MEDIA RELEASE

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First-time discovery of a common pattern in gene regulation could provide clues for new treatments for cancer and other diseases.

Cancer and many other diseases are caused by mistakes in the body's gene regulation process, which can occur when damaged cells do not properly self-regulate. Understanding the process which determines whether or not genes are successfully controlled, is the key to treating and finding cures for cancers and many other diseases.

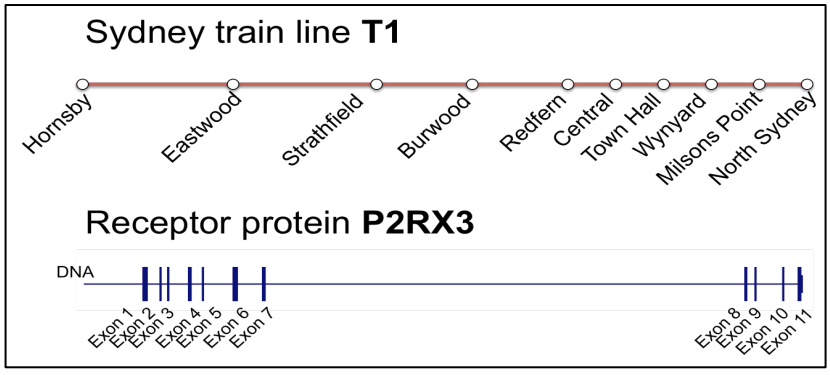
Dr Ulf Schmitz and Centenary Institute's Gene & Stem Cell Therapy Program, led by Professor John Rasko AO, have – for the first time – discovered a common pattern in the process of gene regulation in humans, mice, dogs, chickens and zebrafish.

A better understanding of this common process will help scientists identify abnormal behaviour and help develop direct therapeutic interventions to correct the 'mistake' and find possible cures for diseases. The extreme significance of this work has been recognised, with the research published today in the highly renowned scientific journal, the highly ranked, *Genome Biology*.

The team of scientists used a state-of-the-art experimental system and high performance computing to find that this mechanism of gene regulation evolved over time into a highly calibrated system, facilitating smooth functioning of the animals' immune systems.

"Comparing patterns of gene regulation between species is important because we have learnt in the past that mechanisms which are evolutionarily conserved are often essential for the survival of a species. We found a mechanism and associated characteristics that are well conserved, which suggests that it is important and gives species a selective-advantage" said Dr Ulf Schmitz. This is a world- first study of this type, "What is special about our study is that we used a single, highly purified cell type with highly preserved characteristics," Dr Schmitz said.

To come to their ground-breaking conclusions, the team studied the genetic code imprinted in our DNA, which is organised like a train line. The valuable cargo is lined up at stations that are connected by interspersed tracks of variable length which have long been referred to as 'junk DNA'. Genetic trains load valuable cargo from the stations onto carriages named 'exons' and nonsense-cargo from the tracks onto carriages named 'introns'. Intron carriages are usually removed from the train during their journey to the protein production factory.



Scientists were astonished to find that the systematic phenomenon of intron carriage removal was preserved in at least 400 million years of evolution. This is the estimated time at which a common ancestral organism lived from which all the animals studied in this project descended.

To study this evolution more closely, they retrieved white blood cells from human, mouse, dog, chicken, and zebrafish – all important model organisms which help scientists understand how cells work and how diseases emerge.

Researchers determined that the number of intron carriages in genetic trains and compared their characteristics. They found that preserved intron carriages are abundant in white blood cells of all these species and have very similar features such as their length, composition and location within the genetic train.

The discovery of a clear pattern in gene regulation in the group of vastly different animal species, could bring researchers around the globe, a step closer to understanding the reasons some damaged cells repair themselves and others become diseased. This understanding is highly significant as it could inform future treatments for deadly diseases including various types of cancers.

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