Quest for the Clr2 protein

In the yeast *Schizosaccharomyces pombe*, by expression and purification from *Pichia pastoris*

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It is more or less self evident that understanding the function of an object is easier when observing the three dimensional structure of said object. The simplest example of this is a lock and key model of an object, where lock and key are designed to protect something by fitting only to each other. Changes in shape of the lock due to some problem or insertion of the wrong key would fail to safeguard the object.

Similarly the proteins in any living organism's body, like in us human beings, have specific structures to perform a particular function and protect us from various diseases. The majority of dysfunctions found in proteins are mostly due to changes in their native structures which may lead to diseases like cancer, schizophrenia, etc. Proteins are large molecules consisting of many amino acids.

Each protein has a specific structure on which its function is dependant. To understand the function of a protein it is therefore important to know its structure. In order to produce drugs against diseases like cancer structural studies are important.

The aim of this study was to understand the structure of the Clr2 protein in the yeast *S. pombe.* For example the *S. pombe* shares some similarities with the centre part of the chromosome in human beings. Some previous studies have showed that the Clr2 protein helps in heterochromatin formation, which is important to regulate the gene expression. But the structure of the Clr2 protein is still unknown. It is important to reveal the structure of the Clr2 protein in order to understand the function of this protein in more detail. Though this has not yet been achieved, the study led us further on the path to obtaining the structure.

One of the essential steps of the project was to obtain the protein and to purify it. Here we used yeast called *Pichia pastoris* (which is not similar to baker's yeast) to produce the Clr2 protein. When the protein was obtained, it was purified by affinity chromatography. This is one of the protein purification processes needed in order to enable future structural studies.

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