INTRODUCTION

Alternative splicing is a complex post-transcriptional mechanism which generates different mRNA isoforms allowing large diversity of proteins synthesised from a small number of genes.

Alteration of splicing events can cause or modify human disease, so a reliable method to measure the expression levels of splice variants is essential. Real-time PCR is the most sensitive method for RNA quantification developed to date.

Our aim is to apply Real-Time PCR technology to quantify the different splice variants generated by Major Histocompatibility Complex (MHC) class III region genes, potentially implicated in diseases.

We are now focusing in studying NFKBIL1 (nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1) gene, which is a susceptibility gene for rheumatoid arthritis.

THE HUMAN MHC CLASS III REGION


REFERENCES
