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Deciphering the epigenetic code with innovative insect models

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The modern field of epigenetics is driven by a deluge of raw sequencing data that reveal a very complex portrait of epigenomic dynamics operating at multiple levels interacting with each other and remaining in a constant flux. We and others have recently discussed this multifaceted and versatile regulatory network in the context of an epigenetic code as a prime driver of organismal complexity, robustness, plasticity and disease development. We proposed that by providing organisms with a large repertoire of alternative functional interactions, the epigenetic code increases their adaptability to unforeseen environments. But how do we evaluate what these chemical modifications mean in a functional context? How environment is linked to the genome and how external cues are translated into cellular responses via epigenomic changes? When do these changes go above threshold and guide organisms into another direction, such as an alternate developmental trajectory? How does malfunctioning of epigenetic mechanisms result in diseases? To what extent sequence variants such as single nucleotide polymorphism (SNPs) affect epigenomic marks? We are using the social honey bee to develop a framework for explaining the functional significance of environmentally-driven epigenetic modifications in genomic DNA. Specifically, we aim to obtain empirical evidence supporting the idea that epigenomic dynamics is not only influenced by polymorphic changes in DNA but sequence variants may be necessary to ensure the high level of flexibility of the epigenetic code. We also aspire to shed light on the effects of nutrition on methylation and gene splicing and to determine if the enzymatic machinery implicated in adding/removing epigenetic marks has sequence specificity.

Biography

Ryszard Maleszka received his MSc and a PhD in Genetics from the University of Warsaw and has done Postdoctoral work at the National Research Council of Canada before moving to Australia in 1987. He is spearheading a research theme called 'From Molecules to Behaviour' that uses invertebrate model systems to study the genotype to phenotype link and to understand how epigenetic networks contribute to environmentally-driven phenotypic plasticity. He is a member of several genomic consortia and advisor to genomic databases. He authored over 135 articles and book chapters including a number of landmark papers in Science and Nature.

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