We describe a digestion-capture membrane (DCM) that bridges the transition between electrophoretic separation of proteins (SDS-PAGE) and detection of peptides by MALDI. Proteins blotted into the membrane are digested into peptides, captured and concentrated while maintaining spatial resolution, and eluted into liquid optimized for mass spectrometry. Protein standards demonstrate 87% protein digestion precision, quantitative capture of ~20 pmol peptides in 25 mm² of membrane, and recovery of 83%. Following SDS-PAGE PAGE of yeast lysate and blotting onto the membrane, 72% of identified proteins were localized to a single fraction and 87% in 2 fractions (2 mm size, n=30). This workflow does not require specialized equipment, and is compatible with protein identification by protein mass fingerprinting (PMF) or MS/MS.

### Methods

- Prepare bi-functional DCM from glass/fiber paper
- Run SDS gel
- Blot onto DCM
- Isolate membrane for digestion
- Cut membrane into fractions
- Gel
- Gather MALDI spectra
- Externally calibrate
- Identify proteins by PMF using ChromApe

### Conclusions

- This workflow useful for quick characterization of protein preparations.
- Peptide recovery similar to in-gel digestion.
- TPMS identifies up to ~10 proteins per slice.
- This workflow useful for quick characterization of protein preparations.

### References