world in the food which we consume daily and in the milk which is so important for our babies.

In this study, our aim is to produce monoclonal antibodies against SEA antigen by using hybridoma technology and to use for antibody based diagnostic systems.

For this purpose, SEA antigen was obtained commercially and used for immunisation of 6–8 weeks old BALB/c mice in the experiments. By using hybridoma technology, three fusion studies were carried out with mice giving high immune response. The spleen was used as lymphocyte source in the fusion studies. Spleen and myeloma cells were fused using polyethylene glycol 4000. As a result of fusion, 8 positive hybrid clones were obtained. Among these clones it is observed that one (1D3) produces specific monoclonal antibody against SEA by indirect ELISA.

In conclusion, using this monoclonal antibody it will be possible to develope a quick, easy and cheap diagnostic systems to detect the SEA amount in milk.

http://dx.doi.org/10.1016/j.nbt.2012.08.359

Poster 3.2.25

Production of galactooligosaccharides by beta-galactosidase from *Thermus oshimai* DSM 12092

Yuksel Gezgin, Rengin Eltem*

Bioengineering Department, Engineering Faculty, Ege University, Bornova, Izmir 35100, Turkey

Beta-galactosidases (EC 3.2.1.23) have both transferase and hydrolase activities. Hydrolase activity is very important in milk and whey lactose because of the occurrence of lactose intolerance in many populations. Also, galactooligosaccharides (GOSs) are the products of transferase activities catalyzed by these enzymes. GOSs are non-digestible oligosaccharides which consist of 2–20 molecules of galactose and one glucose. Moreover, GOSs can be used as functional foods such as prebiotics and it has beneficial physiological effects for humans The aim of this study was to describe the enzymatic production of galactooligosaccharides by beta-galactosidase from *Thermus oshimai* DSM 12092. In this study, the beta-galactosidase from *T. oshimai* was firstly purified and then the effects of initial lactose concentrations, pH, temperature and different concentrations of the purified enzyme on the production of GOS were investigated. Transferase activity of enzyme and synthesis of galactooligosaccharide (GOS) were detected in HPLC and it was revealed that two types of galactooligosaccharides; trisaccharides and tetrasaccharides were synthesized during lactose conversion.

The maximum total GOS concentration with crude enzyme was found as 27 g L^{-1} which was obtained at 50% (w/v) lactose level, 80 °C, pH 7.5 and 48 h reaction time. When pure enzyme was used, however, this value was 42 g L^{-1} which was almost 56% higher comparing to that of crude enzyme for the similar working conditions (50%, w/v lactose level, 85 °C, pH 6.5, 48 h reaction time). These results have clearly indicated that lactose concentration and the purity of the enzyme are important for GOS production.

Keywords: Galactooligosaccharides (GOS); Beta-galactosidase; *T. oshimai* DSM 12092; Transferase activity; Prebiotic

http://dx.doi.org/10.1016/j.nbt.2012.08.360

Poster 3.2.26

Proteomic investigation of compatible interaction between wheat and yellow rust

Yahya Emin Demirci[1,*], Cihan Inan[2], Zafer Mert[3], Dilara Maytalman[4], Ahmet Tarık Baykal[5], Aslıhan Günel[6], Şenay Vural Korkut[1], Semra Hasançebi[5]

[1] *Yildiz Technical University, Faculty of Arts and Science, Department of Molecular Biology and Genetics, Istanbul, Turkey*
[2] *Istanbul University, Faculty of Science, Department of Molecular Biology and Genetics, Istanbul, Turkey*
[3] *Field Crop Research Institute, P.O Box: 226, Lodumlu, Ankara, Turkey*
[4] *Istanbul University, Faculty of Science, Department of Biology, 34118, Vezneciler, Istanbul, Turkey*
[5] *TUBITAK Marmara Research Center, Genetic Engineering and Biotechnology Institute, Gebze, Kocaeli, Turkey*
[6] *Ahi Evran University, Faculty of Science and Letters, Department of Chemistry, Kırsehir, Turkey*

The largest portion of yield loss in wheat harvesting results from the diseases caused by various pathogenes. One of the most devastating diseases is the yellow rust (Puccinia striiformis f.sp. tritici-Pst) that causes high losses in efficiency and quality. Fungiside using and conventional agricultural methods are not effective as expected. Elucidation of the compatible interaction between the host and pathogen, especially identification of the differentially expressed proteins during infection provide to develop new strategies for disease control. Recently, genomic and transcriptomic studies have been reported about compatible interactions and disease development in plant tissue. However, as known, all processes in a biologic system is being formed by the contribution of various proteins and proteomic is accepted as a powerful tool for elucidation of complex cellular responses such as susceptibility and resistance.

In this study, aimed to identify differentially expressed proteins during disease development in susceptible Turkish bread wheat cultivar (Seri82). For this purpose, total proteins were extracted from either infected or mock inoculated susceptible wheat leaves and these proteins were separated by using ProteomeLab PF2D that is a two dimensional liquid chromatography system. After separation, proteome maps of pathogene inoculated and mock inoculated plant leaves were created and compared by using software. Selected differentially expressed proteins were digested by proteases and analysed by nanoLC–ESI-MS/MS. Obtained mass spectra data were processed with ProteinLynx Global Server V2.4 and searched against wheat and fungal reviewed protein database from Uniprot. Identified proteins were assessed about their roles in disease development in wheat.

http://dx.doi.org/10.1016/j.nbt.2012.08.361