



# milestone report

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## Advanced livestock measurement technologies: PorkScan Pty Ltd (Year 2)

Milestones 2 and 3

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## Abstract

The development of the PorkScan Plus system using 3D scanning technologies to predict lean meat yield (LMY) of pig carcasses by the Australian pork industry has been the focus of considerable research and development effort over the past 10 years. This system needs to be available to pork processors for a relatively low capital hardware cost whilst delivering lean meat yield prediction results to an accuracy comparable to more expensive systems. PorkScan Pty Ltd has utilised funds from the four-year Rural R&D for Profit 'Advanced Livestock Measurement Technologies (ALMTech)' project, being led by Meat and Livestock Australia. Australian Pork Limited is a collaborator in this ALMTech project. Greenleaf Enterprises were commissioned by PorkScan Pty Ltd to undertake this project.

Revised lean meat yield algorithms were generated in this study which involved 184 carcasses varying in hot carcass weight and fat depth. All sides were scanned in a commercial laboratory using a full scan acquisition (10 mm axial slices using a GE Bright Speed unit) and each side was retrospectively separated into the forequarter, loin, belly and leg for analysis. The average carcass LMY percentage was 71% and ranged from 67% (loin) to 74% (leg). Predictive algorithms were then installed on PorkScan Plus at the participating abattoir, with 2,154 carcasses scanned and analysed. The LMY for whole carcass was 73.9%, with specific LMY ranging from 70.8 (loin) to 76.9% (belly).

Accurate LMY results will allow producers, abattoirs and wholesalers to target specific pigs for specific markets based on pig performance; will give processors the ability to select specific carcasses for further processing and will help producers make improved genetic selection decisions on-farm. The expected net result is increased efficiency, greater customer satisfaction and industry profitability for all stakeholders.

## Table of contents

1	Milestone description .....	4
1.1	Milestones 2 and 3 .....	4
1.1.1	Criteria .....	4
2	Project objectives .....	4
2.1	Developing indirect LMY systems for pork .....	4
2.1.1	Objectives .....	4
3	Methodology .....	5
3.1	Study Protocols & Processes .....	5
3.1.1	Refining the accuracy and repeatability of lean meat yield predictive algorithms for the PorkScan Plus system for pigs .....	5
4	Success in meeting the milestone .....	5
4.1	Trial Progress .....	5
4.1.1	Preliminary Results .....	5
5	Conclusions/recommendations .....	11
5.1	Key outcomes .....	11

# 1 Milestone description

## 1.1 Milestones 2 and 3

### 1.1.1 Criteria

A report outlining the studies conducted to refine predictive algorithms for determining lean meat yield of carcasses and key primals using PorkScan Plus are described. This work aims to address the objectives of the Round 2 Rural Research and Development for Profit project entitled “Advanced measurement technologies for globally competitive Australian meat” (ALMTech). This project is focused on providing more accurate descriptions of the key attributes that influence the value of sheep, beef and pigs to producers through the use of advanced measurement technologies for determining carcase lean meat yield, eating quality and improve compliance to market specifications.

It is anticipated that the ALMTech objective of realising productivity and profitability improvements for primary producers, will be assisted through PorkScan Plus by:

- a. Generating knowledge, technologies, products or processes that benefit primary producers;
- b. Strengthening pathways to extend the results or rural R&D, including understanding the barriers to adoption; and
- c. Establishing and fostering industry and research collaborations that form the basis for ongoing innovation and growth of Australian agriculture.

This report addresses the milestones of:

2. P1: satisfactory progress as deemed by the Steering Committee’s review of Milestone (year to date) report
3. P1: satisfactory progress as deemed by the Steering Committee’s review of Milestone (quarterly) report.

# 2 Project objectives

## 2.1 Developing indirect LMY systems for pork

### 2.1.1 Objectives

As stated in the Operational Plan 2017/18, Program 1.3 aims to develop indirect LMY measurement devices for use in beef, lamb and pig abattoirs. This study addresses Program 1.3 Output 6(f) – Design prototype technology for the indirect measurement of LMY in an abattoir.

This work aimed to:

- validate carcase and primal lean meat yield prediction equations from PorkScan Plus inputs across carcasses of varying genders, hot carcase weights and fat depths.
- investigate whether P2 fat depth of pigs can be reliably predicted by PorkScan Plus measures to support the opportunity for licensees to increase chain speed without compromising accuracy of data.

The expected net result of improved LMY and P2 assessments through PorkScan Plus will be accurate LMY assessments and enhanced feedback enabling on-farm productivity and efficiency improvements.

### 3 Methodology

#### 3.1 Study Protocols & Processes

##### 3.1.1 Refining the accuracy and repeatability of lean meat yield predictive algorithms for the PorkScan Plus system for pigs.

This study focussed on the use of PorkScan Plus, 3D laser scanning technology. to obtain carcass measures for inclusion in algorithms to accurately predict lean meat yield of pig carcasses and major primals, namely shoulder, loin, belly, leg and middle. PorkScan Plus has been developed with funding from the Pork CRC within Program 3. PorkScan Plus algorithms for LMY prediction were developed through these earlier studies but further work was recommended to improve accuracy of LMY assessments and improvement of algorithms to increase accuracy.

A project was commissioned by PorkScan Plus with Greenleaf Enterprises '*Extending PorkScan Plus Capability and Value – Commercial Validation*'

Study protocols required detailed records to be kept, including, but not limited to, property of origin, measured P2 measurements, 3D scanning on the slaughter floor with PorkScan Plus, and CT scan of carcasses with Dicom images captured and saved for each carcass for use in analysis.

Dicom image sets from CT Scans of each carcass were obtained and medical imaging software was then used to analyse each carcass image set. Measures of meat, fat and bone were taken for whole carcass, and leg, loin, belly and shoulder primals. Additional point measures of P2 and other fat and muscle depths were taken from the images to cross check with ultrasound measures of fat and loin depth taken on the slaughter floor using PorkScan Lite

Updated LMY equations were then integrated into the PorkScan Plus commercial system.

### 4 Success in meeting the milestone

#### 4.1 Trial Progress

##### 4.1.1 Preliminary Results

Carcass selection and scanning has been completed. A total of 184 carcasses were selected on the slaughter floor on the basis of the proposed selection grid (Table 1) and digital scans made using PorkScan Plus obtained for these carcasses. As it was not possible to select animals in the lower weight (<60 kg) + higher P2 (>10 mm) categories (they were simply not available during the trial), a range of 'extra' carcasses for the other parts of the grid were chosen. HCW and P2 specifications of the selected carcasses are detailed in Table 2 and Figure 1. Carcasses were split, chilled overnight, wrapped prior to transport to prevent contamination and delivered to a commercial CR scanning facility in Brisbane for scanning using a commercial CT scanner (GE BrightSpeed unit).

Table 1: Proposed grid for selection of 184 carcasses

Weight range	Porker <60kg			Bacon 60 – 80kg			Heavy bacon >80kg		
P2 Backfat	<10mm	10-13mm	≥14mm	<10mm	10-13mm	≥14mm	<10mm	10-13mm	≥14mm
Male	16	16	*	6	6	6	*	11	11
Female	16	16	*	6	6	6	*	11	11
Improvac	*	*	*	6	6	6	*	11	11

\* Unlikely to get pigs in this category

Table 2: Specifications of carcasses selected for CT scanning

Weight range	Porker <60kg			Bacon 60 – 80kg			Heavy bacon >80kg		
P2 Backfat	<10mm	10-13mm	≥14mm	<10mm	10-13mm	≥14mm	<10mm	10-13mm	≥14mm
Male	0	0	0	8	5	1	14	11	13
Female	16	7	0	8	12	6	2	9	12
Improvac	18	1	0	5	8	8	3	6	11
TOTAL	34	8	0	21	25	15	19	26	36
Total	42			61			81		

This selection of carcasses was considered to be a satisfactory industry representation of pigs processed daily.

The full data set was reviewed and 16 carcasses were removed due to lack of laser scanning data or CT image (168 carcasses used). The HCW measured by the scales immediately adjacent to the P2 station was used rather than HSCW from the kill sheet (since this is what the algorithm will use; average difference between HCW and HSCW was only 0.03% [ranged from -1.57% to 1.79%]). Full details of the methodology and statistical analysis used will be provided in the final report.

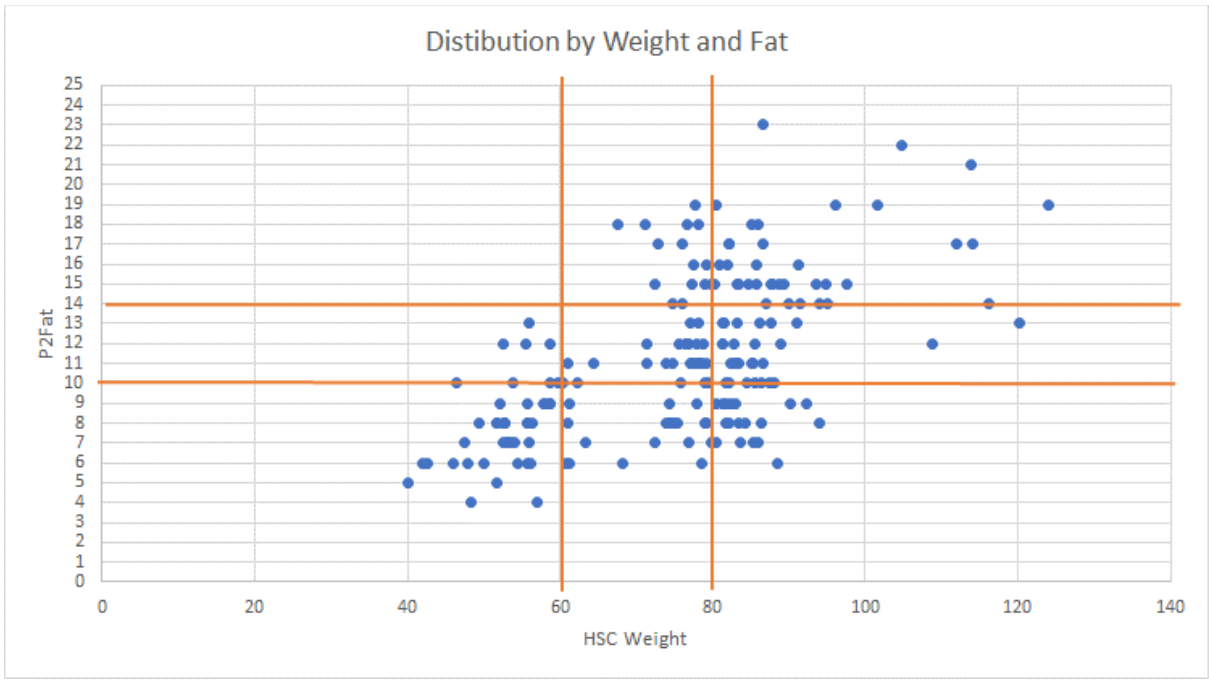


Figure 1: Distribution of P2 fat depth (mm) and HCW (kg) of selected carcasses

The average carcass LMY was 71% and ranged from 67% (loin) to 74% (leg) (Figure 2). In comparison to previous work conducted in 2008 (APL project 2190), carcass LMY values in this study were 12% higher (and 9-16% higher across the primals, Figure 2: Average LMY (%) for carcass and primals ). This accords with increases of 8% and 18% in LMY values in the 2015 and 2016 trials<sup>1</sup>, respectively, compared with APL2190 (Table ). The present study had the lowest mean P2 (Table ), which was inversely correlated to LMY (Figure ).

Questions have been raised and further discussions are in progress regarding the LMY results obtained from the scanning.

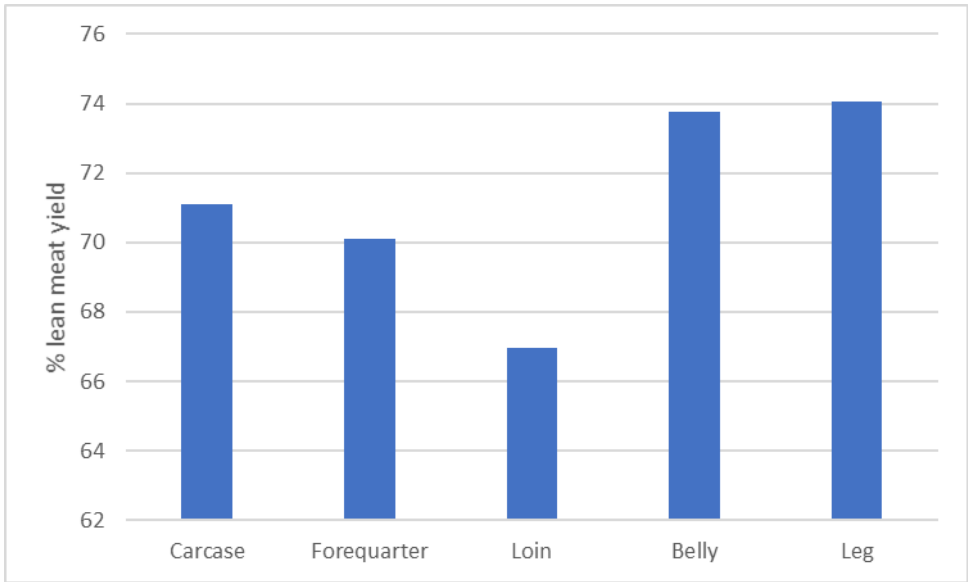


Figure 2: Average LMY (%) for carcass and primals

Table 3: Details and LMY results of current and previous trials

	Year of trial			
	2008	2015	2016	2018
# animals	72	120	82	178
HCW - mean (kg)	78.5	80.2	72.7	75.7
P2 - mean (mm)	12	12	13	11
Carcass (%LMY)	63.7	69.0	76.1	71.1
Forequarter (%LMY)	63.5		72.9	70.1
Middle (%LMY)	59.8		74.5	69.2
Loin (%LMY)	62.4		74.0	67.0
Belly (%LMY)	57.3		75.3	73.8
Leg (%LMY)	68.0		80.5	74.0

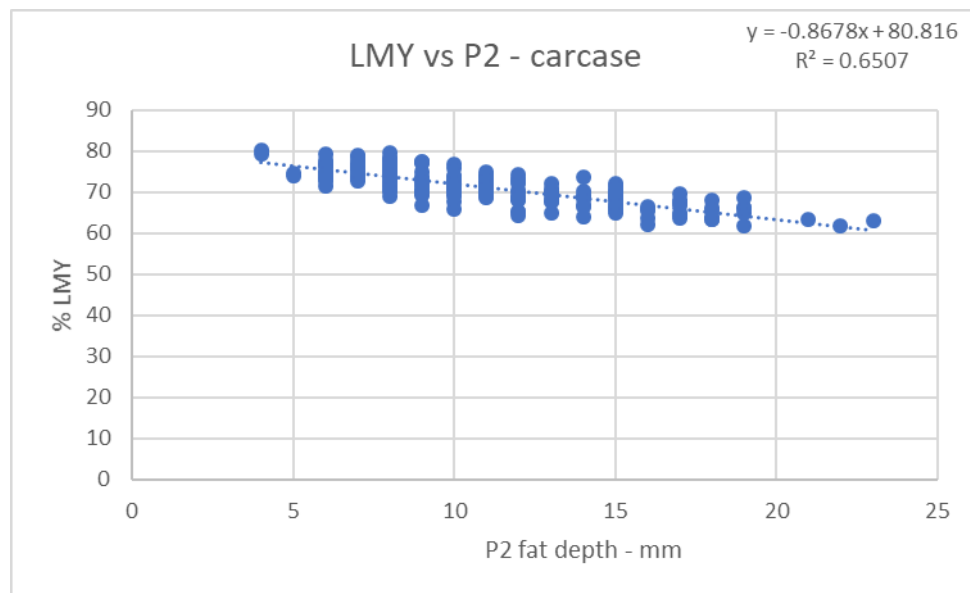


Figure 3: LMY vs P2 (current trial; LMY determined from CT scans and P2 determined from ultrasound measurement on chain)

The P2 fat depth results from ultrasound measurement (measured on chain by PorkScan operator) were similar to the results from CT images, with mean values being  $11.2 \pm 3.9$  mm (ultrasound) and  $10.9 \pm 4.0$  mm (CT image) ( $R^2=0.9404$ ). When the result from CT image was rounded to nearest whole mm (which is how ultrasound measurements were provided), 48% of measurements were identical. Some of the differences in the results may have arisen from:

- Ultrasound measurement was undertaken on full (unsplit) carcass, whereas CT image was captured on one half of split carcass
- Changes occurring during chilling of the carcass (ultrasound was undertaken on hot carcass whilst CT image was captured following ~30 hours of chilling).



Two groups of carcasses, with specific body shapes, were identified to be more highly predictable for LMY using HCW, P2, Sex and point measures (Table ).

Table 4: Models for new LMY algorithm

	Model #	Model name	Applicability	LMY prediction	R <sup>2</sup>	Standard error	RSD
<b>Carcase</b>	1	TopBodyLeft-Down, WaistLeft-Up Model	19%	$0.8420 + 0.0011*HCW + -0.0086*P2 + -0.0131*Sex + 0.0002*TopBodyWidth(mm) + -0.0007*WaistWidth(mm)$	0.87	0.01574	0.0064
	2	TopBodyLeft-Down, ButtLeft-Up, ChestLeft-Down Model	18%	$0.8148 + 0.0008*HCW + -0.0097*P2 + -0.0138*Sex + -0.0006*TopChestLeft148$	0.80	0.01902	0.0094
	3	Remaining Group Model	63%	$0.7969 + 0.0008*HCW + -0.0106*P2 + -0.0122*Sex$	0.81	0.01967	0.0391
	4	HCW, P2, Sex Model	100%	$0.7921 + 0.0008*HCW + -0.0101*P2 + -0.0125*Sex$	0.79	0.01943	0.0619
<b>Forequarter</b>	1	TopBodyLeft-Down, WaistLeft-Up Model	19%	$0.7385 + -0.0069*P2 + -0.0128*Sex + 0.0022*TopBodyLeft268$	0.74	0.01972	0.0109
	2	TopBodyLeft-Down, ButtLeft-Up, ChestLeft-Down Model	18%	$0.8816 + 0.0014*HCW + -0.0069*P2 + -0.0212*Sex + -0.0083*ChestLeft136 + 0.0046*WaistLeft136 + 0.0046*ChestLeft248$	0.79	0.0189	0.0086
	3	Remaining Group Model	63%	$0.7636 + 0.0008*HCW + -0.0086*P2 + -0.0128*Sex$	0.72	0.02062	0.043
	4	HCW, P2, Sex Model	100%	$0.7616 + 0.0008*HCW + -0.0082*P2 + -0.0130*Sex$	0.68	0.02142	0.0752
<b>Loin</b>	1	TopBodyLeft-Down, WaistLeft-Up Model	19%	$0.6707 + 0.0013*HCW + -0.0101*P2 + -0.0008*TopChestWidth(mm) + -0.0002*ButtRight268 + 0.0094*ChestLeft136 + 0.0094*TopBodyLeft134 + 0.0001*WaistLeft134$	0.92	0.01563	0.0059
	2	TopBodyLeft-Down, ButtLeft-Up, ChestLeft-Down Model	18%	$0.7575 + 0.0015*HCW + -0.0142*P2 + -0.0017*TopChestLeft138$	0.77	0.02442	0.0161
	3	Remaining Group Model	63%	$0.7794 + 0.0008*HCW + -0.0140*P2 + -0.0086*Sex$	0.77	0.02785	0.0783
	4	HCW, P2, Sex Model	100%	$0.7681 + 0.0009*HCW + -0.0132*P2 + -0.0093*Sex$	0.76	0.02709	0.1204
<b>Belly</b>	1	TopBodyLeft-Down, WaistLeft-Up Model	19%	$1.0141 + -0.0095*P2 + -0.0298*Sex + -0.0012*WaistWidth(mm) + -0.0003*ButtRight168 + 0.0067*ChestLeft136 + 0.0067*TopBodyLeft134$	0.91	0.02166	0.0117
	2	TopBodyLeft-Down, ButtLeft-Up, ChestLeft-Down Model	18%	$0.9951 + -0.0132*P2 + -0.0312*Sex + -0.0011*TopChestLeft148$	0.76	0.03174	0.0272
	3	Remaining Group Model	63%	$0.9450 + -0.0136*P2 + -0.0261*Sex + -0.0027*ChestLeft268 + 0.0026*ChestRight268$	0.77	0.03384	0.1145
	4	HCW, P2, Sex Model	100%	$0.9413 + -0.0132*P2 + -0.0274*Sex$	0.75	0.0337	0.1873
<b>Leg</b>	1	TopBodyLeft-Down, WaistLeft-Up Model	19%	$0.7737 + 0.0015*HCW + -0.0071*P2 + 0.0003*ChestWidth(mm) + -0.0006*WaistWidth(mm) + -0.0004*TopChestWidth(mm) + -0.0004*ChestLeft136 + -0.0002*ButtRight268$	0.89	0.01237	0.0037
	2	TopBodyLeft-Down, ButtLeft-Up, ChestLeft-Down Model	18%	$0.7808 + 0.0011*HCW + -0.0087*P2 + -0.0004*WaistLeft148$	0.68	0.02044	0.0113
	3	Remaining Group Model	63%	$0.7972 + 0.0008*HCW + -0.0088*P2 + -0.0089*Sex + -0.0002*TopChestLeft268 + 0.0004*WaistLeft278 + 0.0004*TopBodyLeft237$	0.74	0.01909	0.0357
	4	HCW, P2, Sex Model	100%	$0.7934 + 0.0008*HCW + -0.0082*P2 + -0.0089*Sex$	0.70	0.01971	0.0637

The new algorithm was successfully implemented into the laser scanning system on 22 May. On initial analysis of the calculated LMY from the 2,165 carcasses that were scanned, the results appeared realistic and had means and standard deviations not dissimilar to those of the trial carcasses (Table 5).

Table 5: Mean and standard deviation of calculated LMY following implementation of new algorithm (22/5/18, n=2165) and results from the trial (LMY determined by CT, February 2018, n=179)

	Carcase	Forequarter	Loin	Belly	Leg
<i>22/05/2018</i>					
<b>Mean LMY</b>	73.9%	72.6%	70.8%	76.9%	73.9%
<b>Standard deviation</b>	5.1%	3.7%	5.7%	6.9%	5.8%
<i>Trial carcasses</i>					
<b>Mean LMY</b>	71.1%	70.1%	67.0%	73.8%	74.0%
<b>Standard deviation</b>	4.2%	3.8%	5.4%	6.7%	3.5%

In comparison with previous results (2015 and 2016<sup>2</sup>), the LMY predictions were better in the current trial (Table to Table 1). Some of the improvement relative to the 2016 results presumably arose from measurement of actual HCW in the 2018 trial (rather than having to back calculate to get an estimated HCW for 2016 data). Furthermore, the larger number of animals (168 [2018] vs 90 [2015] or 81 [2016]), greater diversity of suppliers and utilisation of CT to determine LMY (rather than DEXA in 2015 and 2016), in the present trial, were improvements. Looking at the trend in the small amount of data available, it appears that in cases where HCW, P2, Sex model has a lower R<sup>2</sup> the addition of point measures provides a larger % increase.

Table 6: R<sup>2</sup> comparison (whole carcass)

Measurement Group	2015 R <sup>2</sup>	2016 R <sup>2</sup>	2018 R <sup>2</sup>
HCW, P2, Sex	0.71	0.51	0.79-0.81
HCW, P2, Sex, Point measures	0.72-0.79	0.57-0.73	0.80-0.87

Table 7 R<sup>2</sup> comparison (forequarter)

Measurement Group	2016 R <sup>2</sup>	2018 R <sup>2</sup>
HCW, P2, Sex	0.46	0.68-0.72
HCW, P2, Sex, Point measures	0.51-0.70	0.74-0.79

Table 8: R<sup>2</sup> comparison (loin)

Measurement Group	2016 R <sup>2</sup>	2018 R <sup>2</sup>
HCW, P2, Sex	0.10	0.76-0.77
HCW, P2, Sex, Point measures	0.22-0.38	0.77-0.92

Table 9: R<sup>2</sup> comparison (belly)

Measurement Group	2016 R <sup>2</sup>	2018 R <sup>2</sup>
HCW, P2, Sex	0.57	0.75
HCW, P2, Sex, Point measures	0.57-0.69	0.76-0.91

Table 1: R<sup>2</sup> comparison (leg)

Measurement Group	2016 R <sup>2</sup>	2018 R <sup>2</sup>
HCW, P2, Sex	0.32	0.70
HCW, P2, Sex, Point measures	0.39-0.65	0.68-0.89

For the P2 fat depth measurements by ultrasound, the use of point measures to predict P2 improved the model R<sup>2</sup> by 34% (from 0.41 to 0.55; Figure 4).

<sup>2</sup> APL 2015/525. 3D scanning for LMY – System completion and prediction algorithms. 2017.

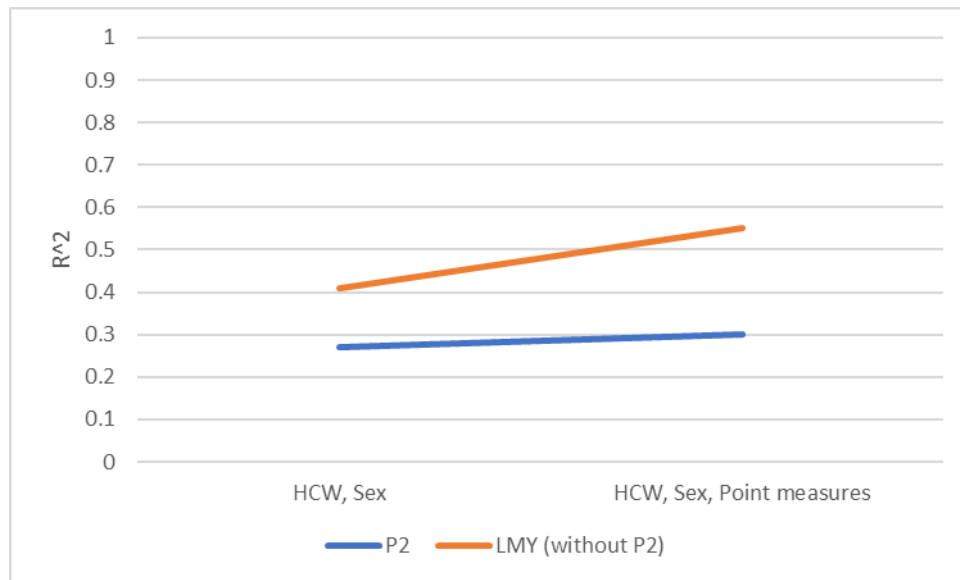


Figure 4: Comparison of  $R^2$  for P2 and LMY prediction equations

## 5 Conclusions/recommendations

### 5.1 Key outcomes

- Refined algorithms were determined which significantly increase the prediction of LMY prediction over existing P2, Sex and HCW inputs from earlier Pork CRC funded studies.
- A new algorithm was implemented into the PorkScan Plus system which has prediction accuracy of 0.68-0.92 for LMY in carcase and primals.
- The PorkScan Plus system could not predict P2 ( $R^2 0.55$ ) with sufficient accuracy to replace manual ultrasound measurement.
- Follow-up is underway to confirm LMY data of Australian pigs as determined by CT in this study.
- The final results and outcomes of the trial will be presented as the Milestone 4 report.