Genes differentially expressed between tissues: a statistical approach to EST data.

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Different methods are used for the analysis of gene expression in tissues: cDNA libraries construction and the EST sequencing, SAGE (Serial Analysis of Gene Expression) and DNA arrays. The analysis of groups of genes co-regulated under different conditions, presumably sharing some functional or regulation characteristics can aid the understanding of regulative networks and control sequences and make easier the prediction of gene function.
On the other hand, the study of genes differentially expressed in different human tissues or in the same tissue in different conditions (e.g. normal and cancer cells) can shed light on biological phenomena. The power of the methodology strongly depends on the availability of appropriate statistical methods for the analysis.
The exploitation of a very large amount of data, mostly from EST sequencing projects, available on public domain genome databases enabled us to reconstruct and analyse transcriptional profiles of human tissues (Skeletal muscle, Heart, and Retina) by using a computational approach (Bortoluzzi and Danieli, 1999, Bortoluzzi et al, 2000 a, b, c).
Recently, we were concentrating on the comparison of transcriptional profiles of different human tissues with the aim of:
- investigate conserved properties of the expression profiles (e.g the frequency distribution of the expression levels);
- outline genes differentially expressed among tissues by applying a statistical approach. This analysis was based on the statistical treatment developed by Audic and Claverie to test differential expression in pairwise conditions comparisons and on the "R" test for the comparison of gene expression from multiple cDNA libraries proposed by Stekel and colleagues.
In particular, as a pilot study, the expression of a set of 89 ribosomal protein genes in six different adult human tissues (brain, liver, skeletal muscle, ovary, retina and uterus) was considered. In each of the analysed tissues a large variations in the expression of ribosomal protein genes was observed. Moreover, when comparing the expression levels of ribosomal protein genes in six different tissues, 13 genes appeared differentially expressed among tissues. Five of them were mostly expressed in ovary (RPL14, RPL38, RPS9, RPS10, and RPS19) and eight were mostly expressed in the skeletal muscle (RPL37, RPL37a, RPL41, RPL44, RPS13, RPS17, and RPS23).
Previous studies documented the over-expression of single RP genes in specific developmental or pathological conditions, whereas we investigated on the possible differences in expression within the entire set of RP genes, in different normal adult human tissues. The hypothesis that an over-expression of some RP genes could be typical of some specific conditions, included the differentiated state of some human tissues and that the upregulation of some RP genes could be related to the involvement of their products in extraribosomal functions should deserve further consideration.