

Beef tenderness markers in the three main French breeds: a proteomic analyses

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▶ To cite this version:

Brigitte B. Picard, Thibault T. Chaze, Bruno Meunier, Gilles G. Renand, Laurent L. Journaux, et al.. Beef tenderness markers in the three main French breeds: a proteomic analyses. 2. World DNA and genome Day, Apr 2011, Dalian, China. pp.185-185. hal-00999830

HAL Id: hal-00999830

https://hal.science/hal-00999830

Submitted on 3 Jun 2020

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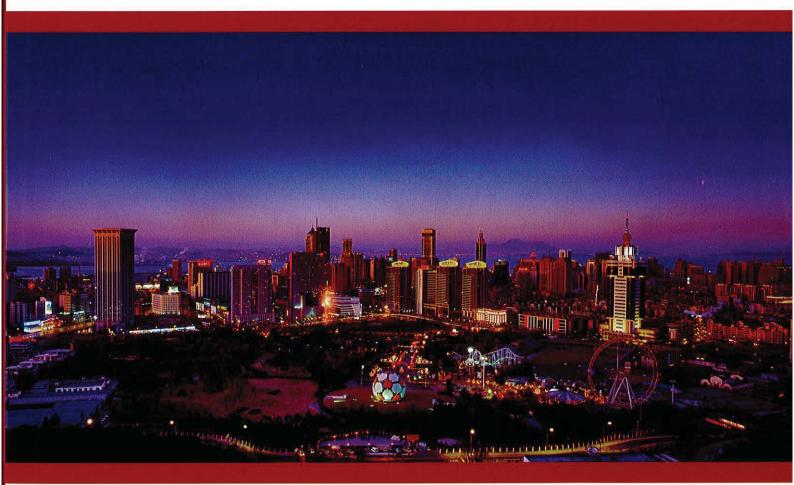


第二届中国大连国际DNA和基因组活动周BIT's 2nd World DNA and Genome Day - 2011

主题: 绿色经济时代重启生物之门

Theme: Reopen Bio-Gateway in Green Economy Era

时间: 2011年4月25-30日 地点: 中国大连世界博览广场 Time: April 25-30, 2011 Place: Dalian World EXPO Center, China



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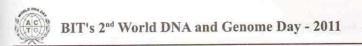


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Title: Beef Tenderness Markers in the Three Main French Beef Breeds: A Proteomic Analysis

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Abstract

In order to identify new markers of beef tenderness, a proteomic analysis was performed on Longissimus thoracis (LT) muscle of two extreme groups of 10 animals each of the three main French beef breeds: Blond d'Aquitaine (BA), Charolaise (Ch), Limousine (Li). Groups were constituted on the basis of an index combining tenderness score estimated by a trained panel and mechanical shear force measurement (Warner-Bratzler). The great number of recorded animals (3349 young bulls, Qualvigene French program, Genanimal-APISGENE) allowed choosing animals with contrasted meat tenderness but similar muscle characteristics: fibres, collagen, lipids. Muscle proteins were analysed by twodimensional electrophoresis and mass spectrometry. ANOVA analysis revealed 15% of spots with a differential abundance between tenderness groups in BA breed, 8% in Ch and 10% in Li. In the three breeds, we observed a higher abundance of fast glycolytic property proteins in the toughest group such as troponin T fast isoforms in Ch and BA, β enolase in Li and BA, phosphoglucomutase in Ch and glyceraldehyde phosphate dehydrogenase in Li. The opposite was found in the tender group with higher abundance of slow oxidative type proteins. The structural protein α actin was a positive marker of tenderness in the three breeds. We revealed 12 different spots of HSP27 protein with positive or negative correlation with tenderness and differences between tenderness groups were greater in BA and Li than in Ch breed. We confirmed a role in tenderness of proteins involved in the oxidative stress such as DJ-1. We revealed differential abundances of proteolytic proteins such as 26S protease regulatory subunit and proteasome subunit β2, more abundant in the tender Li and Ch groups respectively. Other proteins for which a role in tenderness has never been described before were revealed: protein 14.3.3 epsilon (involved in different functions as cell survival), a stress induced-phosphoprotein STIP1, glutathione S transferase involved in oxidative stress, geranyl transferase α type 2 and Rab GDP dissociation inhibitor factor β, involved in cellular transport and calcium releasing. These results will be used in the construction of a phenotyping tool for application in beef production.

Biography

Jean-François Hocquette was born in France, in 1962. He graduated as an Engineer in Agronomy from the National Institute of Agronomy, Paris-Grignon in 1985 and received a Ph.D. from the University of Paris XI in 1990 (specialty: endocrinology). Since 1991, JF Hocquette has been a research scientist at the National Institute of Agricultural Research, Animal Husbandry and Nutrition Department, Growth and Metabolism Unit. In 1999, he was appointed head of the "Muscle Growth and Metabolism" Group (5 scientists) of the Herbivore Research Unit in the same Institute. He is currently the Director of the Herbivore Research Unit (172 staff). JF Hocquette's research interest mainly concerns muscle biology as relevant to beef quality He has co-authored a patent for a genomic marker for meat tenderness and has been invited as the main speaker to more than fifteen conferences in international meetings. JF Hocquette is strongly involved in the activity of the Cattle Commission of the European Association for Animal Production. In 2005, he edited a book entitled "Indicators of milk and beef quality" (460 pages, 20 review papers), EAAP Publication No. 112. He is also a member of the French Meat Academy.