

Bio-Bridge Initiative Pilot Project Convention on Biological Diversity





National Institute of Biological Resources Republic of Korea







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I. Introduction

Division	Contents		
Titles	Transfer of DNA Barcode Analysis for Biodiversity Monitoring		
Duration	Sept. ~ Dec. 2016	Budget	\$ 42,735
Department	Plant and Animal resources divisions		
Staffs	Total 13 people		
The Results	 12 trainee from Asia for DNA Barcoding Analysis Report from the project Implementation of Strategic plans BD 2011~2020 		



I. Introduction



An Objective and Backgrounds

- ▶ To facilitate technical and scientific cooperation(TSC) among Parties to the CBD and to its Protocols on Cartagena and Nagoya
- ► CBD COP X/39 and COP XI/29 recommended sharing taxonomic tools such as DNA barcoding for identification and analysis of threatened species, invasive alien species, and species subject to illegal trafficking etc.

ABT 9 Invasive alien species/ ABT12 Reducing risk of extinction ABT13 Safeguarding genetic diversity ABT19 Sharing Information and Knowledge





Operation Method :

Collaboration with related divisions of NIBR in aspects which are facilities,
 experts for lectures and training program etc.

< The procedures>

Government employees, experts, and students who investigate biodiversity in Asia region(dispatch e-mail to CBD focal points or related Institutions of Parties) ⇒ trainee confirmation ⇒ financial supporting to participate the program (Sending invitation letters etc.)⇒ the workshop (including Field trips) ⇒ Presentation of outcomes of the workshop (side event in CBD cop13)⇒ A final report





- Priorities to participate the workshop
 - **⇒** Trainee recommended by the CBD focal points of parties
 - ⇒ Trainee have degree of master or Ph.D. in Taxonomy, Ecology and Biology, and Subjects related to Biodiversity etc.
 - People who are officials, experts, students related to Biodiversity works (People who were born since 1975)
 - People have experiences which are Capacity Building Program in Global Taxonomy Initiative
 - ⇒ People from East Asia region(Southeast Asia, Northeast Asia)
 - Asian parties do not relatively have enough taxonomists
 - to build up long term cooperation for technology transfer
 - to solve the Asia-issued common problems with outreach (e.g., CITES-listed species identification)
 - ⇒ Gender balance





▶ 16 people in 12countries ⇒ 12 people in 8 countries







- ▶ Lab experiences from DNA extraction to DNA sequences
- ▶ Roundtable discussions to solve potential obstacles in applying DNA barcoding analysis tools in each party
- Schedule of the workshop:14, Nov.(Mon) ~ 25 Nov.(Fri) 12days
- ▶ Dividing into 2 team
 - Plant and Animal Resources





- Materials for analyses :
 - CITES species, Invasive species Unknown powdery herbal medicines, feces, and hairs without recognizable morphological characteristics
- ► For identifying species which is necessary for:
 - (1) prioritization and management of protected area,
 - (2) agriculture and aquaculture relevant to food security,
 - (3) control and management of invasive alien species,
 - (4) species inventories and monitoring in the ABS era





Date	Date	Activity	Action in detail
1	14(Mon) Nov	- Arrival at the lodge and Registration	
2	15(Tue) Nov	RegistrationOpening ceremony, Lecture(1~3)	Ceremony with President of NIBR
3	16(Wed) Nov	Lecture(4~6)Demonstration of lab works(1 and Discussion	DNA extraction
4	17(Thu) Nov	Demonstration of lab works(2)Discussion	PCR (Polymerase Chain Reaction)
5	18(Fri) Nov	Experiments (participants in person)Discussion	DNA extraction, PCR
6,7	19(Sat], 20(Sun) Nov	 Field trips (other institute related to Biodiversity) 	
8	21(Mon) Nov	Lecture(7~9)Experiments and Discussion	Assembling of sequences
9	22(Tue) Nov	- Field trip (visiting Amore-Pacific)	
10	23(Wed) Nov	Lecture(10~12)Experiments and Discussion	Alignment of sequences, Making NJ tree and Analysis
11	24(Thu) Nov	Experiments and Round table discussionSurvey for participants	Farewell Ceremony with President of NIBR
12	25(Fri) Nov	Closing ceremonyDeparture to each country	













III. Outcomes



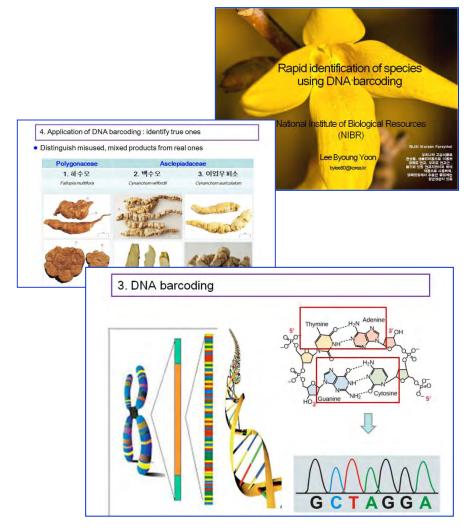


III. Outcomes



Preparation the final report







III. Outcomes



- ► Contribution to Implement Strategic Plan for Bio diversity 2011-2020 and Achievement of Achi Targets in Asia
 - → to make them understand some technologies of species identification using advanced tools
- Many developing countries would be able to monitor and manage their biodiversity
 - → can identify species of interests and unknown species
 - → can enhance capacity building of parties which have high(mega) biodiversity
- ► A gap would be narrowed between developing countries and developed countries in scientific and technical aspects



IV. Consideration of the program



- ➤ So diverse situations of parties
 - knowledge and lab experiences on DNA barcoding
 - experimental facilities and experts
- ▶ One way training is not a good model for BBI
 - transfer technologies to be applicable to recipient parties
 - real support such as lab setting, facilities, expert dispatch
- ► Connection is needed from technology transfer to application
 - Person-based training is good, but institution-based is better for future collaboration
 - More programs will be developed and expanded to narrow technology gaps by triggering





Thank you very much



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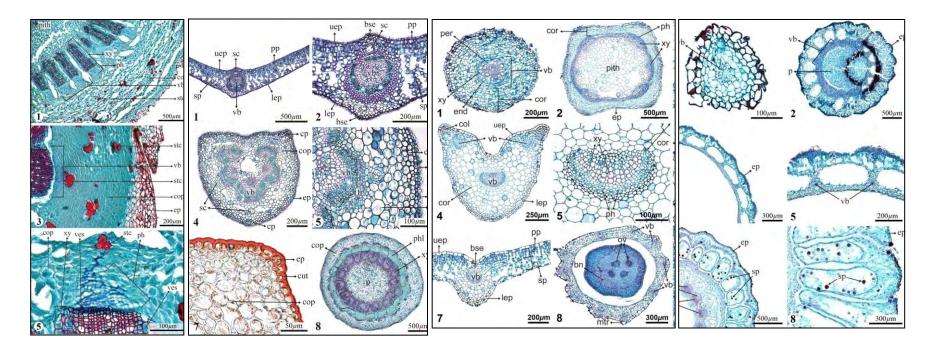
Species identification: morphology

- External morphology
 - Vegetative characters: leaf shape and arrangement (opposite, alternate, simple, compound), stem habit (vine, woody, herbaceous), and etc.
 - Sexual characters: inflorescence, flowers (calyx, petals, stamen, and pistil)
- Taxonomic keys to the genus Bupleurum in Korea
 - 1. cauline leaf narrow, leaf base not covered stems ----- B. falcatum
 - 1. cauline leaf broad, leaf base covered stems
 - 2. bracts and bractlets linear ----- *B. longiradiatum*
 - 2. bracts and bractlets not linear
 - 3. cauline leaf oval to lanceolate, sessile ----- *B. euphorbioides*
 - 3. cauline leaf reniform to ovate, long petiolated ----- B. latissimum

- Terminology is not familiar, not understandable to the public
- No typical form, too many variation of morphology in the Nature

Species identification: anatomy

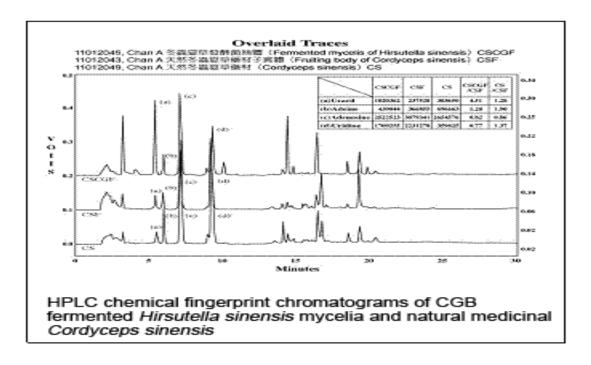
- Anatomical morphology
 - Compare shapes and arrangement of cells, tissues and fibers from cross sections of roots, stems, leaves, petioles, fruits or seeds



- Terminology is not familiar, not understandable to the public
- Good at the genus level, but weak at the species level

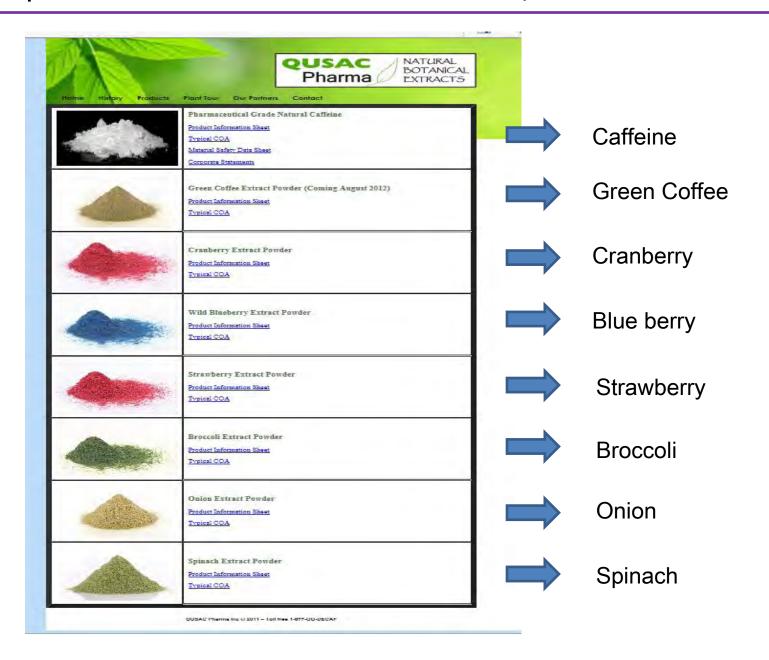
Species identification: chemical fingerprinting

- Chemical taxonomy
 - Classify organisms based on the distribution of natural products;
 chemical extracts in the case of vascular plants



- No quantitative indication is given, presence (traced, big spots) or absence
- Secondary metabolisms are turned on or off by environmental or developmental factors

Species identification: which one is a spinach?



Species identification: Molecule (DNA)

- Molecular phylogenetics
 - Compare homologous sequences for genes using sequence alignment techniques to identify similarity among species

- No quantitative indication is given, presence (traced, big spots) or absence
- Secondary metabolisms are turned on or off by environmental or developmental factors



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Biological identifications through DNA barcodes

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Although much biological research depends upon species diagnoses, taxonomic expertise is collapsing. We are convinced that the sole prospect for a sustainable identification capability lies in the construction of systems that employ DNA sequences as taxon 'barcodes'. We establish that the mitochondrial gene cytochrome c oxidase I (COI) can serve as the core of a global bioidentification system for animals. First, we demonstrate that COI profiles, derived from the low-density sampling of higher taxonomic categories, ordinarily assign newly analysed taxa to the appropriate phylum or order. Second, we demonstrate that species-level assignments can be obtained by creating comprehensive COI profiles. A model COI profile, based upon the analysis of a single individual from each of 200 closely allied species of lepidopterans, was 100% successful in correctly identifying subsequent specimens. When fully developed, a COI identification system will provide a reliable, cost-effective and accessible solution to the current problem of species identification. Its assembly will also generate important new insights into the diversification of life and the rules of molecular evolution.

Keywords: molecular taxonomy; mitochondrial DNA; animals; insects; sequence diversity; evolution

- Universality: same primers to amplify all of specific DNA regions
- High quality of amplified DNA sequences
- Amplified sequences: good enough for species discrimination

4. 반성 및 발전 방안

