Rahul

Define your research question

Public level

Genetic information is stored in the form of DNA, but for it to have any effect, it needs to be translated into proteins, and we're interested in learning about a new mechanism by which this occurs.

Disciplinary level

Discipline: Developmental Biology

The majority of messenger RNAs in eukaryotes are translated through a canonical process that depends on the presence of a 5'- cap. There is increasing evidence that up to 10% of transcripts may utilize an alternative translation mechanism involving internal ribosome entry sites (IRES). We are interested in understanding how IRES function and how their activity is regulated.

Subfield level

Subfield: Gene Expression

We are interested in the cis- and trans- mechanisms that regulate cell IRES in eukaryotes. It's surprising but up to 10% of mRNAs are not translated through the canonical Kozak mechanism. While people have a reasonable idea of how viral IRES work, they don't really understand the cis- and trans- mechanisms that regulate cellular IRES. We are looking at IRES present in a group of genes that function in the same genetic pathway as a model to approach this problem.

Lab level

We need to generate a series of deletion constructs to identify the cis- elements and the specific sequences that are essential for IRES function in Gene X. We will test these both by generating transgenic animals and using transfection assays in S2 cells.

Elevator Pitch

Headline

I'm really interested in how IRES function.

Elaboration

There's increasing evidence that up to 10% of eukaryotic mRNAs use IRES. And while we have a reasonable idea of how viral IRES work, there's really no basis to understand how their cellular counterparts function. There's no consensus sequence that can predict the presence of an IRES, and IRES-transacting factors are not known. We have a powerful system to study this problem that bypasses the artefacts in cell culture approaches and allows us to use genetics as well.