RNA splicing

Dr. X is a biochemist that studies RNA processing. Messenger RNA (mRNA) is the molecule that serves, as its name implies, as a kind of messenger between DNA and protein. DNA is transcribed into mRNA, which is then translated into proteins that go on to perform the majority of cellular tasks. Typically, freshly-transcribed mRNA molecules are much longer than the mRNA that gets translated into protein. A newly-made piece of RNA must undergo a set of steps that prepare the molecule for making protein, and together these steps are called "processing." RNA processing involves an event called splicing, which executes the removal, rearrangement, and subsequent reassembly of an mRNA polymer prior to protein construction. The pieces that are removed from a strand of mRNA are called introns, and the coding pieces that remain are called exons. Splicing adds a level of diversity to the proteins a single mRNA can code for. Almost all human genes require mRNA splicing to generate the correct protein product.

X-ray Crystallography

X-ray crystallography is a biophysical method that gives researchers a direct look at the 3D structure of the atoms that make up the macromolecule they are interested in. This direct look reveals information about how the protein or RNA functions and can lead to the generation of additional hypotheses about what the molecule is used for. Crystallographic data facilitates the development of research tools and therapeutics that target specific surfaces of a molecule.

To obtain information about the shape of a protein using X-ray crystallography, one must first generate crystals of the protein being studied. Growing crystals requires large amounts of very pure protein, so many crystallographers are also expert biochemists. Purified protein is added to hundreds of different crystallization experiments in an attempt to find conditions that will trigger the formation of protein crystals. Once adequate crystals are grown, they are frozen and shot with an X-ray beam. This beam is diffracted by the electrons within the atoms of the protein and form a speckled pattern on a detector. From this pattern researchers can back-calculate the positions of the atoms within the crystal, thus describing the shape of the protein. These models are subsequently deposited in an electronic database when they are published and can be accessed online by anyone.

Bacteriophage

Bacteriophages (phages) are viruses that infect bacteria. Phages make up an incredibly old and genetically diverse population and have evolved many different types of tools for invading and controlling bacterial cells. Information gained from the study of phages can be used to design novel antibiotics, therapeutics, and research tools. To learn about this gigantic virus family, Dr. X identifies and characterizes new phages. Specifically, he studies phages that infect the bacterial species *Mycobacterium smegmatis*. This is a close, non-pathogenic relative of the species *Mycobacterium tuberculosis*, which is the causative agent of tuberculosis. Dr. X works to use phages and their bacteria-killing strategies to develop new antibacterial tools to help the world stay ahead of antibiotic resistance.

When a bacteriophage enters a host cell, it makes a decision about how to use its genetic material: it can either replicate it within the host cell to generate more phage or insert it into the host's genome to lie dormant until the environment is conducive to replication. Insertion into the host's genome relies on enzymes called integrases. Integrases make incisions in the host DNA and mediate the integration/excision of the phage genome. These enzymes are key to a phage's ability to persist within a population without killing the host cells. The mechanisms of integration are unique to different types of phage and provide options for the development of tuberculosis therapeutics and genetic tools.

Disease ecology

One of the main questions Dr. X focuses on is how variation among different members of a group influence parasite transmission dynamics through a population. In her most recent manuscript, Dr. X evaluated whether there were differences in the transmission rates between guppies with different infection histories or ones that were at different stages of infection. To test this, she exposed a group of guppies that were “parasite naive” to guppies that had different levels of parasite infestation, and quantified parasite transmission. Through these studies, Dr. X found that increases in infection load raise the rate of transmission, but curiously, this did not happen at a linear rate (i.e. the transmission rate was not uniformly proportional to the parasite load), suggesting other interesting factors must be at play. Even more interestingly, her data shows that hosts who are more resistant to the parasites have a higher transmission rate (resistance is measured experimentally in the lab and assigned a numerical value). Additionally, Dr. X found that the parasites grew more slowly within organisms that had previously been exposed to them. This suggests some type of immunity is attainable within her study system.