Chromatin-associated lncRNA: Influence on Transcription and Seed Dormancy.

DNA is a simple polymer built of four types of nucleotides. All the genetic information about any living creature is stored in DNA chains. However, the genetic code would be useless without the complicated interpretation machinery. The variety of ways to read the genetic information stored in DNA has amazed biologists for several decades. Every cell must transcribe specific pieces within DNA (called genes) into mRNA molecules to survive. Then, these transcripts must be translated into proteins, which serve as building blocks or active nanomachines. However, protein-coding sequences constitute only a few percent of the entire information stored in DNA (in humans about 2%). What happens with the rest? Since DNA is only a simple polymer, how does the DNA reading enzyme (polymerase) know that this 2% is essential and the other 98% is irrelevant? It turns out that the polymerase that reads DNA and produces RNA does not know that and, as a consequence, transcribes about 75-85% of the entire genome. Transcripts produced by polymerase II can be divided into coding (mRNA) and non-coding (ncRNA) based on their utilisation for protein production. Does studying ncRNAs have any purpose since they do not produce proteins and are almost immediately digested? Just as in the hive, the life of each bee has a profound meaning (the queen alone cannot give birth to bees, care for larvae, defend the hive, and gather food), so in the nucleus for many ncRNAs, exhibiting short half-lives, physiological relevance has been discovered. Additionally, most non-coding RNAs do not leave the nucleus. During research, I found that modifications to the 3' end of RNA molecules are crucial for their activity and localisation. However, they do not affect stability, i.e. being eaten by the exosome. In addition, they are used as regulators of hormonal pathways and sensors of temperature rise, regulating the depth of seed dormancy. RNAs, compared to DNA, are very unstable and sensitive to chemical and physical factors, but they have essential biological functions regulating, among other things, the depth of seed dormancy.

Seed dormancy is an evolutionary mechanism that helps plants avoid germination under unsuitable conditions by protecting them from unfriendly environmental conditions such as drought or cold. In many plant species, dormancy depth is regulated by abscisic acid(ABA) and the DOG1 protein. Both high levels correlate with deep seed dormancy, and their interaction with other factors such as temperature, light, humidity and other plant hormones are essential to eventually breaking dormancy and triggering the germination process. Dry seeds suffer extensive DNA damage during storage. A DNA damage checkpoint has been postulated as one of the first events during seed imbibition. How the DNA repair in seeds is linked with ABA and DOG1 pathways has not been addressed. We found that long non-coding RNAs (lncRNAs) can be used as regulators of hormonal pathways and sensors of high temperature, regulating the depth of seed dormancy by coordination of DOG1, ABA and DNA repair pathways.

To comprehensively describe the potential mechanism, I will use seeds of Arabidopsis thaliana, a model plant used in molecular biology. Even though seeds, as the survival stage of plants, appear to be dormant and very static, an astonishing amount of molecular processes are happening inside. Seeds must integrate current environmental signals about the life experiences transmitted by the mother plant. The seed goes through stages of maturation, repeatedly entering a state of awakening and dormancy, to finally commit the irreversible decision to germinate. All these dramatic changes are reflected at the level of RNA - its synthesis, processing, storage, and degradation.

During the realisation of this grant proposal, I would like to answer two questions:

1. How does long non-coding RNA link three seemingly independent physiological pathways?

2. How do the modifications of the 3' end of non-coding transcripts direct their localisation, and what is their effect on seed function?

I plan better to understand the mechanisms of lncRNA's association with chromatin. The results of my work will provide a better understanding of seeds' molecular adaptations to the environment.