

## Estimation of crossbred beef carcass chemical composition by DXA scan of half-carcass or 11<sup>th</sup> rib

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The aim was to estimate beef half carcass (HC) composition by using dual X-ray absorptiometry (DXA), from either HC or 11<sup>th</sup> rib analysis. 42 cold left HC (94±49 kg, 17 to 157 kg) and their 11<sup>th</sup> rib were obtained from bulls of the three most Swiss-widespread crossbreeds in dairy herds (♀ Brown Swiss x ♂ Angus, Limousin or Simmental). Lean, fat, bone mineral content (BMC) and total masses of cold HC and 11<sup>th</sup> rib were determined with a DXA scanner (iLunar, GE, "Right Arm" mode). HC was then grinded, before chemical analyses (lipid: Soxhlet, protein: Dumas, ash: 550°C). Regressions (R software, v3.6.3) were tested between the HC and 11<sup>th</sup> rib DXA values and HC chemical composition. HC contained 11±8.3 (0.8 to 29.1) kg lipid, 18±9.2 (3.1 to 30.6) kg protein and 4±1.8 (0.8 to 6.5) kg ash. The cold HC weight explained a large part of chemical component masses (lipid:  $R^2=0.884$ , residual coefficient of variation (rCV)=25.3%; protein  $R^2=0.996$ , rCV=3.4%; ash  $R^2=0.971$ , rCV=7.8%). It was also well estimated from HC DXA total mass with a  $R^2$  of 0.999 (rCV=1.3%). Estimations of lipid, protein and ash masses with a single HC DXA variable were precise with fat ( $R^2=0.983$ , rCV=9.7%), lean ( $R^2=0.996$ , rCV=3.4%) and BMC ( $R^2=0.975$ , rCV=7.8%), respectively. Multiple models were even more accurate with HC DXA fat, lean and BMC masses for lipid mass ( $R^2=0.990$ , rCV=7.7%), cold HC weight and DXA fat mass for protein mass ( $R^2=0.997$  and rCV=2.9%), and cold HC weight, DXA fat and BMC masses for ash mass ( $R^2=0.979$  and rCV=7.2%). Multiple regressions of HC lipid and protein masses with 11<sup>th</sup> rib DXA variables provided  $R^2$  very close to the previous ones established from HC DXA scan. But the rCV was twice higher for lipid mass (rCV=14.8%) and remained equal for protein mass (rCV=2.9%). Crossbreed effect was rarely significant in models and only improved slightly their accuracy (maximum of +1% for the  $R^2$  and -1.5% for rCV for HC lipid mass from 11<sup>th</sup> rib DXA variables). A single rib DXA scan appears to be a promising method to estimate carcass composition in a simple, quick, reproducible, accurate and non-destructive way.