



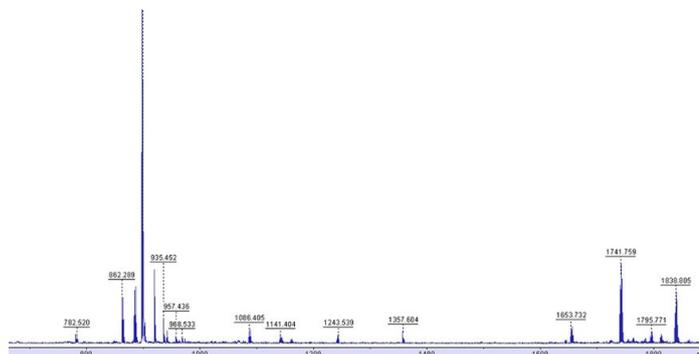
Computational system for detection of mutant proteins and SNPs in MS/MS data

Introduction:

Mutations cause a wide spectrum of diseases including cancers. Knowledge of mutation profiles allows scientists and clinicians to understand altered cellular processes and to guide selection of therapies. Screening of alterations is routinely done using modern high-throughput methods such as Single Nucleotide Polymorphism (SNP) chips or Next-Generation Sequencing (NGS). However, mass spectrometry of proteome, method with a great potential in personalized medicine, is not used for this purpose yet.

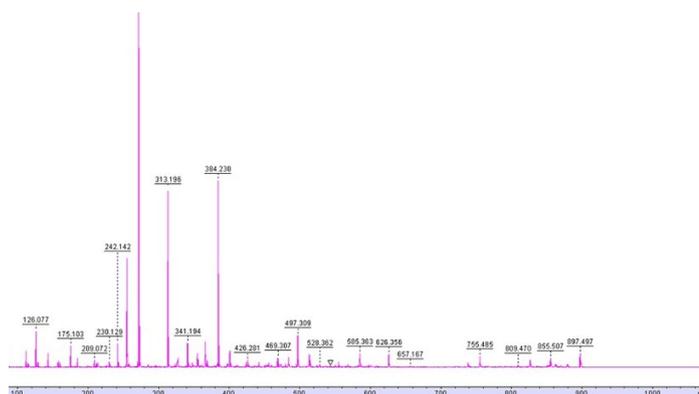
Technology description:

The technology consists of a computational system, named *claire*, used for direct detection of mutant and polymorphic proteins in MS/MS data. At its core, the system holds large protein variant database, used to match MS/MS spectra. The reliability of detection is based on our probabilistic algorithm (Patent pending, EP 18184710.4), which was verified under variety of circumstances. Furthermore, given high computational efficiency of the algorithm and modularity of the software design, the system can be easily adapted to novel circumstances. For instance, the system was recently improved to identify intact variant N-glycopeptides, utilizing the same detection principles.



Advantages:

The software allows to advance mass spectrometer into a tool for reading of mutations and polymorphisms. This type of information is critical not only in cancer research but can be also used for other applications. For instance, our analyses have shown the capacity to authenticate cell lines or identify individuals from high-resolution MS/MS spectral data. Another advantage is the potential to directly observe effect of mutation on post-translational modifications.



Development status:

Fully functional version of the software, named *claire*, available through web interface (claire.imtm.cz). At present, the system is accessible within network of Palacky University and for authorized users only.

IP protection:

EP 18184710.4

Commercial offer:

Exclusive or non-exclusive license to the software

Ownership:

Institute of Molecular and Translational Medicine, Faculty of Medicine and Dentistry, Palacky University, Olomouc

Contact:

More information is available upon signing a CDA/NDA. Please contact IMTM's director (director@imtm.upol.cz) or the technology transfer office (tto@imtm.upol.cz)

