

**Non-Confidential Description - PSU No. 4152**  
**"A Process to Accelerate Trait Improvements in Crop Plants and  
Prioritization of Genes for Anti-biological Compound Production"**

**Keywords/Field of Invention:**

Plant and Tree Breeding, Genetic diversity, Pathogen Resistance, R Gene

**Inventors:**

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**Background**

The conventional approach to improving crops involves breeding and selecting for the desired heritable trait. Recently, the use of genetic linkage mapping (i.e. quantitative trait loci "QTL") may identify a trait's chromosomal region and/or individual genes. However, the time consuming, expensive QTL method is only applicable to plants that interbreed, works best when genome sequence is available, and is not economically suited for tree species and other slow breeding plants.

**Invention Description**

The subject invention relies on a combination of bioinformatics and functional genomic approaches to identify trait-associated genes from a single generation of plants. As there is no breeding, this invention enables the characterization of trait-related genetic diversity across broad collections of crop varieties and even wild plants, thereby opening up unexploited reservoirs of beneficial genetic variation – a very important potential breakthrough. This process takes a different approach than previous methods for identifying functionally important polymorphisms, including the QTL method. Because of its ability to identify polymorphisms in any type of plant gene, the invention may be used to rapidly identify loci harboring variation potentially affecting crop features that have been subjected to directional or diversifying selection. The inventors have so far used this fully developed process to characterize protein diversity created by disease resistance ("R") genes. Utilizing the invention's process of material collection and genetic analyses, the deliverables of this invention can be used to guide marker assisted breeding, gene editing and transgenics.

In addition to crop improvement, the invention is useful for rapidly identifying plant genes likely to be sources of useful anti-biological compounds. For example, a typical plant species harbors 20-40 genes encoding chitinases, only a few of which are likely to produce potent anti-fungals. Rather than functionally test each one, the invention identifies by well-established biology methods a short list of genes that are the best candidates to test for anti-biological compounds.

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**Status of the Invention**

The invention has been reduced to practice and can be demonstrated to potential licensees. Because of *Theobroma cacao*'s economic importance (chocolate) and the yield reduction caused by its fungal pathogen, collaborating researchers are presently applying this technology to this tree species. This invention has the potential to produce large increases in plant resistance within a single generation and at a fraction of the cost of the QTL method. This invention can facilitate the stacking of resistance alleles, which would enable more durable disease resistance. The inventors believe that this invention has particular economic utility for crop plants such as rubber, cacao, grape, citrus, apple, pear, nut, coffee and other slow maturation woody species, which do not fully benefit from marker-assisted breeding programs. In the case of R gene enhanced plants, the invention should reduce the use of fungicides, thereby lowering the cost to farmers and the environment. In the case of anti-biological compounds, there are a large number of potential source plant species (including wild plants) and uses.

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