Pelvic organ prolapse (POP) is a disorder in which one or more of the pelvic organs drop from their normal position. This disorder has substantial negative impact on physical function and quality of life. The prevalence of POP increase with age reaching up to 10% in women aged 20 to 39 years, up to 30% of the women between 40-59 years, up to 40% of women age 60 to 79 years and up to 50% of the women aged 80 years or greater. The risk of POP varies by race, Caucasian women have highest risk because have longer levator hiatus and bony pelvis than non-Caucasian women. The etiology of POP is multifactorial and several risk factors including age, parity, genetic variants and lifestyle contribute to the development of POP. It is though that main cause of prolapse is biomechanical weakness of the pelvic support apparatus (i.e., muscles, fascia and ligaments), which results from the disturbance of the connective tissue metabolism. Apart from connective tissues, impairment of the smooth muscle function of the pelvic floor may also contribute in POP, however, their clinical significance is not clearly understood.

Current genetic analyses focus mainly on the single nucleotide polymorphisms (SNPs) in genes encoding proteins engage in the connective tissue structure and remodeling. Up to date few genetic studies investigated small number of women suffered from POP, mostly in postmenopausal women. In a more recent study, sequencing of whole exome was applied in 8 sporadic POP patients of Chinese Han origin. Screening of genetic variants in young women suffering from POP, using whole-exome sequencing (WES), seems to be interesting approach for better understanding the complex nature of the prolapse.

We assume that the genetic factors can play crucial role in the development of POP in young woman because there are no important risk factors such as age and age-related loss of sex hormones. In the case of POPs, there are limited data on the use of next-generation sequencing (NGS), a technique that could accelerate the discovery of new genetic variants important for the development of pelvic organ statics disorders.

The objective of this project is to identify genetic variants in 40 young women (under 40 years of age), with (n=20) and without (n=20) family history of POP, using WES sequencing that allows to analyze coding parts of the human genome. The data on clinically relevant genetic variants obtained in this study will be correlated with the phenotype of patients, and their origin will be identified, i.e. the sequencing of selected variants will be carried out in the parents of patients. Moreover, the concentration of the procollagen III N-terminal propeptide (PIIINP) in serum will be measured to assess if there is a difference in the turnover of collagen in a group of women with family history of POP compared to a group without family transmission.