

Multicellular organisms including plants and mammals are very complex and precisely synchronized machineries. The information about composition and function of organs built up of billions of cells, forming complex organism, is encoded in DNA, in genes. From these genes the specialized multiprotein complexes read encoded information and transcribe it to messenger RNA particle (mRNA). From one gene may be produced several transcripts due to alternative splicing. Transcripts are moved to endoplasmic reticulum where ribosomes translate the functional proteins. Proteins are constructed all machineries responsible for specialized cellular processes i.e. enzymes converting glucose into energy, enzymes repairing DNA damages etc.

The human DNA is about 2 meter long but is stored in the cell nucleus which is featured by very small, about 10 μ m diameter. Given this, DNA must be compacted in higher structures. Such structure is chromatin which is composed of nucleosomes, the basic unit of chromatin organization. Nucleosome is formed by DNA strand and protein core composed by basic histone proteins. Chromatin is very tightly packaged in cell nucleus, therefore the access for protein factors initiating transcription is frequently restricted. Thus, in eucaryotic cell exist highly specialized chromatin remodeling complexes enabling other proteins i.e. transcription factors the access to their target sequences in particular genes.

Among four families of these complexes identified so far, the biggest and most exhaustively studied by molecular biologists is SWI/SNF complex. The functional core of SWI/SNF complex is composed of four subunits. Such complex is able to remodel chromatin in the laboratory conditions. The number of other accessory subunits is variable (usually 5 to 8). These subunits are responsible for targeting of SWI/SNF complex to proper places in chromatin as well as enable its contact with other proteins. SWP73 protein is the most frequently isolated accessory subunit of SWI/SNF complex. In *Arabidopsis* (*Arabidopsis thaliana*) genome there are encoded two SWP73 proteins: SWP73A and SWP73B. SWP73B protein is involved in leaf development, flowering time control as well as in callus formation, UV radiation response and cell cycle control. Additionally, recently published data indicate global function of SWP73A and SWP73B proteins in chromatin by nucleosome positioning and also suggest that both SWP73 proteins have unique and common functions.

SWP73A acts in flowering time control and embryogenesis while SWP73B is general modulator of various developmental pathways including leaf and flower development. Inactivation of SWP73A gene doesn't cause phenotypic alterations, the mutant plant resemble wild type while *swp73b* plant is dwarfed, exhibits altered leaf and flower development and is completely sterile. Interestingly, plant lacking both SWP73- type proteins dies at very early stage of embryonic development. This indicates that SWP73A may be functionally substituted by SWP73B and both proteins may act the same processes. By contrast, SWP73B protein has additional unique functions which can't be functionally substituted by SWP73A protein. Therefore, the full effect of partial or complete loss of SWP73A is visible only when SWP73B is absent. The exact function of SWP73A and interplay between SWP73A and SWP73B in the context of SWI/SNF function remains so far unknown. Given this, during execution of this project we plan to use the most modern molecular biology methods and will identify a pool of genes controlled by SWP73A. Dłatego wpływ czciowej lub całkowitej utraty SWP73A widoczny jest dopiero przy braku SWP73B. We will test if their expression depends on functional SWP73A and check whether their function is dependent also on properly functioning SWP73B. We will also identify the SWP73A target regions in chromatin. Subsequently we plan to check using the most modern molecular biology and microscopy techniques which processes are dependent on SWP73A and SWP73B.