AG Oncogenetic

The AG Oncogenetic focuses on the biological backround of somatic and hereditary cancer diseases. The group leader is Dr. med. Christopher Schroeder who was trained in the field of human genetics in Tuebingen. The two PhD student Ilanaz Saph (hereditary cancer syndromes) and Franz J. Hilke (somatic oncogenetics) are completing the group together with the technician Diana Stuermer. The major goal in the field of hereditary cancer syndromes is classification of genetic variants and their impact on the development of the disease. Therefore especially the DNA repair pathway is studied extensively. The goal of the somatic oncogenetics is translational research. Therefore we especially study clinical targetable variants and employ minimal invasive methods like liquid biopsy. The experiments are carried out by high-throughput analysis. Together with the bioinformatics research group we are implementing new analysis tools and NGS methods, permanently.

Molecular Inversion Probes and molecular barcodes

The field of next generation sequencing technologies and analysis tools is evolving constantly. Over the past 3 years a new capture technology has entered the field: it is called molecular inversion probes (MIPs). An advancement of the amplicon (library, system, with a strand specific capture and possibilis yield of the targeted loci). The probes are an easy designing tools to sequence a specific area of the genome. This method is especially useful in combination with the amplicon sequencing which enables the sequencing of a single target region (stand for about 2000). The design is highly meaning just one gene or up to hundreds can be targeted. However so far not all loci are available for the MIPs.

Here we present data from 505 patients with family history suspicious for hereditary breast and/or ovarian cancer according to S3 Guidelines who underwent genetic testing at our institute between May 2013 and May 2015. Patients were tested for 11 diagnostic core genes as well as more than 45 candidate genes which are part of the DNA repair pathway or direct interactors of BRCA1/2. One aim of the project is the identification of rare variants in genes that may have an influence or even cause the disease in the families. Besides the variant interpretation of genes that have a research background, we will follow up on interesting variants by segregation and DNA-analysis. Number of genetic loss of function mutations identified in different genes. The majority of classified variants are variants of unknown significance or carriers of variants in the DNA repair machinery which are parts of DNA-repair machinery or directly interact with BRCA1/2. We plan to analyze two colorectal cancer patient panels from the TCGA and the International Cancer Genome Archive (TCGA) and the International Cancer Genome Consortium (ICGC) study. The goal is to  get further insight in the cancer development and progression. The results have made it possible to understand the principles of cancer development and progression. We aim to get further inside in the genetic alterations occurring in the cell to find targets that can be used to find drugs or develop new drugs. Together with the bioinformatics research group we are implementing new analysis tools and NGS methods, permanently.

DNA-Repair Study

BRCA1 and BRCA2 were the first two genes identified to cause hereditary breast and ovarian cancer. There is a broad number of genes encoding protein involved in DNA repair pathways. GWAS identified several loci which are likely to modify the age at onset but each locus only explain small penetrance. Moreover penetrance can greatly differ between families with the same mutation. DNA-Repair Study.

Data analysis and processing

With our results, we hope to be able to predict the age of onset based on an individual mutation load of low risk BRCA1/2 mutation carriers. We plan to analyze two colorectal cancer patient panels from the TCGA and the International Cancer Genome Archive (TCGA) and the International Cancer Genome Consortium (ICGC) study. We plan to analyze two colorectal cancer patient panels from the TCGA and the International Cancer Genome Archive (TCGA) and the International Cancer Genome Consortium (ICGC) study. The goal is to  get further insight in the cancer development and progression. The results have made it possible to understand the principles of cancer development and progression. We aim to get further inside in the genetic alterations occurring in the cell to find targets that can be used to find drugs or develop new drugs. Together with the bioinformatics research group we are implementing new analysis tools and NGS methods, permanently.

Heredity Breast and Ovarian Cancer

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Benign

Likely Benign

MUTYH

MME

RAD51B

FAM175A

TP53BP1

XRCC2

MRE11A

PMS1

BLM

FANCG

MUTYH

MMR

PRSS1

SBDS

HR

SMO

VHL

FA

ATR

OBSL1

APC

KANK4

Total=113

Age at Onset <35

Breast cancer

1%

Likely Benign

No breast cancer

27%

MUTYH

MME

RAD51B

FAM175A

TP53BP1

XRCC2

MRE11A

PMS1

BLM

FANCG

MUTYH

MMR

PRSS1

SBDS

HR

SMO

VHL

FA

ATR

OBSL1

APC

KANK4

Total=113

Age at Onset >60

Breast cancer

1%

Likely Benign

No breast cancer

27%
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dicant in Graecis legendis operam malle consumere. Postremo aliquos futuros suspicor, qui me ad alias litteras vocent, genus hoc

temperantiam postulant in eo, quod semel

Diagnostikthema 2

Beschreibung: ... Non eram nescius, Brute, cum, quae summis ingeniis exquisitaque doctrina philosophi Graeco sermone tractavissent,

Diagnostikthema 3

Beschreibung: ... Homo ait, quod semel a nobis philosophia defensa et collaudata est, cum esset accusata et vituperata ab

Diagnostikthema 4

Beschreibung: ... Non eram nescius, Brute, cum, quae summis ingeniis exquisitaque doctrina philosophi Graeco sermone tractavissent,

Diagnostikthema 1

Beschreibung: ... Non eram nescius, Brute, cum, quae summis ingeniis exquisitaque doctrina philosophi Graeco sermone tractavissent,