

P006 Aspects of the barley seed proteome during development and germination illustrated by a targeted study of thioredoxin h
Christine Finnie¹, Kenji Maeda¹, Ole Østergaard¹, Kristian Sass Bak-Jensen¹, Jørgen Larsen², Birte Svensson¹
¹*Department of Chemistry, Carlsberg Laboratory, and* ²*Carlsberg Research Laboratory, Gamle Carlsberg Vej 10, DK-2500 Valby, Copenhagen, Denmark*

By mass spectrometry, about 200 different proteins in 500 spots in the two pH ranges 4–7 and 6–11 have been identified on 2D-gels of water-soluble extracts from barley seeds. The fate of individual protein spots has been followed during grain filling and germination. Proteomes of dissected aleurone layer, embryo and starchy endosperm show the distribution of the proteins in the seed tissues. Proteins varying among cultivars with differing properties have been observed and the genetic basis for the variation studied using a double haploid population. Detailed information gained from 2D-gels and mass spectrometry has enabled the cloning, expression and characterisation of two isoforms of thioredoxin h, a redox-regulator of many proteins important in germination. An improved technique has been used for specific Cy5-labelling of the free thiol groups generated by thioredoxin h in barley seed extracts. Proteins in about 30 spots on 2D-gels have been identified as likely target proteins of thioredoxin h. A bonus of this technique is that it also provides data on the presence or absence of free cysteines in other proteins identified on our 2D-gels.