The genomic research has been altered by the introduction of next-generation sequencing (NGS) which provide a comprehensive and accurate tool for molecular mutations detection. Otherwise, finding among large lists of candidate genes the most promising ones is time consuming and considered a gene prioritization challenge. It is also necessary to predict the amino acid changes' potential impact on gene functions to provide computational proposing of disease phenotypes' casual variants. Then, confirm the selected candidates by performing familial segregation studies and *in vitro* or *in vivo* functional analysis.

Ciliopathies is a group of disorders associated with genetic mutations yielding defects in the cilia structures, the basal body or the ciliary function. In this study, we aimed to propose candidate variants using data from whole exome NGS of five unrelated patients clinically diagnosed to be suffering from ciliopathies. The variants have been filtered and prioritized by a manual approach and in parallel by using bioinformatics prioritization tools. These prioritized variants have been checked for their pathogenicity to exclude neutral effect variants and have been sequenced to exclude false positive variants. Segregation analysis was performed when possible. One of the prioritized genes (*DOCK6)* has been checked *in vitro* for its effect on cilia structure.

All variants have been found *in silico* to be pathogenic except *CCDC88B* associated variant and all are expected to be related to cilia and responsible for the patients' phenotypes. Family v646 variants are coherent with the family phenotype pedigree. *DOCK6* variant in this family did not show observable effect on cilia structure and needs further investigations. Family v645 variants appeared as heterozygous in the affected male patient (57) supposing there are other variants responsible for the male patient phenotype without excluding their rule in the affected female (54). All family v633 variants have been confirmed in the patient while INCENP showed another variant in one of its affected codons. We did not find promising homozygous candidates in family v636 and family v647 suggesting other mechanisms of inheritance responsible for the disorder. In this research we characterize new *in silico* pathogenic variants as promising candidates for ciliopathies disorders.