Analysis of Expressed Sequence Tags from the Embryogenic Callus of Korean Ginseng (*Panax ginseng C.A. Meyer*)

Jun Gyo In¹⁾, Bum Soo Lee¹⁾, Yong Eui Choi³⁾, Deok Chun Yang^{2)*}

DioPia Co., Ltd., Kyunghee Oriental Medicine Material and Processing Center, Kyunggi-do 449-701, Korea

²⁾Department of Oriental Medicine Material and Processing, Kyunghee Univerdity, Kyunggi-do 449-701, Korea

³⁾Ginseng Research Institute, Chungang University, Ansung-shi 456-756, Korea

In order to study gene expression transcribted during the embryo development, we constructed a cDNA library of embryogenic callus induced from cotylendon of Korean ginseng and generated expressed sequence tags (ESTs) of 3,359 clones randomly selected. The ESTs could be clustered into 1,910 (59.1%) non-redundant groups. Similarity search of the non-redundant ESTs against public non-redundant databases of both protein and DNA indicated that 2,217 groups show similarity to genes of known function. These ESTs clones were divided into eighteen categories depending upon gene function. Most abundant transcripts were ribosomal protein small subunit 28kDa(40), tumor-related protein(35), metallothionein (31), small heat-shock protein class 18.6K(24), and cyclophilin(20). There are no useful informations of gene expression during the embryo development in Korean ginseng. These results could help to understand the embryo development in Korean ginseng.