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# Focused Plant Biotechnological Research to Preserve Biodiversity

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Biodiversity simply defined as the rich variety of life and of habitats on planet earth is a vital corner stone for both the survival and welfare of our existence as a species. The continual degradation of biodiversity has economic, environmental, and social consequences. The failure to preserve the biological resources especially the plant life on which we depend for food, clothing, medicine and more recently energy in the form of biofuels lays open the fact that we may also be losing potentially beneficial compounds and materials that have not yet been discovered [1]. Added to this, the fact that climate changes will now significantly affect the world agricultural output and in turn directly influence world food security is not lost upon the scientific, political and industrial communities [2]. The world food security for decades depended on both conventional breeding as well as biotechnological crop improvement strategies [3]. The diverse array of biotechnological strategies that were the focus of research in developing improved novel varieties of crops were witness to concerted efforts between conventional and molecular breeders [4]. These efforts can now be extended to research focused on preserving and enhancing plant biodiversity.

Plant biotechnological research is an immense storehouse of cutting edge technologies [5] and it is a challenge for current researchers to identify contextual research strategies and not get lost in the diverse array of biotechnological strategies that unfold every year. In order to develop novel strategies to preserve plant biodiversity [6], researchers will be best advised to focus on certain crucial aspects of plant molecular biology to better utilize the tools of biotechnology that are available.

## Identifying Effective Experimental Model Crop Plant Systems

The identification of model plant species to study the genetic, biochemical and molecular basis of plant biodiversity is still not fully realized. Plant molecular biology has christened *Arabidopsis thaliana* as a model system due to its complete genomic sequence in the public domain, easy transformation protocols, short generation times, availability of expressed sequence tags (EST), microarray and proteomics data, and a large set of well-characterized mutants as exemplified by the *Arabidopsis* information resource (TAIR) database (http://www.arabidopsis.org). Efforts geared towards identifying model plant systems by utilizing the molecular and genetic data available on TAIR through bioinformatic analyses can be a good starting point for researchers. The successful completion of complete genomes of rice [7,8] and sorghum [9] and more recently banana [10] opens the doors for analyses of specific genes as illustrated by studies made in *Arabidopsis* [11]. A comprehensive database for model experimental plants among edible crops, forest species, pharmaceutically important plants and biofuel crops aimed at data related to transformation protocols, ESTs, microarray, experimental mutants, transcriptome and proteome data in line with the TAIR database will be an effective resource for breeders aiming to develop novel plants to preserve biodiversity.

## Plant Databases for Targeted Gene Discovery

Existing databases such as TAIR (http://www.arabidopsis.org), Gene Ontology (http://www.geneontology.org), Plant GO slim (http://www.geneontology.org/GO.slims.shtml) and the more recent TRY (http://www.try-db.org) with over 3 million trait records for 69000 plant species with the integrated whole genome profiling information can be utilized towards concerted efforts aimed at identifying a vast number of target genes related to preserving plant biodiversity. The identified target genes with crucial molecular functions related to preserving and enhancing plant biodiversity can then be evaluated for their biotechnological potential by genetically engineering them into popular cultivars and forest species.

## The World of Small RNAs

A more recent development in the form of the discovery of microRNAs involved in an array of molecular processes in popular crop plants such as rice [12] and sorghum [13] is opening an entirely new and effective field of plant molecular research [14]. Techniques are now available in designing and silencing miRNAs for various traits across plant species [15-17] and a dedicated web site makes the technology readily accessible (http://wmd3.weigelworld.org/cgi-bin/webapp.cgi). Researchers can effectively use the technology to design artificial 21-mer microRNAs (amiRNAs) that can be genetically engineered and function to specifically silence single or multiple genes of interest across plant species according to the previously determined parameters of target gene selection.

Charles Darwin in his monumental work *The Origin of Species*, focused on biodiversity to unravel the biological mechanics behind the rich variety of life forms on our planet [18]. Darwin attributed the evolution of diverse species on earth to the ability of plants and animals adapted to their environment to breed and pass on their characteristics to their offspring. In the revolutionary conclusion to his classic theory, Darwin reflected on the crucial principle of the importance of relationships between species a contemplated an "entangled bank" where various life forms live in unison. This unraveled the fact that no species including our own *Homo sapiens* can exist in isolation from other living things. Every species on earth is dependent on natural processes for its own survival and in doing so contributes to the natural balance of the environment that translates into the very survival of our planet. We as human beings can thus be the agents of change to the preservation as well as degradation of the rich biodiversity on our planet. With the ever growing field of plant biotechnology that has a diverse array of technological applications

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to choose from, a planned contextual strategy to best utilize the available state of art techniques will richly benefit future researchers and their studies. The planned research strategies will help fulfill our existence as a human race in being the very agents of change that are responsibly preserving and enhancing the rich plant biodiversity to benefit planet earth, while systematically exploiting its resources to better our lives.

**References**

1. The organization for economic co-operation and development (OECD) policy brief (2005)
2. White JW, McMaster GS, Edmeades GO (2004) Genomics and crop response to global change: what have we learned? Field Crops Res 90: 165-169.
3. Kropiwnicka M (2005) Biotechnology and food security in developing countries: the case for strengthening international environmental regimes. ISYP Journal on Science and World Affairs1: 45-60.
4. Van Buerren ETL, Backes G, de Vriend H, Ostergard H (2010) The role of molecular markers and marker assisted selection in breeding for organic agriculture. Euphytica 175: 51-64.
5. Kumar P, Gupta VK, Misra AK, Modi DR, Pandey BK (2009) Potential of molecular markers in plant biotechnology. Plant Omics Journal 2: 141-162.
6. Pijut PM, Lawson SS, Michler CS (2011) Biotechnological efforts for preserving and enhancing temperate hardwood tree biodiversity, health, and productivity. In Vitro Cell Dev Biol Plant 47: 123-147.
7. Yu J, Hu S, Wang J, Wong GK, Li S, et al. (2002) A Draft Sequence of the Rice Genome (*Oryza sativa* L. ssp. *indica*). Science 296: 79-92.
8. Goff SA, Ricke D, Lan TH, Presting G, Wang R, et al. (2002) A Draft Sequence of the Rice Genome (*Oryza sativa* L. ssp. *japonica*). Science 296: 92-100.
9. Paterson AH, Bowers JE, Bruggmann R, Dubchak I, Grimwood J, et al. (2009) The *Sorghum bicolor* genome and the diversification of grasses. Nature 457: 551-556.
10. D'Hont A, Denoeud F, Aury JM, Baurens FC, Carreel F, et al. (2012) The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants. Nature 1038: 11241
11. Denby K, Gehring C (2005) Engineering drought and salinity stress tolerance in plants: lessons from genome-wide expression profiling in *Arabidopsis*. Trends Biotechnol 23: 547-552.
12. Li YF, Zheng Y, Addo-Quaye C, Zhang L, Saini A, et al. (2010). Transcriptome-wide identification of microRNA targets in rice. Plant J 62: 742-759.
13. Zhang L, Zheng Y, Jagadeeswaran G, Li Y, Gowdu K, et al. (2011) Identification and temporal expression analysis of conserved and novel microRNAs in Sorghum. Genomics 98: 460-468 .
14. Nelson P, Kiriakidou M, Sharma A, Maniataki E, Mourelatos Z (2003) The microRNA world: small is mighty. Trends Biochem Sci 28: 534-540.
15. Ossowski S, Schwab R, Weigel D (2008) Gene silencing in plants using artificial microRNAs and other small RNAs. Plant J 53: 674-690.
16. Warthmann N, Chen H, Ossowski S, Weigel D, Herve P (2008) Highly Specific Gene Silencing by Artificial miRNAs in Rice. PLoS one 3: e1829
17. Schwab R, Ossowski S, Riester M, Warthmann N, Weigel D (2006) Highly Specific Gene Silencing by Artificial MicroRNAs in *Arabidopsis*. Plant Cell 18: 1121-1133.
18. Darwin CR (1859) On the origin of species by means of natural selection, or the preservation of favoured races in the struggle for life. (1stedn), London: John Murray.

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