3. CAPACITY BUILDING WORKSHOPS

6. ABS Workshop in 2021: Data mining from DNA barcoding research

Name	Counterpart	Title
Iskandar Z. Siregar, Muhammad Majiidu	B14	Data mining on DNA barcode research

Background and Objectives

DNA barcoding is a method used for rapid identification of species using a sequence of bases from an organism's tissue (Kress *et al*., 2002; Lahaye *et al*., 2008). Hajibabaei *et al*. (2007), Meier *et al*. (2006) and Virgilio *et al*. (2012) stated that the process of identifying a molecular scale by DNA barcoding is rapid, accurate, and unambiguous compared to the morphological identification. DNA barcoding requires only a small sample of the specimen taken from all body tissues of the organism. Unfortunately, this method is not yet sufficiently developed in plants compared to animals. The markers commonly used in plants are maturase-K (matK) and *ribulase-1,3-biphosphate carboxylase oxygenase (rbcL)* (Kress *et al*. 2005; Wicke & Quandt 2009). Current technology development based on the 3rd NGS technologies that employ long-read and short read sequences has potentials to improve the traditional DNA barcode analysis. Considering both technologies, we conduct specific activities aimed at: i) building capacity for the use of genomics data for SNPs and microsatellites markers and ii) supporting the finalisation of pending manuscripts on plant DNA barcodes on Fabaceae and Anacardiaceae.

Picture 6. Mini workshop on genomic research, held at IPB University for 14 undergraduate and postgraduate students from IPB University, Bengkulu University and Jambi University.

ABS Workshop

- A mini workshop was conducted at IPB University; it was attended by undergraduate and postgraduate students from IPB University, Bengkulu University and Jambi University (Picture 6).
- The workshop aimed at discussing about genomic research and its applications such as DNA barcode primers design. Dr. Deden Derajat Matra, a lecturer from Agronomy and Horticulture, Faculty of Agriculture, IPB University, was a speaker in this mini workshop. Fourteen students participated in the workshop and were trained to use bioinformatics tools (e. g. Geneous, MASER platform from NIG Japan).

Pemanfaatan marka DNA *barcode* untuk identifikasi spesies dari genus terpilih pada famili Fabaceae

Utilization of DNA barcode markers for species identification in selected genera of Fabaceae

I Quati Ayu Kusuma Wardani[a], Fitri Yola Amandita[b], Iskandar Z Siregar[a]

[a] Tropical Silviculture Study Program, Department of Silviculture, Faculty of Forestry and Environment, Bogor Agricultural University (IPB). Darnaga IPB Campus Bogor, 16680, Indonesia [+62]
[b] Center for Quality Research and Development and Environmental Laboratory, Ministry of Environment and Forestry, Building 210 Center for Science and Technology Research Area, South Tangerang, Indonesia [+62-21-756-3114]

Abstract: *Fabaceae is an invaluable plant family with considerable ecological and economic importance, for example, as food sources, bio-fertilizer, and medicinal plants. However, this plant has been overexploited in Indonesia, thereby critically endangering and the existence of several species belonging to this family. Therefore, it is essential to support the associated conservation efforts provided to ensure the overall survival of this plant family through morphological similarity, rapid and accurate identification of Fabaceae species. Nowadays, species identification through DNA barcoding has become an effective taxonomic classification tool. This study aims to evaluate the effectiveness of chloroplast and combination markers, such as matK, rbcL, and matK+rbcL, as DNA barcodes for identifying selected genera in Fabaceae. The result showed that matK+rbcL, and matK had the highest level of investigated genera identification at 90% and 82.05%, respectively. Additionally, matK had the highest mean of interspecific and intraspecific distances*

Figure 3

Outcome

- Two manuscripts result from this work: one article (Fig. 3) has been accepted by the *Jurnal Pengelolaan Sumber Daya Alam dan Lingkungan*. Another manuscript is in the final stage of preparation.

References

Hajibabaei M, Singer GAC, Clare EL, Hebert. 2007. Design and applicability of DNA arrays and DNA barcodes in biodiversity monitoring. BMC Biology 5(24):1-7.

Kress WJ, Prince LM, Williams KJ. 2002. The phylogeny and a new classification of the gingers (Zingiberaceae): evidence from molecular data. *Journal Bot*. 89: 1682-1696.

Kress WJ, Wurdack KJ, Zimmer EA, Weigt AL, Janzen DH. 2005. Use of DNA barcodes to identify flowering plants. Proc Natl Acad Sci USA. 102(23):8369-8374.

Lahaye R, Vander BM, Bogarin D, Warner J, Pupulin F, Gigot G, Maurin O, Duthoit S, Barraclough TG, Savolainen V. 2008. DNA barcoding the floras of biodiversity hotspots. Proc Natl Acad Sci USA. 105(8):2923-8.

Meier R, Shiyang K, Vaidya G, Peter KL. 2006. DNA barcoding and taxonomy in Diptera: a tale of high intraspecific variability and low identification success. Systematic Biology. 55(5):715-728.

Virgilio M, Jordaens K, Breman F, Barr N, Backeljau T, Meyer MD. 2012. Turning DNA barcodes into an alternative tool for identification: African fruit flies as a model [Internet]. [diunduh 2019 Mar 8]. Tersedia pada: https//www.ippc.int/static/media/files/publications/en/1300372559_POSTE R-deMeyer_KJETT.pdf.

Wicke S, Quandt D. 2009. Universal primers for the amplification or the plastid trnK/matK region in land plants. Anales Jard Bot Madrid. 66(2):285-288.