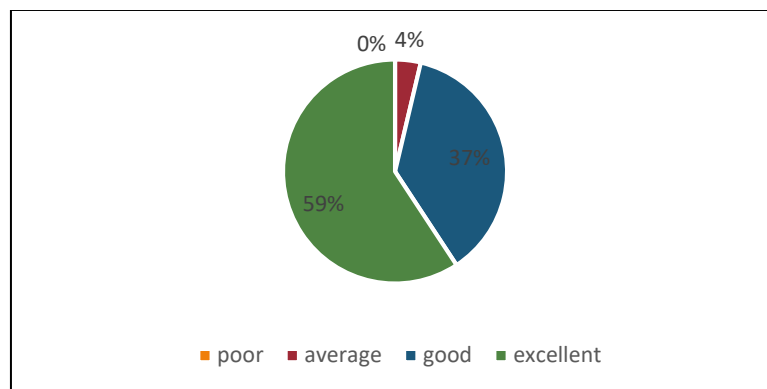
Question 2: Was the content of workshop appropriate?



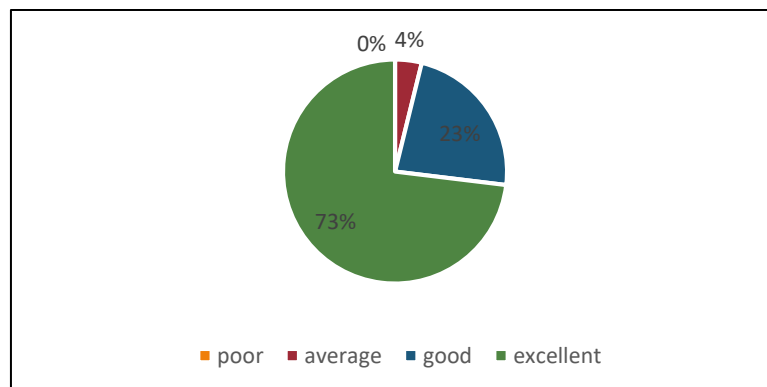
Question 3: Were you satisfied with hands-on practicals?



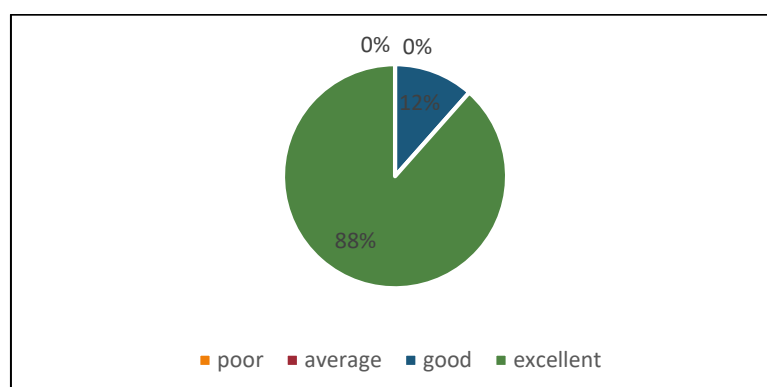
Question 4: Were teaching /training techniques were appropriate?



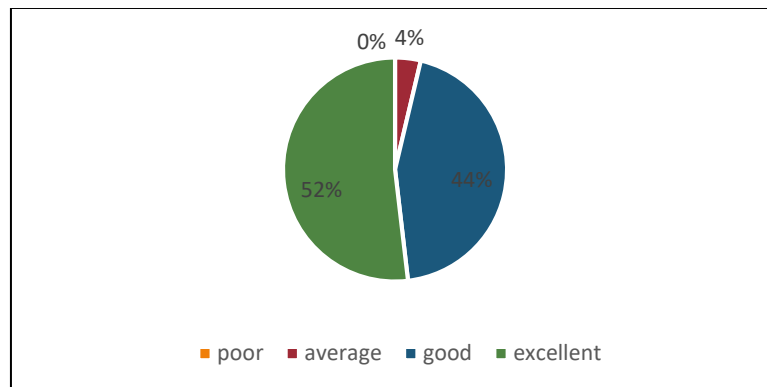
Question 5: Did instructors answer your questions in appropriate way?



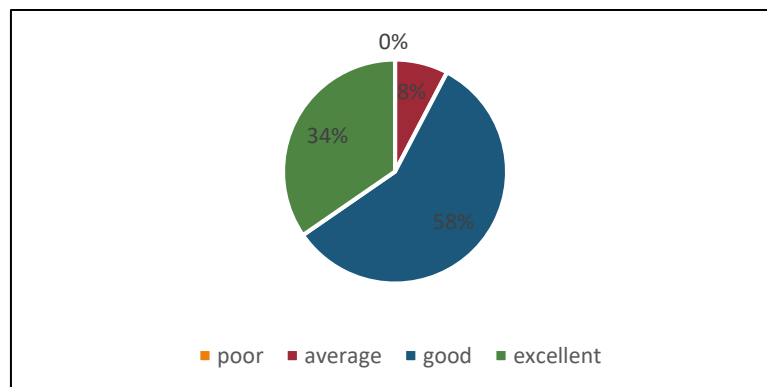
Question 6: How do you rate knowledge of resource person (s)?



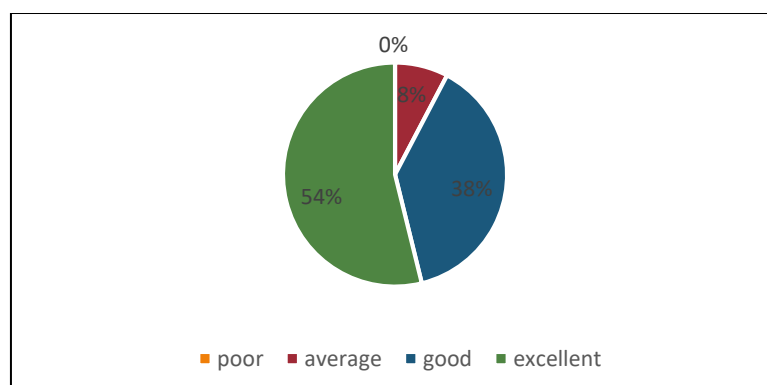
Question 7: Knowledge gained in the workshop will be useful to you in future works.



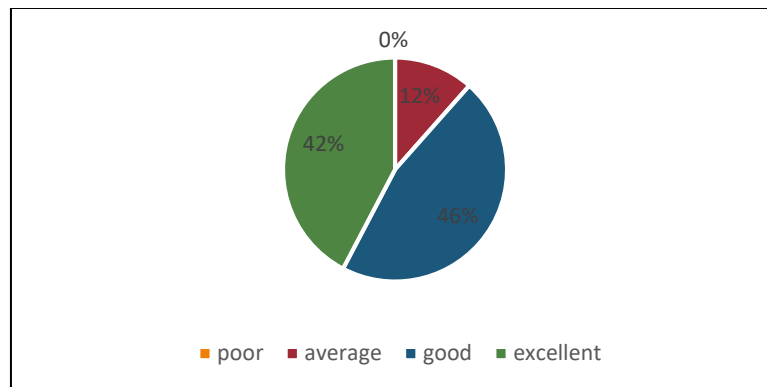
Question 8: To what extent were concepts clear after attending the workshop?



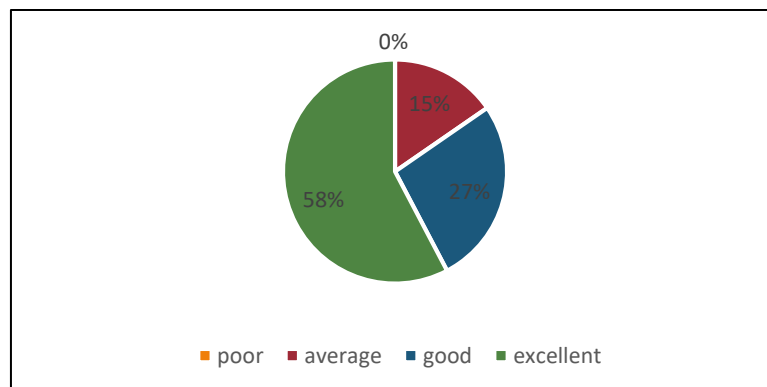
Question 9: Rate instructor's presentation styles?



Question 10: How do you rate useful visual aids and handouts?



Question 11: Instructors facilitated interactions among participants well, rate them.



Question 12: How do you rate the venue for the workshop?

