

**The best proteomics:
combination of upfront
reduction of sample complexity,
reproducible resolution, and
effective follow up**

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OUTLINE

- I. Proteomics analysis of actions of a dietary supplement, grape seed extract (GSE), in the brain;
- II. DIGE analysis of protein differences in rat tissues at different developmental stages to determine basis for cancer risk

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Our principal goal: to understand the molecular basis of human chronic conditions/diseases, to develop prevention or therapies.

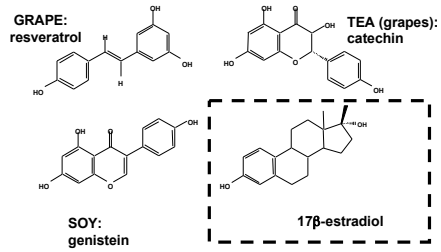
Strategy: a proteomics approach

Hypothesis: Actions of “beneficial” agents such as dietary anti-oxidants in normal and disease tissue will reveal subproteomes of proteins “at risk” for disease-relevant changes.

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POLYPHENOLS: similar structures among themselves, and with 17 β -estradiol



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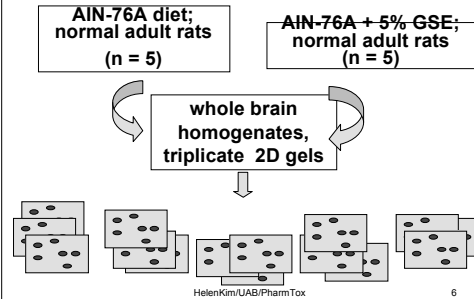
RATIONALE for predicting grape seed extract (GSE) polyphenols will have neuroprotective actions:

Joseph et al., 1999;
blueberry extract supplement protected against age-related cognitive impairment
Pan et al., 2000;
soy isoflavones protected against ovariectomy-induced cognitive dysfunction
Peng et al., 2005;
our own studies showed GSE enhanced cognition in estrogen-depleted (ovx'd) rats;

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The experiment, and the dataset:

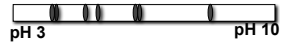


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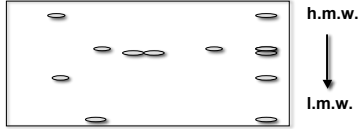
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Basics of 2-D electrophoresis

- 1st dimension: Isoelectric focusing on flat plastic strips containing immobilized pH gradients (IPG) (separation according to charge)



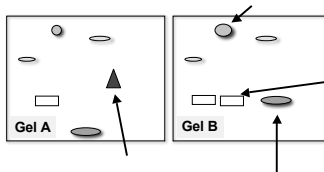
- 2nd dimension: (SDS)-polyacrylamide gel electrophoresis (separation according to size)



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Critical part of 2-D gel proteomics: Image analysis

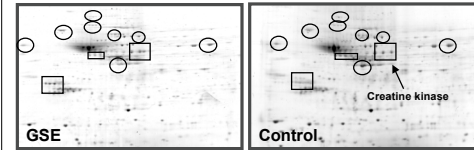


The arrows indicate the types of information suggested by image analysis data.

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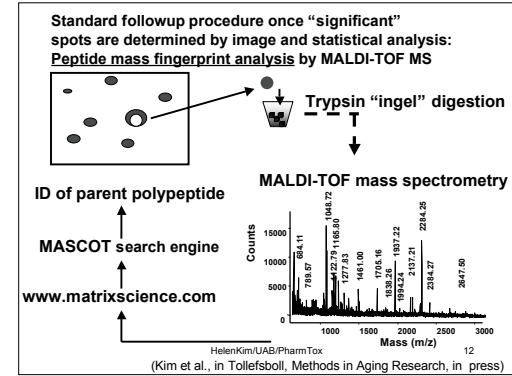
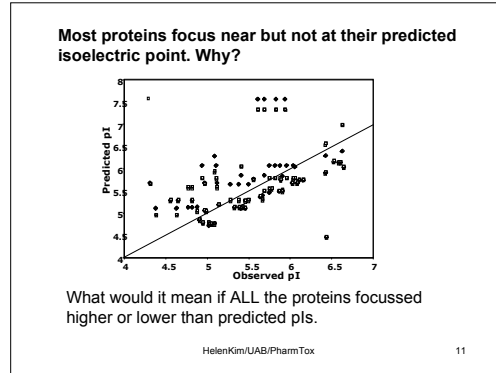
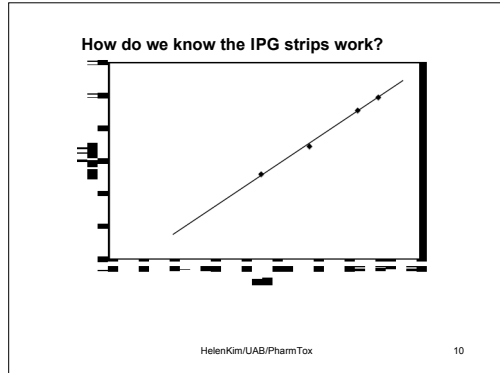
Image analysis indicated spots that differed between the two sets of gels;

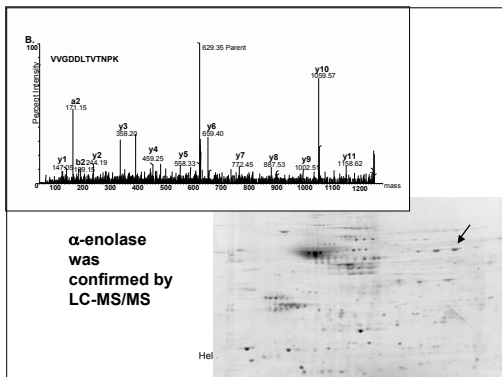


- Different in intensity
- Different in position (variability)

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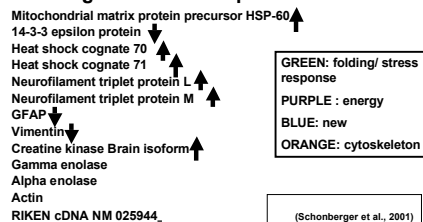


Database of protein differences in GSE vs CT brains

| Protein Name | Accession # | Accession # | Score | Mass | Size | Score | Score of change in GSE vs CT |
|---|-------------|-------------|-------|-------|------|-------|------------------------------|
| Mitochondrial matrix protein precursor HSP-60 | F03158 | F03158 | 11.25 | 72000 | 650 | 11.25 | -1.2 |
| Heat shock cognate 70 | P04648 | P04648 | 11.25 | 70000 | 700 | 11.25 | -1.2 |
| Heat shock cognate 71 | P04649 | P04649 | 11.25 | 70000 | 700 | 11.25 | -1.2 |
| Neurofilament triplet protein L | P02558 | P02558 | 11.25 | 66000 | 660 | 11.25 | -1.2 |
| Neurofilament triplet protein M | P02559 | P02559 | 11.25 | 66000 | 660 | 11.25 | -1.2 |
| GFAP | P02559 | P02559 | 11.25 | 66000 | 660 | 11.25 | -1.2 |
| Vimentin | P02559 | P02559 | 11.25 | 66000 | 660 | 11.25 | -1.2 |
| Creatine kinase Brain isoform | P02559 | P02559 | 11.25 | 66000 | 660 | 11.25 | -1.2 |
| Gamma enolase | P02559 | P02559 | 11.25 | 66000 | 660 | 11.25 | -1.2 |
| Alpha enolase | P02559 | P02559 | 11.25 | 66000 | 660 | 11.25 | -1.2 |
| Actin | P02559 | P02559 | 11.25 | 66000 | 660 | 11.25 | -1.2 |
| RIKEN cDNA NM 025944 | | | | | | | |

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(Deshane et al., 2004. J. Agric. Food Chem.)

Initial conclusion: GSE is neuroprotective, since its effects on proteins are counter to the directions of change for the same proteins in disease.



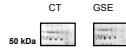
GREEN: folding/ stress response
PURPLE: energy
BLUE: new
ORANGE: cytoskeleton

(Schonberger et al., 2001)
(Tillemann et al., 2002a)
(Tillemann et al., 2002b)

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(Deshane et al., 2004. J. Agric. Food Chem.)

Western blot analysis of 2D gel image and statistical analysis

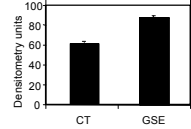
A. Stained gel for HSP-60



B. Western Blots



C. Quantitative Densitometry



Don't discount the power of conventional/"old" methods..

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Validation of protein identifications and quantitations

| Protein | LC-MS/MS | Western blot |
|-------------------|----------|--------------|
| CK-BB | + | + |
| Hsp60 | + | + |
| GFAP | -- | -- |
| Actin | -- | + |
| NFL-M | + | -- |
| α -enolase | + | -- |
| γ -enolase | + | -- |
| Hsc70 | -- | -- |
| Hsc71 | -- | -- |
| 14-3-3e | -- | + |
| NFL-L | -- | + |

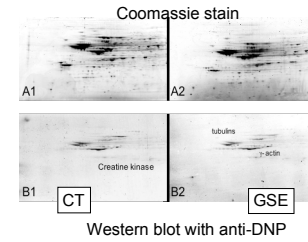
Interesting note:
Only for spots from 2D gels, journals accept PMF data, without sequence data, because of the information from the 2D gel (mass, pI).

(Kim et al., 2005, in Luo and Packer, Oxidative Stress & Neurodegeneration)

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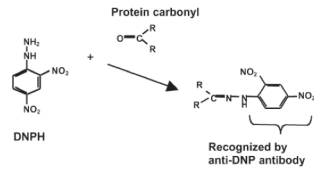
Proteomics can indicate protein oxidations: an increasingly important area of study in chronic diseases



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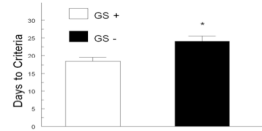
To study protein oxidations, must understand chemistry involved, make use of biological reagents



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The strongest validation of proteomic data can come from completely different (orthogonal) experimental procedures that usually test for function.



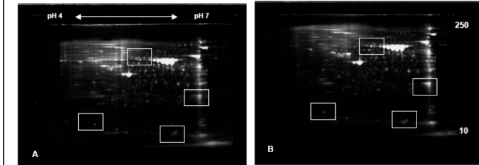
In this case, GSE fed to young female rats enhanced learning and memory over those fed control diets. This data was consistent with GSE having neuroprotective actions.

(Peng et al., 2005)

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DIGE (difference gel electrophoresis): powerful, but quality control issues need to be addressed to ensure robust data.



Issue addressed here: does the same sample bind the two cy-dyes, cy3 and cy5, equivalently?

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How do you deal with running multiple samples on 2D gels as objectively as possible

| Gel # | 1 | 2 | 3 | 4 | 5 |
|-------|-------------------|-------------------|-------------------|-------------------|-------------------|
| Cy 2 | Internal Standard | Internal Standard | Internal Standard | Internal Standard | Internal Standard |
| Cy 3 | Day 21 | Day 50 | Day 21 | Day 50 | Day 21 |
| Cy 5 | Day 50 | Day 21 | Day 50 | Day 21 | Day 50 |

Grid assigns random pairs of samples per gel; In this experiment, the different days were swapped to make sure that there wasn't preferential dye binding of one day over the other.

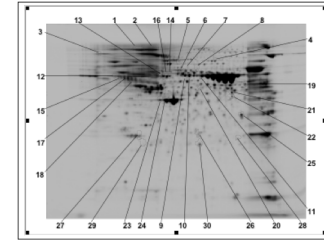
Real data from a DIGE experiment

Table 2. Fold change, significance and FDR of proteins that were significantly different between days 21 and 50

| Master Spot | Figure 4 spot number | Protein Identification | Fold change, Day 21/50 | T-Test value | FDR | Pred. Mass (Da) | Mature Mass (Da) | Obs. Mass (Da) | Pred. pI | Mature pI | Obs. pI |
|-------------|----------------------|--|------------------------|--------------|--------|-----------------|------------------|----------------|----------|-----------|---------|
| 192 | 1 | alpha-1-antitrypsin III | 1.2925 | 0.0024 | 0.0091 | 165.038 | 164.975 | 132.210 | 5.70 | 5.69 | 4.97 |
| 192 | 1 | procollagen, type XIV, alpha 1 (triplehelix), glycom (Glyc) a | 1.2925 | 0.0024 | 0.0500 | 192.494 | * | 132.210 | 5.08 | * | 4.97 |
| 193 | 2 | similar to Collagen alpha-1(VI) chain precursor | 1.0945 | 0.0003 | 0.0333 | 198.738 | * | 132.210 | 5.21 | * | 5.14 |
| 215 | 3 | alpha-1-antitrypsin III | 2.8150 | 0.0004 | 0.0052 | 165.038 | 164.976 | 122.763 | 5.70 | 5.67 | 4.31 |
| | | PREDICTED: similar to Drosophila heavy chain of BMD CC11842-PA | 1.2709 | 0.0107 | 0.1345 | 438.140 | 432.262 | 117.590 | 5.87 | 6.08 | 5.41 |
| 292 | | heat shock protein 4 | 1.4585 | 0.0101 | 0.1098 | 93.997 | 94.057 | 110.030 | 5.13 | 5.13 | 5.46 |
| 302 | | heat shock protein 4 | 1.3668 | 0.0145 | 0.1289 | 93.997 | 94.057 | 109.179 | 5.13 | 5.13 | 5.41 |
| 309 | | similar to alpha glucosidase 2 alpha neutral isoenzyme | 0.8315 | 0.0392 | 0.2249 | 109.390 | * | 108.753 | 5.76 | * | 6.11 |
| 310 | 4 | similar to alpha glucosidase 2 alpha neutral isoenzyme | 0.8153 | 0.0047 | 0.0704 | 109.390 | * | 109.179 | 5.76 | * | 6.16 |
| 344 | 5 | PREDICTED: similar to ribosome binding protein 1 gpl009g.1 | 1.4174 | 0.0082 | 0.0955 | 109.068 | * | 103.388 | 5.79 | * | 5.58 |

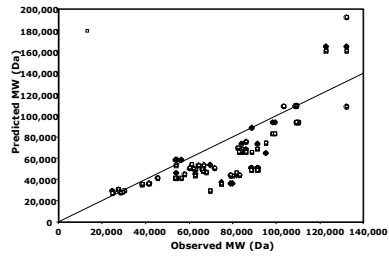
(from Kim et al., J. Proteome Res, 2008)

Image analysis generates "significant" spots for MS analysis



On this gel, half the spots didn't contain enough protein for MS analysis; solution?

Analysis of observed mw over predicted mw: many polypeptides run at mw higher than predicted.

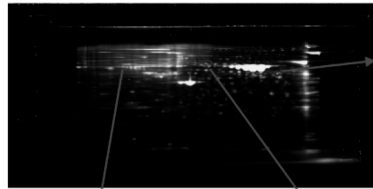


What would it mean if every single spot ran at a higher mw than predicted?

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Some protein markers for rat development



Serine protease inhibitor 2b,
2x, 50day/21day
p = 0.0063
FDR = 0.0311

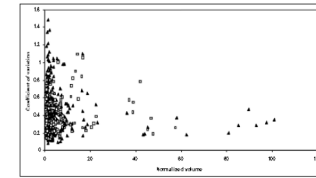
Homopexin
1/2, 50day/21day
p = 0.0004
FDR = 0.0242

Coronin
1.4x, 50day/21day
p = 0.0081
FDR = 0.0227

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Coefficient of variance: statistical tool that assesses the extent of variation over the range of samples:



Bottom line here: there was no difference in coefficient of variance between the different groups, thus the differences were due to the true means. (Kim et al., J Prot Res, 2008)

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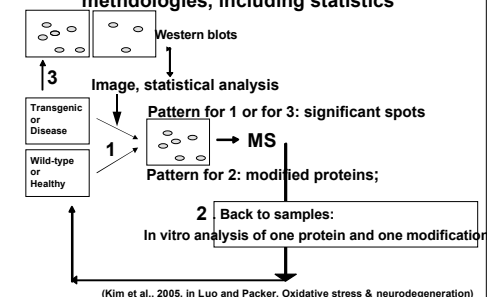
Take home lessons, part I

- Proteomics suggests GSE has pleiotropic effects in the brain:
 - gene expression/protein turnover;
 - (Deshane et al., J. Agric. Food Chem.,2004)
 - How would you follow up?
 - protein oxidations;
 - Informatics helps you relate your data to the rest of the world; in the case of actions of GSE, we know that many of the proteins affected in normal brain are also differentially expressed in AD brain.
 - *What will make the GSE effects consistent with neuroprotection?*
 - *How do we PROVE that any one effect of GSE actually prevents neuronal impairment?*

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Optimal data analysis: Iterative process may start with proteomics but can/should include other methodologies, including statistics



Take home lessons, part II

- DIGE: powerful, but room for lots of quality control;
- In the case of the data presented, these were differences in protein abundance between two developmental ages in female rat tissues;
- How do we know which are important in the actions of a carcinogen which is given at the later age?
- How do we know which cell type these occurred in, and minimize blood protein (albumin) differences?

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