

عنوان مقاله:

In Silico Identification of Housekeeping Genes by Expressed Sequence Tags

محل انتشار:

سومین کنگره بین المللی و پانزدهمین کنگره ملی ژنتیک ایران (سال: 1397)

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خلاصه مقاله:

Introduction: In gene expression studies, for validation and obtain reliable results, normalization of qRT-PCR data by Housekeeping Genes (HKGs) is required. Failure to select an appropriate HKGs may lead to biased gene expression data. HKGs are critical for maintenance of basic cellular functions and existence of a cell. They are constantly expressed in different types of cells, tissues and in different experimental conditions. However, several reports have indicated that they are not expressed in all cells/tissues and experimental treatment or have variable expressions. Expressed Sequence Tags (ESTs) are a high-throughput method providing a new dimension to transcriptome analysis and discovering genes. ESTs represent the amount of mRNA expressed in the cell or tissue. **Methods:** In this study, the EST profile of 17242 protein-coding genes was randomly selected from the UniGene database. Based on the definition of HKGs mentioned above, only 100 genes were expressed in 7 developmental stages, 45 normal and 25 normal tumor tissues. In order to normalize EST counts across normal and tumor tissues, we used Log2 (TPM + 2) scale. Then fold changes in 15 normal and tumor tissues were analyzed. **Results:** Our results showed that 57 genes not only have no expression changes between the normal and tumor tissues but also show overlapping expression in some tissues. **Discussion:** Our findings demonstrate that some of the common HKGs are not suitable for gene expression normalization and may suggest novel genes as potential HKGs but its proof requires further investigations and another high-throughput data.

کلمات کلیدی:

Housekeeping gene, EST, In Silico

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