Bioanalytical Proteomics and Interactomics

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November 19, 2019

Introduction

- Most proteomic studies are based on mass spectrometry
- The program will be finished in December, in January we will only do exercises
- The examination is composed in a poster presentation and an oral part
  - A poster is a self-sufficient work
  - Usually it is prepared at the begininning of a scientist's career
  - We should base our poster on selected papers
  - The poster is not mandatory, but if we do it we will only be asked 1 question in the exam
- Proteomics is one of the main omics, but also interactomics and secretomics are becaming really interesting
- The data produced by omics are on the order of zetta and yottabytes
- Personalized medicine is important, and now we have the tools to implement it
- Proteomics can be structural, functional and differential (expression)
- Three main approaches: top-down, bottom-up and shotgun
- Many funding sources now require researchers to share raw data
- In silico-cloning: we need to know at least one software
- Other useful softwares are Pymol, Graphpad Prism, ImageJ
  - Graphpad Prism is a spreadsheet used to elaborate data and do statistics
- Proteomics is the large scale study of proteins, the proteome is the total amount of proteins coded in the genome
- Proteomics involves a spatial and temporal dimension, while the genome is static
  - It is really noisy (!)
  - Proteins are really diverse, and their processing is complex
  - They are present in a really broad concentration range
  - There is no PCR for proteins (!)
- Unnatural amino acids are really interesting, and there are many patens about them
  - They are used frequently in cosmetics (!)
- Proteases are everywhere (!)
- Aromatic amino acid tend to be in β conformations
- MALEK tend to be in α helices
- 1/3 of drugs target GPCR receptors
- Membrane proteins are hard to study
- An antibody is around 150 kDa, it is a big protein
- Is of huge clinical interest to find fluorescent proteins that emit in the red spectrum
  - Most tissues absorb really well green light, and red is the least absorbed part of the spectrum
- Mutagenesis can be performed rationally or randomly
  - Random mutagenesis is made with kits that make an imprecise PCR
  - We can substitute any possible aminoacid in a specific postion that we know to be important
- The top-down aprroach starts from the protein
- The bottom-up approach uses peptides deriving form digestion of the protein
- The shotgun approach uses different peptides deriving from many proteins

- The less complex the protein mixture, the better (!)
- Informations on chemical compounds can be retrieved in PubChem
- PubMed does not indicize articles outside of biology and medicine (!)
  - Better to use Scopus or Web of Science for chemistry and other fileds
  - For patens, Espacenet is the main database
- A volcano plot has the fold change in expression in the x axis and the significance in the y axis
  - It is used to rapidly identify differentially expressed proteins (it is also applicable to other fields)

Protein separation

- Proteins can be separed with different chromatographies or electrophoresis, microdialysis
- We can use depletion techniques to remove typical high-abbundance proteins
  - There are kits to remove albumin with spin columns
- Protein electrophoresis can be done in native conformation or by SDS-PAGE
- Immunological techniques are Western blot, ELISA, immunoprecipitation
  - Antibodies have affinity constants ranging from 10^9 to 10^12 M
- The upper limit for the number of resolvable proteins in a 2D-PAGE is 10000
- Spot identification in 2D-PAGE can be done by MS or by image analysis
  - Image analysis can be done by comparing our image with gel images of identified proteins present in databases
  - I usually work on master images created by combining 5-10 images of gels run in the same condition, to reduce noise
- Databases for 2D-PAGE, like ExPasy proteomic server, allow to search for images of specific tissues or cells, or conditions
  - I can then compare my spots with the ones already identified
- Differential PAGE (DIGE) runs 2 samples on the same gel, with different labels, so to be able to compare expression differences between them
  - It is a good practice to repeat the experiment by switching labels
  - Labels called cyainine derivatives (CyDies) are available with many different emission spectra
    - Labelling is done prior to IEF
    - We can use many samples at the same time (multiplexing)
    - They are really small and bind to the ϵ amino group of Lys in proteins
- The staining method for 2D-PAGE should be chosen considering the sensitivity required
- 2D-PAGE is generally speaking non-quantitative
- We can perform WB also on 2D-PAGE (!)
- HILC (Hydrophilic interaction liquid chromatography) uses a polar stationary phase and a polar mobile phase
  - It is really useful for glycosilated proteins
  - Elution is done in water gradient
- N-terminal microsequencing is based on Edman degradation and can be used for spot indentification, but it is obsolete
  - It has been replaced by MS
  - It uses phenyl-isothiocyanate that reacts with the N-termini forming thiazolinone derivatives
  - The derivative is then released and identified by cromatography or electrophoreys, before repeating the cycle
  - Amino acids are red at 269 nm

Mass spectrometry - basis is not for exam

- A mass spectrometer contains an ion source, a mass filter and a detector
- Some ion sources can be interfaced with a separation technique, others must be operated manually
- Soft ionization method do not break chemical bonds, while hard methods do that
  - In proteomics we use soft ionization: MALDI or ESI

  - There is also a semi-soft technique: fast atom bombardment (FAB)
    - It is used for small proteins and peptides
    - It uses typically a glycerol matrix
  - In ionization techniques, the matrix is used in order to prevent sample fragmentation
- In ESI the sample is in solution and it is sprayed by a small tube in a really strong electric field in presence of a hot nitrogen flow
  - The ionization is performed at atmosferic pressure
  - The sample forms droplets that evaporate concentrating charge, until they undergo columbic explosion
  - The produce ions are multiple-charged, and this is useful for detecting big molecules
  - We can operate both in positive or negative ionization
    - In positive mode I need to add formic acid to the solvent, in negative mode ammonia
    - If I have acidic groups in my analite I want to operate in negative modality, while with basic groups I want to operate in positive modality
  - It is possible to form protonated ions, deprotonated ions or cation adducts
    - It is very sensitive to salts and detergents
  - Since I have multiple-charged ions, I have many peaks for each analite
    - With molecules under 1200 Da I tend to have single ions
    - The multiple peaks are normally distributed and can be deconvoluted via software to derive the MW of the ion
  - Native and complexed proteins tend to have non-normal distribution of ions
  - It is very sensitive, but I need really pure samples
- In MALDI the solid sample is heated by a laser while embedded in the matrix
  - The matrix becomes ionized and transfer charge to the analite, while exploding at supersonic speed
  - We can operate in negative or positive modality
  - It generates single-charged ions M+H and M-H
  - It is more tolerant to contaminats
  - It can directly analize cells (!)
  - MALDI resolution can be influenced by the differential time of ionization of analite molecules, and differential initial velocity of the ions before the TOF acceleration
- A mass spectrum is a plot with m/z on the x axis and relative abundance in the y axis
  - Peaks are typically really sharp
  - From each ion I get a carachteristic pattern of peaks, due to spontaneous fragmentation
  - I have spontaneous fragmentation only if my ionizing source is strongh enough
- The accuracy of the mass spectrometer is measured in ppm
- The resolution of a mass specrtrometer is obtained by dividing height of the peak by its width at half height
- A mass filter is a device that separates analite ions based on their m/z
- A magnetic sensor mass analyzer (MSA) deflect the ions by differen radii depending on their m/z
- The quadrupole mass filter allows a stable path only for a selected m/z, and we can get a spectrum by scanning all the target m/z values
  - It is used also in tandem MS
- Orbitrap (Makarov, 2000) is the newest and most sensitive analyzer
  - There is a spindle-like electrode around which the analite ions spin and a barrel-like electrode
  - The ions oscillate with a frequency related to their m/z, giving a signal
  - The signal is deconvoluted with the Fourier transform to yeld the fundamental armonics, which are related to m/z
- The time of flight analyzer (TOF) accelarates ions with an electric field in a way that is proportional to m/z
  - The time that is required for the ions to reach the detector is proportional to m/z
- The reflectron is a variant of TOF that improve resolution by compensating for different initial velocities
- MS detectors are diods that generate secondary electrons when struck by an ion
  - Electron multipliers produce many secondary electron for each ion. and therefore are more sensitive, but require extensive maintenance

- Tandem MS combines 2 MS in the same instrument
  - I avoid fragmentation in the first step using a soft ionization of the molecular ion
  - A collision cell between the 2 MS filled with inert gas allows to fragment the analite

Peptide mass fingerprinting

- It is the main bottom-up approach
- The standard workflow starts with 2D-PAGE that allows to recover unique spots
- It is important to chose a staining method that is compatible with MS
- We can also use multidimensional HPLC as an alternative to 2D-PAGE
- Spots are then cut and destained
- Spot picking can be done manually or with a robot
  - Manual picking is susceptible to keratin contamination
  - There is a risk for gel deformation
- The protein is then digested by trypsin to yeld peptides
  - Trypsin cuts after K or R, but only if not followed by P
  - It is important to have a complete digestion to avoid missing cleavage sites
  - Better to use volatile buffers to eliminate them easily afterwards
  - Trypsin can also self-digest (!) and the deriving peptides are really useful as a standard for MS
    - It is an internal calibrator
- Peptides are then purified by reverse chromatography or Zip tips
  - RC uses apolar stationary phase on polar mobile phase
  - Zip tips are a miniature RC column (!)
- We perform MS on the peptides, getting a fingerprint of the protein
  - In MS peptides must be ionized in a gas phase
  - MS measures the m/z ratio of the peptide ions
- I can then identify the protein by searching for my fingerprint in databases
- Masses can be reported as monoisotopic or average
  - Entry level instrument cannot differentiate isotopes, therefore report only average masses
- To match a fingerprint with a database, I check how many hits on the same protein I have with my masses
  - I choose the protein with the maximum number of hits
- Main PMF databases are Mascot and ProFound

Peptide de novo sequencing

- Peptide de novo sequencing uses MS/MS spectra to determine the sequence of a protein without using any previous knowledge
- This is in contrast with database search, that identifies the peptide using databases
- The fragmentation process produces different kinds of ions
  - Give the low collision energy employed, most fragmentations involve peptide bonds
  - If the charge is retained in the N-terminal fragment, the ion is termed a, b or c
  - If the charge is retained in the C-terminal fragment, the ion is termed x, y or z
  - Fragmentation of the peptide bond produces y or b fragments
- I can recover the mass of the residues by analyzing the mass difference between ions
- Given a MS/MS spectrum, the sofware Peaks can give the protein sequence, with a confidence for each residue

Synthetic biology - Not for exam

- In order to provide proprieties that are not available in nature we can use non-natural amino acids

- We can also modify polymerases in order to use non-natural nucleotides that still pair among themselves in a specific way

Molecular cloning - Not for exam

- Molecular cloning is essential because it is our only way to obtain high amounts of proteins
- The general workflow is to isolate the cDNA of the protein, insert it in a plasmid and transfect bacteria with it
  - The cDNA is amplified with primers containing a 3' overhang that allows to introduce the appropriate restriction sites
- When I cut my plasmid, I want to use single cutters so to avoid that the plasmid could close on itself
  - Usually I can cut exactly where I want because plasmids are engineered to have many restriction sites
- Selection of recombinants is done with antibioitics for bacteria and mammalian cells, and with auxotrofs for yeast
- Cells are made competent with a $CaCl_2$ solution
- Commercially available competent cells are usually much more efficient, even though a little bit more expensive
- Transfection can be done by heat-shock or electroporation
- Plasmids tend to be toxic for bacteria, because of their metabolic burden
- DNA absorbs at 260 nm, proteins at 280 nm
- Protein biotinylation can be performed in vivo or chemically
  - Chemically, I usually bind biotin to Lys residues
  - In vivo I can fuse my protein with a biotin binding domain and clone it toghether with BirA, a biotinylating enzyme
- For in silico cloning, we can use Vector NTI Advance or the online platform Benchling