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Biomarker development to improve dry cured ham quality

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Q-PORK CHAINS

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Introduction

- Improving pork quality is a major aim in pig breeding
- Special products like dry cured hams are high price / high quality products
  - Deviating qualities are expensive for producers

- The proteome is a major constituent of meat
- Changes in the proteome will affect meat quality
  -> Proteomic Biomarkers may predict pork quality

Biomarkers: Why and How

- To **Monitor** and **Predict** Biological processes
- **Difficult** or **Expensive** to measure Biological processes
- **Easy** and **Cheap** measurable molecules

- Can be used to **direct** industrial processes

Aim of the study

- **Develop Proteome biomarkers** that monitor and predict:
  - Pork quality in general
  - Ham quality in advance of processing the ham

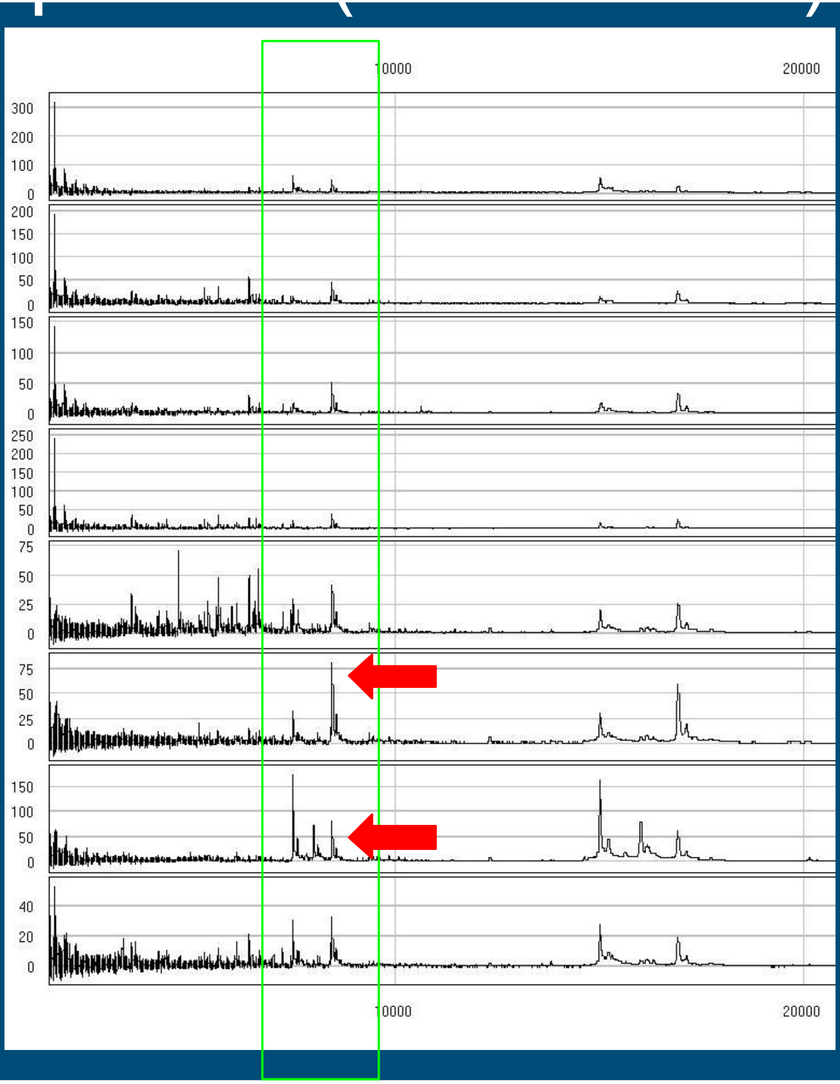
- Help the industry to select to best hams to reduce costs and improve overall dry cured ham quality

Experimental design

- Investigate the relationships between proteome profiles and meat quality

- Material:
  - 2 batches (N=70 each) of pigs with terminal Duroc sire
    - Increase the IMF (food) for high quality dry cured ham
  - 2 independent producers each batch
  - Measure: Carcass lean, FOM, pH, drip loss, IMF (GM)
  - Sample: LD

Proteomics profiles (SELDI-TOF): Example



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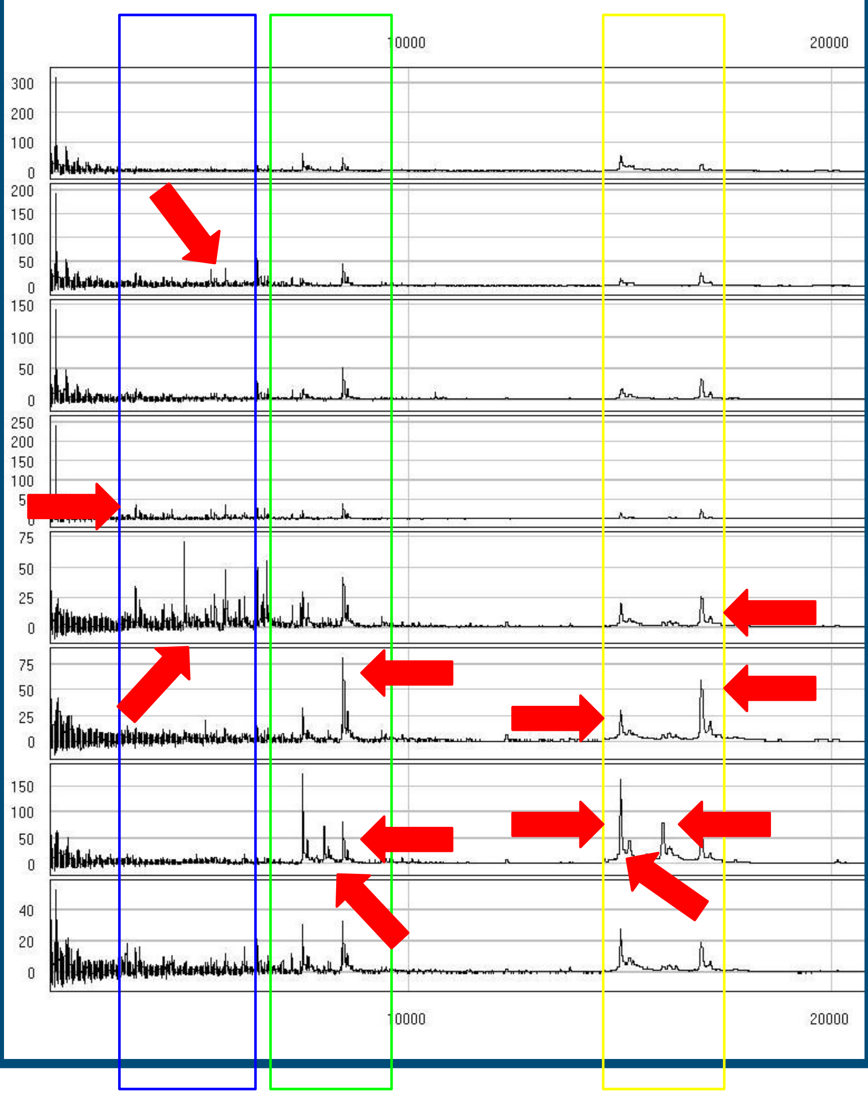


Associations between peak height and meat quality traits

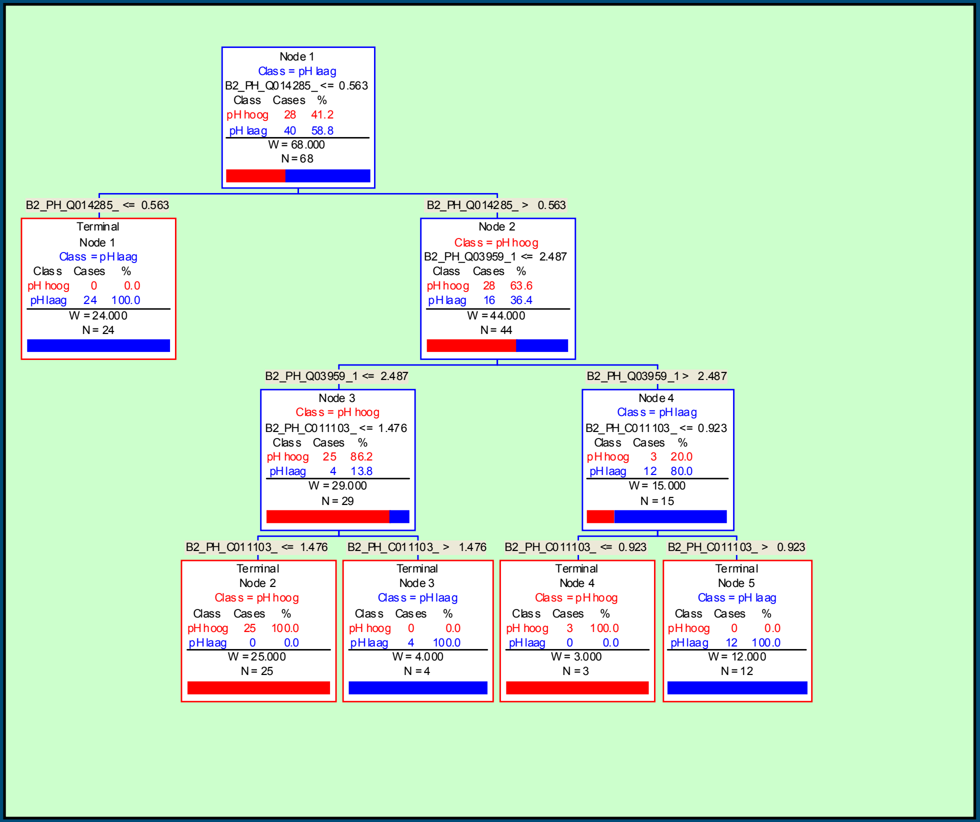
Trait	Peak (M/Z)	P (batch 1)	Sensitivity	Specificity	P (batch 2)	Sensitivity	Specificity
Drip-loss	8474	0.016	**82**	**55**	0.005	**72**	**36**
	17017	0.00069	**92**	**44**	0.0028	**96**	**50**
	9627	0.037	**88**	**40**	0.043	**74**	**33**
IMF G medius	13888	0.012	**45**	**56**	0.026	**62**	**69**
	3903	0.02	**47**	**61**	0.04	**76**	**65**
	12960	0.008	**51**	**63**	0.049	**65**	**68**
	10159	0.013	**53**	**64**	0.007	**67**	**56**
pH24	8474	0.003	66	82	0.00058	66	81
	21697	0.028	75	45	0.048	73	68
	16646	0.04	71	46	0.02	46	79
	6132	0.047	67	52	0.033	72	70
	12482	0.048	54	41	0.000039	50	71
	4256	0.011	66	51	0.000012	67	88
	3963	0.003	85	31	0.000017	56	81
Carcass lean	6108	0.42	63	34	0.000012	77	35

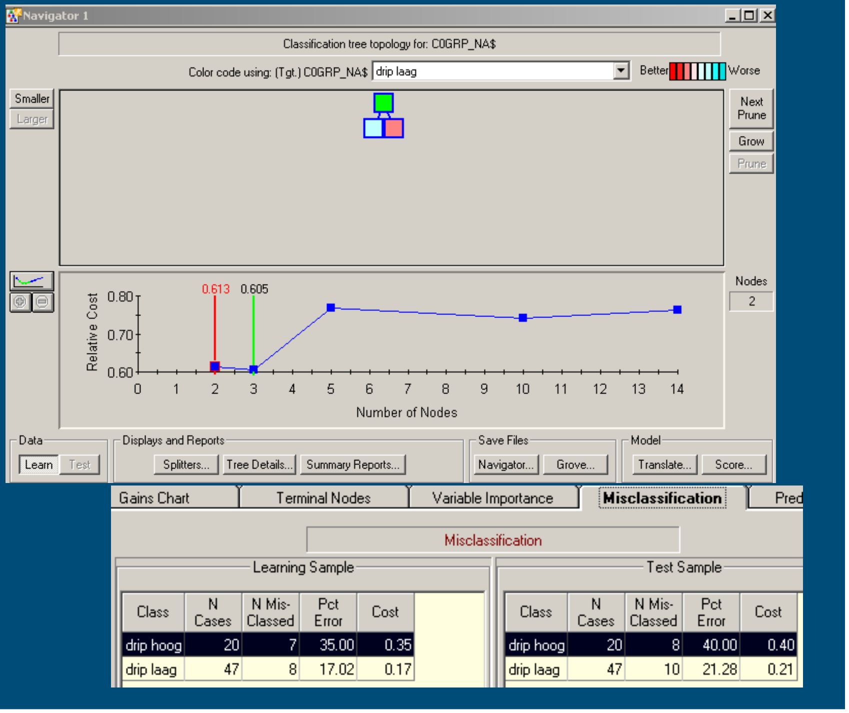
Combining peaks may provide better biomarkers

- If sensitivity and / or specificity is low
- Two peaks may be better than one

- Biomarker Patterns Software package
  - Start with a peak
  - Investigate the improvement of combining with a second peak, third peak, …….
  - Make a tree

Combining peaks may provide better biomarkers





Misclassification

Learning Sample

Class	N Cases	N Mis-Classed	Pct Error	Cost
drip hoog	20	7	35.00	0.35
drip laag	47	8	17.02	0.17

Test Sample

Class	N Cases	N Mis-Classed	Pct Error	Cost
drip hoog	20	8	40.00	0.40
drip laag	47	10	21.28	0.21

Discussion: How can we use these data?

- Biomarker development
  - What is needed to develop the biomarker from these data?
    - Identification of peak
    - Fast, cheap test development
    - Validation in other datasets / other commercial environments
    - Proof of concept in industrial environment
  - …
- Improve the selection of the best hams before processing

Conclusion - summary

- We developed **potential biomarkers**
- **We started the road ahead to develop commercially interesting biomarker tests**

Acknowledgement

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