On the Trail of Genomic Pioneers

Meet Dr. Justin O'Sullivan
Senior Lecturer
Institute of Molecular Biosciences
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1) Can you tell us a bit about your research interests?

My research interests are in systems biology of the genome. In particular we concentrate on the factors that set-up, alter, and maintain the three-dimensional organization of genomes and how this relates to phenotypic changes.

2) Which research study or work has strongly influenced your thought and research goals?

My thoughts and research goals have been hugely influenced by the people I currently have the good fortune to work with and those I have previously worked with. In terms of ideas, I think work on co-transcriptional processing and early studies into nuclear structure have had the biggest impact on my current research interests.

3) Where do you see your research leading in future?

I hope my research contributes to models that predict how changes in genomes, genome three-dimensional structure and genomic processes integrate to cause phenotypic changes. Ideally, such models would then be able to be used to predict novel targets for anti-microbial and anti-viral therapies, or even preventative therapies for somatic cell mutations.

4) A great deal of your work focuses on studying Yeast Genome and variations. What would you say are the most important things that have been discovered in this area over the years? What do you think would be the role of genomics in this area in years to come?

I don't consider myself qualified to say what the most important things are that have been discovered in the field of the Yeast genome and variations thereof. There are so many truly amazing discoveries that have been made or confirmed in yeast. However, it is clear that the recent changes to genomic technologies are enabling a rapid shift in the scale and types of experiments that are being undertaken. As such, I think that genomic scale studies will become much more common place and affordable over the next few years. These changes will mean that as biologists we have to adapt to a new way of designing and analyzing our experiments. As every generation repeats, the next few years will revolutionize the way we do science.

5) How does yeast genome help in understanding genome organization ?

The yeast genome helps us in our quest to understand genome organization because it is a relatively small linear genome that is spread over 16 chromosomes, one parasitic plasmid and a mitochondrial replicon. Moreover, yeast is one of the preeminent model eukaryotes with an extremely well characterized genome, excellent tools and resources.

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6) How does the repeated elements play a central role in the dynamic organization of genome architecture?

We don't really know yet. But we hypothesize that the nucleolus, the most prominent nuclear structure, is important for general nuclear organization. Moreover, clustering of other repetitive elements, for example telomeres, also appears to be important for genome stability and organization.

7) What are the new genomic tools or technologies you used for you research?

We use next generation sequencing and are currently concentrating our work on the SOliD3 (LifeTechnologies) platform. We also develop and incorporate a lot of existing bioinformatic tools into pipelines designed to analyze genome architecture.