The Abdus Salam International Centre for Theoretical Physics

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QUANTITATIVE LIFE SCIENCES SEMINAR

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ICTP
Central Area, 2nd floor, old SISSA building

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Gene expression profiling as a tool for the identification of novel disease signature for neurodegeneration in humans

Prion diseases or transmissible spongiform encephalopathies (TSE) are a class of fatal infectious neurodegenerative disorders whose pathogenesis mechanisms are not fully understood. The diseases manifest as sporadic, genetic or acquired. So far, neither specific biomarkers for early diagnosis nor effective therapeutic targets have been identified. The pathological molecular component of the diseases is a misfolded isoform of the prion protein (PrP) denoted as prion.

Mounting evidence suggests that in addition to gene coding for the PrP (*PRNP*) other genes may contribute to the genetic susceptibility of TSE. In this context, microarray-based gene expression analyses offer unique tools to approach neurodegenerative disorders.
In particular, transcriptome profiling can be used to identify altered transcripts in response to pathogens, and select potential targets for novel therapeutic approaches. Up to date, a number of studies have been carried out in order to investigate the gene expression alterations occurring in prion-infected organisms, but most of them involved animal models such as mice, sheep and cattle, which are not closely related to humans. Several studies have been performed on non-human primates but none of them have investigated the genomic outcome of prion infection. In this presentation, new sets of data will be presented in an attempt to delineate molecular mechanisms of prion diseases and identify genes that can modulate progression of these fatal maladies in humans.