Which genes are best indicators for lesion age determination on the pig carcass – a preliminary study

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Assessing the age of lesions on the carcass may help determine the time of their infliction and identify the causes. This study aimed at identifying which genes are the best indicators of lesion age on the pig carcass. Five identical lesions were inflicted at the same time on the shoulders of 10 pigs (100±20 kg) using a piglet's lower jaw. Five biopsies on each pig were performed at 1, 4, 8, 24 and 48 h after injury (1 biopsy per lesion). Intact skin was the control. Local anaesthetic and analgesics were used to reduce pain. To assess the effect of slaughter and carcass treatment on gene expression, 5 of the 10 pigs were slaughtered 24 h after the infliction of two lesions in the hams. Biopsies were taken before and after slaughter (BS and AS, respectively), and after carcass singeing. The qPCR method was used to quantify the expression of 98 genes involved in wound healing, using the 2^(-DDCT) method. Since carcass handling induced a degradation of the RNA, only samples taken before carcass dehairing were used. Genes that were not differently expressed between BS and AS were first tested on 5 pigs in all lesion age categories. Fourteen selected genes were then tested on all pigs. Statistical analyses were performed using the PROCMIXED procedure of SAS. Eight genes (CCL2, COX2, IL2, IL6, IL8, MMP1, SERPINE1, TIMP1) presented different expression patterns by the age of the lesion ($P<0.05$). In particular, COX2 appears to be a useful indicator of lesions of 1h (1h=6.2 [3.2-12.1], 4h=1.4 [0.7-2.6], 8h=1.7 [0.9-3.4], 24h=1.6 [0.8-3.1], 48h=1.1 [0.6-2.2]; $P<0.01$), and MMP1 of 4-8h (1h=1.9 [0.7-5.5], 4h=35.6 [12.4-102.3],8h=19.2 [6.7-55.3], 24h=4.0 [1.4-11.4], 48h=1.3 [0.4-3.6]; $P<0.001$). Based on their different expression by age of lesion, the identified genes may be used in larger-scale studies to validate on-field methods for this assessment.