Title: A high throughput analyses of glucosyltransferase genes and proteins by using EU-data GRID environment and hunting of novel genes

1. Introduction

Currently we are working about carbohydrate related enzymes, glycosyltransferases, which have important functions in many biological organisms including human. One of our goals is focused on isolating and constructing novel genes (and finally enzymes) with new genetic information through DNA and protein sequence analysis of various existing and new glycosyltransferases. The new enzymes can synthesize useful biomaterials using those enzymes in real world.

For this purpose, informational resources related to glycosyltransferase genes are required to be harvested and analyzed by utilizing analyzing tools such as Blast, Swiss-Prot, etc…, yet currently the gene analyses need much more storages and faster analyzing abilities for computer. Thus, we are thinking that data GRID environment from EU is the best answer for these difficulties. By using GRID system we believe we can analyze more genes' and proteins' information once and fast, and the outcomes make it construct the distinct phylogenetic tree of glycosyltransferases among biological organisms and confirm the relationship between enzyme characteristics and gene sequences. This can also give information about the functionality of glycosides in human proteins and/or enzymes. After isolating the unique characteristic genes of glycosyltransferases, we will designed and evolved further those genes for synthesis of valuable functional carbohydrates and proteins. Furthermore, those results will contribute on potential applications in the foods, cosmetics, and pharmaceuticals-medical industries, understanding on disease mechanisms and therapeutic pathways.

2. Overall Goals

(1) Analysis of glucosyltransferase genes and proteins through EU-data GRID environment and construction of phylogenetic tree based on output results.

(2) Development of oligonucleotide probes for microarray to obtain new genetic information by comparing properties of glucosyltransferase and novel genes.

(3) Identification of new characteristic glucosyltransferase and Synthesis of useful functional biomaterials.

3. Research Content

(1) Bioinformatics becomes stressed for its importance in order to search and systemic develop of valuable genetic information via recent Genome studies, global genes development, DNA and protein sequences data.

(2) For this purpose, data GRID environment from EU was built to compensate current system' drawbacks in that it shows difficulties to handle huge information related to gene sequence comparison and analysis and particularly, to draw the precise correlation from large informational resources for a short time period.

(3) Glucosyltransferase is one of carbohydrates related to enzymes and shows important functions in many biological organisms including human. This study is focused on hunting the novel genes with new genetic information through

DNA and protein sequence analysis of glucosyltransferases and furthermore inventing useful biomaterials using those enzymes in real world.

(4) This study results will contribute on potential applications in the food, cosmetic, and medical industries, understanding on disease mechanisms and therapeutic pathways.

(5) Therefore, the large informational resources related to glucosyltransferase genes are required to be harvested and analyzed by utilizing analyzing tools such as “PROTEOMICS”, yet currently the gene analyses need much more storages and faster analyzing abilities for computer. Thus, data GRID environment from EU is the best answer for these difficulties.

(6) Study outcomes make it produce the distinct phylogenetic tree of glucosyltransferase among biological organisms and confirm the relationship between enzyme characteristics and gene sequences. This can give functionality of glycosides in human proteins and/or enzymes. The unique characteristic genes of glucosyltransferase will be designed and evolved further for synthesis of valuable functional carbohydrates and proteins.

4. Expecting Effects (application fields and practical uses)

(1) Developing and upgrading of tools for fast comparison/analysis of huge genetic information.

(2) Novel-designed genes with unique characteristics will be produced based on the analyzed data, and then biomaterials will be developed and synthesized by using the novel enzymes for practical applications.

(3) Genetic information support for developments and production of new functional

biomaterials as for the Growth Engines of Korea (and others).

(4) Industrial improvements of food, pharmaceutical-medical fields through genetic information gathering and applications.