

## STRATEGY AND INNOVATION FOR SUSTAINABLE PEPPER PRODUCTION AND QUALITY

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### 1.0 Introduction

Malaysia is one of the world's leading producers and exporters of black pepper (*Piper nigrum* L.). In Malaysia, pepper is mainly cultivated in the State of Sarawak where it contributes significantly to the rural population as a source of income. The traditionally practiced pepper cultivation methods are costly and labor intensive. Pepper is extensively cultivated as a single cultivar on gentle to steep slopes, planting on mounds, use of hardwood posts, systematic training of vines, manual harvesting and others. Pepper yield depends significantly on the agricultural chemical inputs, especially pesticides and fungicides for diseases control. This is because pepper is susceptible to various pathogens such as fungus, nematodes and viruses which cause considerable yield loss every year. The high production cost forcing pepper breeders to look into pepper varieties with improved agronomic traits of fast growth rate, high yielding and disease resistance. Therefore, an improvement in pepper yield, quality and resistance is imperative in light of escalating cost, competition and stringent of food standard. Agricultural biotechnology and pepper genome research can provide a solution.

Introduction of agricultural biotechnology into pepper cultivation can be initiated through the fundamental studies on the complexity of gene regulations and gene interactions in pepper metabolisms. Various genomic tools have facilitated greatly the development of improved genotypes / varieties in several crop species. One of these approaches is the genome libraries construction via sequencing technologies. Pepper genome research has been initiated in Malaysia by Malaysian Pepper Board (MPB) since 2008 through collaboration with the local Universities to discover pepper resistance genes. Identifying the sources of resistance becomes important for effective and long term control of the diseases. Although some moderately diseases tolerant lines of black pepper such as varieties 'Balankotta', 'Kalluvally' and 'Neelamundi' were identified earlier, there is a need to screen more accessions / cultures (Turner, 1971; Sarma *et al.*, 1996; Rajagopalan *et al.*, 1998). The informatics database on pepper genome sequences enable the in-depth understanding of genes encoding for pepper yields, vine health and foster the development of improved pepper varieties with desired agronomic traits.

This paper discusses the strategy and innovation for sustainable pepper production and quality through agricultural biotechnology approaches. Pepper genome studies develop a basic knowledge of the structures and functions of pepper genome. This knowledge can be translated to a comprehensive understanding of all aspects of pepper plants and plant processes of potential economic value. By bridging fundamental pepper genome research and pepper plant performance in the field,

pepper genome research can accelerate basic discovery and innovation in pepper plants and enable enhanced management of agricultural practices and breeding programmes in pepper to meet societal needs.

## **2.0 Research Rationale**

The genomic studies on pepper species is gaining momentum, although the understanding on pepper plants has been widely explored in other fields of study such as agriculture, plant breeding and others. The lack of genetic information has become one of the main constraints in production of improved pepper varieties with the desired agronomic traits. Furthermore, there are only 64 Expressed Sequence Tags (ESTs) sequences of *Piper nigrum* L. are available in the database of National Centre for Biotechnology Information (NCBI) GenBank. The majority of these reported ESTs sequences are developed from the *Piper nigrum* variety 'Kalluvally' by researchers from India.

Compared to other crops with plenty of ESTs sequences available in the NCBI GenBank database such as paddy (*Oryza sativa*) with 1,278,747 ESTs sequences are available, tobacco (*Nicotiana tabacum*) with 345,665 ESTs sequences are available, cocoa (*Theobroma cacao*) with 164,375 ESTs sequence are available, papaya (*Carica papaya*) with 77,431 ESTs sequence are available, oil palm (*Elaeis guineensis*) with 40,919 ESTs sequences are available and rubber (*Hevea brasiliensis*) with 13,454 ESTs sequences are available; the lack of information on pepper genetic sequences has limited the progress of genome development on this valuable commodity crop.

## **3.0 Potential of Pepper Genome Research**

### **3.1 Expressed Sequence Tags (ESTs)**

The generation of large-scale pepper ESTs is a very useful approach for identification of gene-rich regions in pepper genome. ESTs are small pieces of DNA that are generated by sequencing either one or both 3' and 5' ends of an expressed gene or complementary DNA (cDNA). ESTs database towards the understanding of genetic controls in pepper metabolisms and provide a quick route to discover novel genes, study on gene regulations, construct pepper genome maps and develop gene-based markers. ESTs database serving as a genome library and contribute to the breeding programme of pepper species. It is an important resource to enhance pepper industry by produces improved planting materials by means of high quality and quantity in yields.

### **3.2 Genome Sequencing**

Transcriptomes sequencing have been performed in rice, papaya and *Eucalyptus* tree for genome investigations (Ray *et al.*, 2008; Eshchar *et al.*, 2010; Lu *et al.*, 2010). The transcriptome is the complete set of transcripts in cell, and their quantity, for a specific developmental stage or physiological condition. Understanding the transcriptome is essential for interpreting the functional elements of the genome and revealing the molecular constituents of cells and tissues, and also for understanding

development and disease (Wang *et al.*, 2009). Exploration of resistance transcripts in pepper is a first step to a broader understanding of the structure and organization of resistance genes in pepper and needs to be conducted in an effort to provide genomic tools for better understanding of disease management of black pepper and provide diseases resistance pepper planting materials in future.

#### 4.0 Conclusions

In conclusion, agricultural biotechnology offers many advantages in sustaining pepper production and quality as well as represents unique applications of science that can be used for the betterment of society through development of pepper variety which is genetically-resistant to pests and diseases. Pepper genome research is beneficial to the country as a foundation in the application of genetics for pepper breeding purposes. Genetic improvements in pepper also must be expanded, accelerated and done much more precisely to meet the growing world demand. Meanwhile, the use of genetically-resistant pepper variety can reduce the adverse effects of chemical pesticides on both the abiotic and biotic components of the environment. Both innovations can provide a better future for pepper industry since the overall goal is to achieve a safe environment, sustainable and improved pepper productivity.

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