Fungi of the genus *Fusarium* are the major source of contamination of food and feed with mycotoxins worldwide. The most frequently occurring are type B trichothecenes, which pose a serious threat to food and feed safety. In Europe, two species: *Fusarium graminearum* sensu stricto and *F. culmorum* are the most common contaminants of cereals with type B trichothecenes. Highly sensitive diagnostics of these pathogens enables to predict contamination of food and feed products with trichothecenes. It requires the use of specific molecular markers allowing for not only detection but quantification of these pathogens. It can be achieved by the use of qPCR (quantitative PCR) technology. To date, all qPCR assays have been designed on the basis of nuclear, single copy genes, which often do not provide highly sensitive quantification. Highly sensitive diagnostics of fungi can be achieved by the use of mitochondrial based assays.

The purpose of this study is the development a highly sensitive FcMito qPCR assay (*F. culmorum* specific mitochondrial based quantitative assay) for quantification of *F. culmorum*. To ensure high sensitivity of the assay, primers and MGB probe will be designed based on multi-copy mitochondrial DNA. Specificity of the assay will be evaluated against all known phylogenetic species of the FGSC complex as well as other *Fusarium* species and fungal cereal pathogens. The assay will be evaluated in terms of efficiency and sensitivity against a test panel of different *F. culmorum* strains. In order to find a correlation between *F. culmorum* DNA and trichothecenes, the FcMito assay will be used to quantify *F. culmorum* from grain samples from Poland and Luxembourg with defined levels of trichothecenes.

The aim of the second part of the planned study is to determine whether the mitogenomes of type B trichothecene producing *Fusarium* spp. may have any value in resolving interspecific evolutionary relationships within these species. To achieve this, we will characterize the mitogenomes of a representative set of 30 geographically diverse strains of *F. culmorum*, *F. cerealis*, *F. pseudograminearum* and phylogenetic species from *Fusarium graminearum* species complex. We will perform comparative analysis to reveal the interspecies variation in their mitogenomes. In addition, mito-phylogenomic analyses will be performed to find a potential barcodes for identification of these species.

The results of the studies presented in this paper will provide new insight into fungal diagnostics and interspecific mitogenome variation of type B trichothecene producers. This part of studies will require bioinformatic analysis which will include assembling and annotation of fungal mitogenomes which will be performed with collaboration with international research workers. It is worth to note that in this study the first complete mitogenomes of *Fusarium* spp. will be sequenced and deposited in NCBI database.