



Effect of horn status on the muscle proteome of cattle. 35th French Society of Electrophoresis and Proteomic Analysis (SFEAP) congress

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PROGRAM & ABSTRACTS

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GRAND THÉÂTRE - ALBI

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Fifty-four Limousin x Swiss dairy breed crossbred young bulls were used of which half had been disbudded under anaesthesia and locally and systemically administered analgesia using a hot iron at the age of 7 weeks. After slaughter at the age of 17 months, Longissimus thoracis samples were obtained and subjected to shotgun proteomic analysis, which identified 281 proteins. Of these, 38 proteins (13.5%) showed different abundances according to horn status. Panther Gene Ontology identified 6 different biological functions: binding (43%), catalytic activity (29%), structural molecule activity (14%), receptor activity (7%), transporter activity (3.5%) and signal transducer activity (3.5%). Within binding functions, 91% corresponded to protein binding (cytoskeletal: 60%; receptor: 40%). Within catalytic functions, 43% corresponded to transferase activity, while oxidoreductase and hydrolase activities represented 28.5% each. Bulls with horns had generally higher levels of all proteins, apart from Myomesin-1 (MYOM1), GRIP and coiled-coil domain containing 2 (GCC2) and Dynein axonemal heavy chain 5 (DNAH5). MYOM1 is the major component of the myofibrillar M-band and binds titin, myosin and light meromyosin in a dose-dependent manner. GCC2 and DNAH5 allow transport or tethering of vesicles to cellular organelles. String database was used to identify interactions between the 38 proteins with different abundances. Horned bulls had higher levels of various stress-induced proteins which formed a hub with proteins accelerating protein folding. Another hub was formed by structural proteins, including MYOM1, Vinculin (VCL), Myosin heavy chain of the slow type (MYH7), CapZ-A2 (CAPZA2), actinin-2 (ACTN2), Cysteine and glycine-rich protein 3 (CSRP3), Tropomodulin 4 (TMOD4), all involved in the correct functioning of contractile system. Results indicate that disbudding may have long-term consequences on the physiological functioning of muscles in male fattening cattle. Particularly, structural and binding proteins were influenced. In addition, stress-induced proteins were lower in disbudded cattle. As both structural and stress-induced proteins are known to play a major role in meat quality determinism, it is possible that disbudding influences ultimate meat quality.

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Brigitte Picard², Claudia Terlouw^{2*}

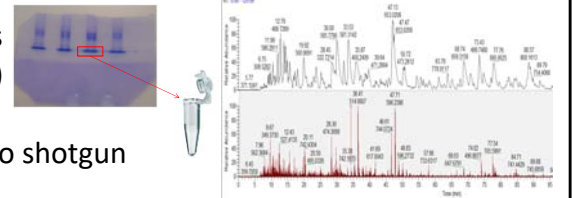
Objectives

Disbudding is frequently used, but little is known of the physiological consequences → The present study evaluates its effects on the muscle proteome



Materials & Methods

- 54 Limousin x Swiss dairy crossbred young bulls, half of which was disbudded (using hot-iron, anaesthetics and analgesic treatments)
- Slaughter at the age of 17 months
- Protein extracts of *Longissimus thoracis* samples were subjected to shotgun proteomic analysis

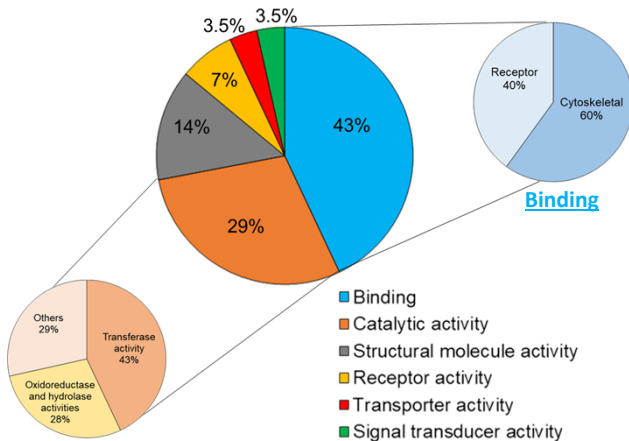


Results

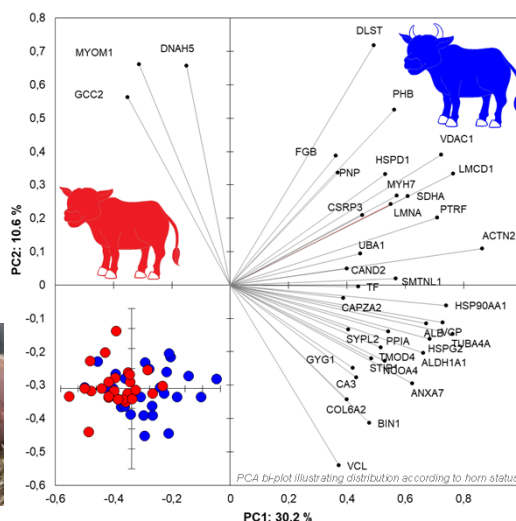
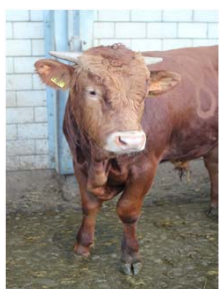
281 proteins identified

- Horn status influenced abundances of 38 proteins (13.5%)
- Bulls with horns had higher level of all proteins, apart from **MYOM1**, **GCC2** and **DNAH5**

Panther Gene Ontology identified 6 different biological functions

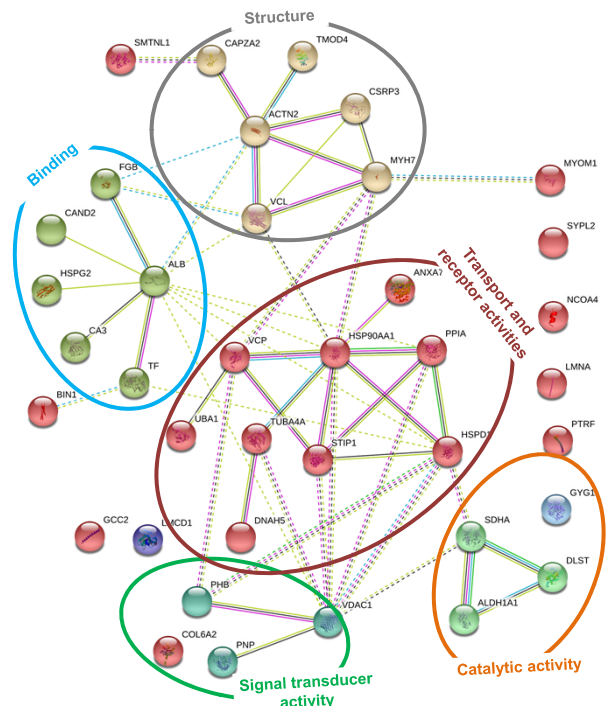


Catalytic activity



The interactome of Protein-Protein-Interaction identified several sub-networks that grouped various

- Stress-induced and folding proteins
- Structural proteins
- Binding proteins



Conclusion

Disbudding may have long-term consequences on the physiological functioning of muscles in male fattening cattle, reducing abundancies of stress-induced proteins, structural and binding proteins. Further studies will evaluate if disbudding influences meat quality, including tenderness.

Acknowledgments

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