

## Germline variants in cancer patients with personal and family history of colorectal cancer

Asta Försti

Hopp Children's Cancer Center (KiTZ), Heidelberg, Germany; Division of Pediatric Neurooncology, German Cancer Research Center (DKFZ), German Cancer Consortium (DKTK), Heidelberg, Germany

Multiple primary cancers in a single individual, as well as family history of the same cancer, are features of hereditary cancer. About 15% of colorectal cancer (CRC) patients have first-degree relatives affected by the same malignancy. However, for most families the cause of familial aggregation of CRC is unknown. To identify novel high-to-moderate-penetrance germline variants underlying CRC susceptibility, we performed whole genome sequencing (WGS) in germline DNA of Polish CRC patients with personal and family history of colorectal cancer. After WGS, we used *in silico* tools to evaluate the effect of the identified nonsynonymous and loss-of-function (STOPgain, frameshift and splice site) variants on the function of the corresponding proteins. We identified variants in genes known to be involved in CRC biology, chromatin and transcription regulation, general cellular processes and immune response. Our findings contribute to the identification of unrecognized genetic causes of familial CRC.