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MEAT QUALITY MAPPING IN NORWEGIAN PIGS AND TESTING LINKS WITH KNOWN MUTATIONS

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I. INTRODUCTION

Technological meat quality is affected by a multitude of factors, including farming-practices, feed, diverse stressors and genetics. In particular, the last decades' rapid development of breeding strategies have markedly improved main sustainability attributes in pig production by selecting genetics for more rapid growth and better feed conversion. However, changes in muscle growth are typically linked to changed muscle physiology, e.g., by a shift towards faster growing 'white', glycolytic (type IIB) muscle fibers. Such changes can also impact technological meat quality, along with the presence of known quality-related SNPs ('mutations'). Among such mutations are *200Q* ('Rendement Napole'), *199V*, *hal+* ('*RYR1_hal+'*) and PHKG1 [1, and references therein]. Together with producer- and often country-specific farm and slaughterhouse practices, nowadays' technological pork quality might therefore be different from typical textbook values for pork pH and color. Therefore, and to better understand the risk of more severe meat quality defects, large scale mapping data is needed to establish the status quo for main pork quality attributes.
Here we assessed pH and color for a large, heterogenous Norwegian pig population. We then explored possible relations of pH and color with known quality-related mutations for the tested population.

II. MATERIALS AND METHODS

We collected ham cuts with the *musculus semimembranosus* (SEM) from 291 pigs in early 2020 at six Norwegian meat cutting plants, representing a total of 43 producers. Convenience sampling was applied. Our previous study [1, compare also [2]] confirmed that the sample population comprised various cross-breds with genetics of the most commonly used breeds in Norway: Landrace, Duroc, Large White, Hampshire. Preslaughter handling, stunning and slaughtering were in accordance with EC regulations. Samples were obtained 12-24h post-slaughter, shortly after cutting. pH values were obtained at two defined SEM locations: in the center of the muscle ("central") and at the tapered, distal location ("distal"), either with a pH 3110 Set 2 (WTW Germany, pH electrode BlueLine 21 pHT) or with a testo 205 pH meter (Testo, Germany). pH meters were routinly calibrated using buffer solutions with pH 4.0 and 7.0. For the same two locations as with pH testing, subjective color assessment was done using the six grade Japanese Color Scale (JCS), were 1 represents the palest grade. Ahead of color-testing sample surfaces were left to bloom for at least 30min. SNP ('mutation') screening data were previously published, and were obtained using a PCR-RFLP assay [[1]. Possible location-dependet pH and JCS differences between the two locations were explored using a paired *t*-test. Mutation-dependent quality data differences ($pH_{central}$ vs. pH_{distal}, $JCS_{mutation+}$ vs. $JCS_{mutation-}$) were explored using the Welch's t-test, which is more robust against unbalanced sample numbers, e.g., when only a smaller number of individuals were mutation-positive. Statistical testing was performed with Minitab® (v. 22.2.2).

III. RESULTS AND DISCUSSION

Meat quality mapping revealed average pH-values of $pH_{central}$=5.49 (SD=0.10, Fig. 1A) and pH_{distal}=5.46 (SD=0.10, Fig1C) for the two SEM muscle locations. Visual color assessment using the Japanese Color Scale revealed average values of $JCS_{central}$=2.7 (SD=0.6, Fig. 1B) and JCS_{distal}=1.7 (SD=0.7, Fig. 1D) for the same two locations. The distal location showed significantly lower pH-values (T=7.46; P<0.001) and paler color (T=27.81; P<0.001), indicating marked differences within an individual muscle, and poorer quality for thinner, distal SEM areas.
A subset of N=135 pigs was screened for four mutations with known links to quality changes: *200Q, 199 V, hal+, PHKG1* [1]. Only for *200Q*, significant associations with meat quality could be established. Specifically, carriers of the *200Q* allele showed significantly lower pH values for the central ($P_{pH/N=86,49}$ <0.001) and the distal location

($P_{pH/N=86,49}$ <0.05). However, significant *200Q*-related color differences, were only detected for the distal ($P_{JCS/N=86,49}$ <0.001) and not the central location ($P_{JCS/N=86,49}$=0.063). Notably, *200Q* was associated with seemingly opposing changes on the two quality attributes: while *200Q*-positive samples showed a lower pH, indicating poorer quality, the *200Q*-positive samples were also darker, indicating better color quality. As previously reported, *hal+* was not detected in the Norwegian test population and associations could not be tested [1].

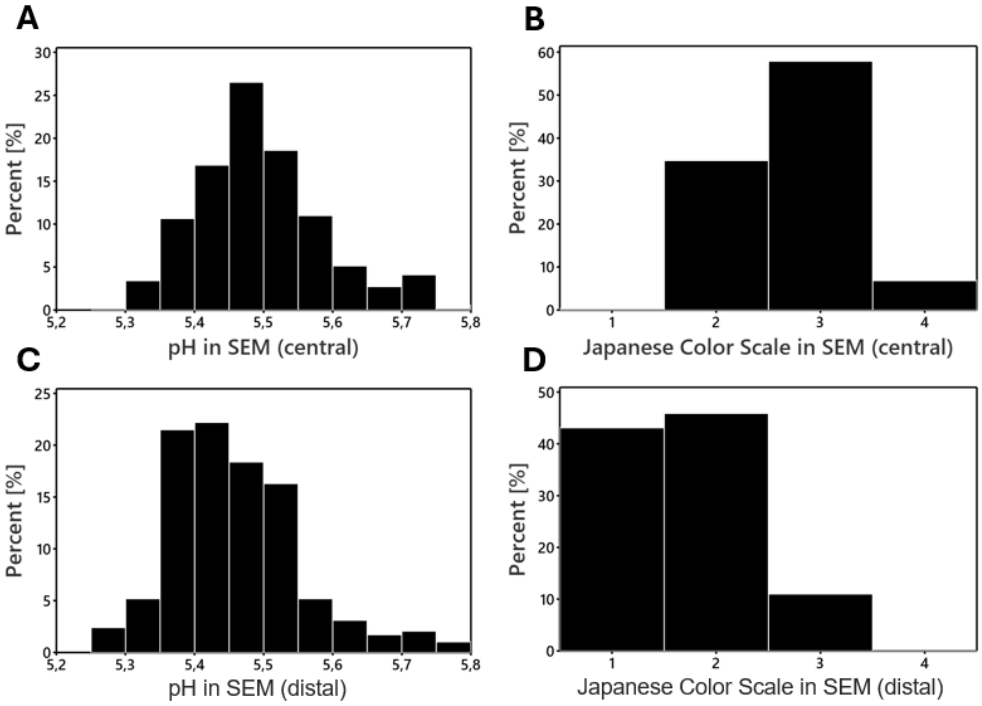


Figure 1. Technological meat qualities mapped for N=291 pigs collected from 6 different meat plants. pH and color (Japanese Color Scale) were tested at 2 specific ham location, i.e., at one central (A, B) and one distal (C, D) *semimembranosus* muscle (SEM) position.

IV. CONCLUSION

- We show marked, location-dependent pH and color differences within an individual muscle, with a declining technological meat quality from the muscle's thicker center to its thinner periphery.
- The Norwegian test population showed pH and color values that were lower than 'standard values', which are typically reported in textbooks and other compendia on pork quality. While most references give values for another main muscle, our data might point to a generally lower pH and paler color.
- Among the four tested mutations, an association with quality could only be established for *200Q*. Overall, however, the results on pH and color seem contradictory, since *200Q* was linked to a reduced pH but improved color.
- In sum, low pH and relatively pale color could not simply be explained by individual mutations. Rather, our data warrants studies on other factors to explore underpinnings of changed technological meat quality, including on transport and slaughter stress, feed, as well as on genetical and physiological attributes.

ACKNOWLEDGEMENTS

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