Poster I-17

Identification of novel imprinted genes in human.

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Short Abstract: Identification of imprinted genes is expensive mainly due the difficulty to the paternal allele expression evaluation. In this work we developed a large scale approach, based in the integration of public data from SNPs, SAGE and MPSS, for the identification of new imprinted genes candidates.

Long Abstract:
Genomic imprinting is an epigenetic phenomenon in which alleles of a gene are differentially expressed depending on their parental origin. Genomic imprinting plays an important role in both normal development and diseases such as diabetes and cancer.

Recently, our group, in collaboration with the group of Biology Molecular and Genomic of the Ludwig Institute, generated a database of Single Nucleotide Polimorfisms (SNPs) associated alternative SAGE (Serial Analysis of Gene Expression) and massively parallel signature sequencing (MPSS) tags. SAGE and MPSS are techniques developed for genome-wide analysis of gene expression and both techniques rely on the production of short tags adjacent to the 3' most restriction site of a given enzyme (NlaIII for SAGE and DpnII for MPSS). Tags are then sequenced in large scale and tag counts are used to measure the relative abundance of their corresponding transcripts.

The presence of SNPs in the restriction sites or in the tag sequence can generate an allelic-specific tags that allows us to study allele-specific gene expression. In this work we used the database of SNP-associated alternative tags to identify imprinted genes with a mono-allelic expression pattern.

Basically, we searched for genes with SNP-associated alternative tags and for which both allele-specific tags are never observed concomitantly in the different SAGE and MPSS libraries, suggesting that only one allele is expressed. Using this approach we have been identified 351 candidate genes and found among these candidates 5 known imprinted genes.

Finally, we submitted eight candidate genes for experimental validation to confirm the mono-allelic expression. Three genes presented an imprinting pattern, other three genes presented differential expression between its alleles and for two genes we couldn't finds heterozygote individual to test the allelic expression. These results suggest that our

approach may contribute significantly to the identification of new imprinted genes.

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