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The utility of transcriptomics in the conservation of sensitive and economically important species

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The connection between the central dogma of biology [DNA → (Transcription) → RNA → (Translation) → Protein] and the 'omics' resources obtained from each molecule are now being exploited by conservation managers to protect biodiversity and ecosystems for sustainable development. Biodiversity doesn't necessarily mean the total number of species, it is more complex and includes genetic diversity within species and the diversity of habitats. Land-use changes, direct harvest, various forms of pollution, and climate change are the biggest threats to biodiversity, most of which are hardly documented at the molecular level to guide conservation actions and stop extinctions. Justifying the plasticity of species adaptability could ensure informed decisions on proposing suitable habitats for species translocations if the current distributional range is disturbed. The 'omics' resources (especially generated by high-throughput RNA and DNA sequencing approaches) have intervened on a larger scale recently to understand species physiology, evolutionary biology and ecology. This has supported enriched information on the evolution and evaluation of adaptive phenotypes in natural populations as well as the mechanism of physiological responses to various environmental perturbations (Alvarez *et al.*, 2015; De Wit *et al.*, 2015; Evans, 2015; Connon *et al.*, 2018).

Transcriptomics can unravel unparalleled mysteries in the context of conservation of sensitive and economically important species. Being smaller than genomes and tissue-specific, it reduces the amount of data generated and focuses on candidate gene expressions, understanding a species' response to environmental changes. It gives sufficient scope for studying the biology of a non-model species at the molecular level by *de novo* assembled transcript generation and annotation involving predicted gene function. Apart from the ontology and homology-based functional annotations, the transcriptomes can also be mined for the discovery of genetic markers such as simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs) vital for assessments of genetic diversity and exploring species from newer habitats. Ultimately, such resources should be effectively integrated into management decisions and policies to contribute towards conservation. Utilization of transcriptome knowledge in conservation remains rare due to unfamiliarity of the interpretation of complex molecular data for managers. Hence, to overcome such a knowledge divide, the physiologists and the data scientists need to build partnerships with regulatory agencies and resource managers to translate transcriptomic evaluations to well-characterized molecular thresholds that can act as sensible markers to predict a species' adaptive plasticity in invoking compensatory mechanisms leading to recovery or non-recovery. Until and unless such conservative benchmarks are designed, the utility of the transcriptomes into management actions and policies seems debated.

I have been associated with the Korean threatened species initiative for the past eight years as a researcher. The initiative has prioritized the Illumina HiSeq-based short-read platform for transcriptome generation and the Trinity suite for *de novo* assembly of clean reads. Further, a locally-curated database known as the PANM database (Protostome DB) has facilitated gene discovery in Red List molluscan and butterfly species of Korea that are threatened of extinction. Mostly, the transcriptomics pipeline adopted under this initiative has cataloged the functional resources in the context of immunity, growth and reproduction of species. Large-scale screening of SSR markers from transcriptome has highlighted the possibility of addressing species richness and diversity in disturbed natural habitats and the feasibility of finding species in newer habitats. This initiative has provided the first report to record ecologically-relevant traits from

endangered lycaenid butterflies such as *Protantigius superans* and *Spindasis takanosis* and the nymphalid butterfly, *Fabriciana nerippe* (Patnaik *et al.*, 2015; Hwang *et al.*, 2016). Further, the transcriptome profile of the Asian giant hornet, *Vespa mandarinia* was able to screen new genes to understand the physiological attributes of the wasp enlisted as threatened species in Korea (Patnaik *et al.*, 2016). Among the threatened molluscan species of Korea, the land snails such as *Aegista chejuensis* and *Aegista quelpartensis* (Kang *et al.*, 2016), *Koreanohadra kurodana* (Kang *et al.*, 2016), *Satsuma myomphala* (Kang *et al.*, 2017) and *Ellobium chinense* (Kang *et al.*, 2018) were prioritized for transcriptome sequencing. The detailed molecular components ascribed to innate immunity pathways were also screened from the transcriptome of a freshwater mussel, *Cristaria plicata* endangered in Korea (Patnaik *et al.*, 2016) and an air-breathing land slug, *Incilaria fruhstorferi* (Patnaik *et al.*, 2019). The discovery of the immunity components was useful in drafting a conceptual map of innate immune signaling in molluscs by addressing the putative involvement of the orthologs at different stages of pathway. Such resources are vital for functional genomics applications as they serve to understand the resistance or susceptibility of the host to microorganisms. *De novo* transcriptome of endangered triton shell, *Charonia lampas sauliae* identified transcripts that are channel proteins blocked by tetrodotoxin synthesized by symbiotic bacteria inhabiting the shells. Additionally, conotoxin superfamily peptides were discovered that could be synthesized for therapeutic interventions such as anti-cancer and pain-relief agents (Fassio *et al.*, 2019; Yao *et al.*, 2019; Hwang *et al.*, 2021). The transcriptome of endangered diving beetle, *Cybister japonicus* and endangered dung beetle *Copris tripartitus* also enriched information on molecular resources including SSR discovery (Hwang *et al.*, 2018; Hwang *et al.*, 2023). With the large-scale availability of 'omics' resources, the threatened species initiative is taking proactive steps to complement local conservation efforts in the country.

In India, there is a lack of similar consortium-based initiatives for understanding the local biodiversity of a region. This has restricted access to high-throughput molecular resources from the local biodiversity for meeting the challenges in health, agrifood and the environment. Hence, a consortium such as the National Biodiversity Genomics (NBG) consortium addressing the genome or transcriptome-guided discovery of molecular resources can act as a knowledge hub supporting environmental sustainability (Fig. 1). The consortium will be able to develop expertise in database development, bigdata analysis and bioinformatics, genetic diversity analysis and functional genomics resources. The consortium will also facilitate new opportunities in bigdata science, research-academia-industry partnerships for new product development, entrepreneurship, and outreach activities and invoke a forum for collaborations with International genomics consortiums. Such a consortium will keep the academics interested in the research supporting environmental

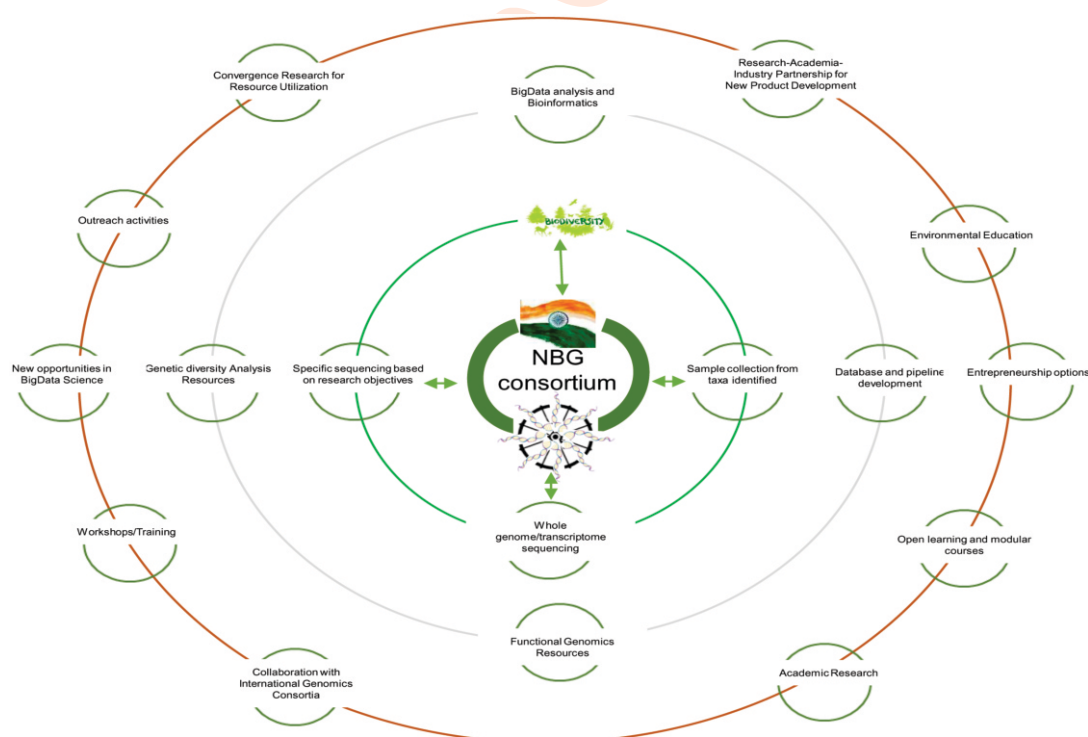


Fig. 1: Native Biodiversity Genomics (NBG) Consortium: A knowledge hub supporting environmental sustainability..

sustainability with opportunities for workshops/ training, open-learning and modular courses, environmental education programs to encourage local action groups and conservation managers and create avenues for convergence research for resource utilization. Building 'omics' data infrastructure in a consortium to study the conservation of sensitive and economically-important species is needed in the country to invigorate attention on biodiversity conservation. In summary, such a consortium will build large-scale data resources, maximize the impact of national research infrastructure, build scientific capabilities, catalyze scientific collaborations and international linkages, and would accelerate research and translation into industry.

I sincerely wish that the reference transcriptome characterization of native flora and fauna would be taken up in a consortium mode to unravel the unparalleled benefits of the resources in multi-dimensional research and development objectives. I am happy to share my research experience and expertise through this editorial on the '*Journal of Environmental Biology* (JEB)' platform- a journal that I have been associated with for the last 15 years in different capacities as an author, reviewer, and editor. I appreciate the visions of Professor Dalela and the hardworking team over the years to make this journal a global environmental outlook tool for the benefit of society.

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