

The overall aim of the project is to study Sialoadhesin binding to rest and activated mouse regulatory T cells (Tregs). The flow cytometry results showed Sialoadhesin had strong binding to activated Tregs but did not bind to rest Tregs. As Sialoadhesin binds to glycans on cell surface, this presence/absence binding pattern was initially thought to reflect an overall dramatic change of glycosylation upon Treg activation. However, when the glycan profile of the Tregs were compared using glycomic strategy, an overall change of glycosylation was not observed. The synthesis of glycans on cell surface was catalysed by two major groups of enzymes known as glycosyltransferases and glycosidases in the ER and Golgi complex. The expression of the glycosyltransferases and glycosidases were then studied using proteomics. Unfortunately, most of the glycosyltransferases and glycosidases were not identified, probably due to the low copy number and high glycosylation of these proteins.

The aim of the RNA-Seq experiment is to investigate the expression of glycosyltransferases and glycosidases upon Treg activation. Four pairs of rest and activated Tregs were prepared and RNA was isolated. The samples were submitted to the Edinburgh Genomics Facility for mRNA sequencing. mRNA from samples was isolated using poly A selection and the libraries were prepared by the facility. The sequencing results have been received in BAM and FASTQ formats.