Serum Metabolites Differ in Late Gestation Sows at Various Risk for Pelvic Organ Prolapse

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Sow mortality is an economic and welfare concern for U.S. pork producers. Specifically, pelvic organ prolapse (POP) is estimated to account for approximately 21% of all sow mortality, and a direct cause of POP has yet to be identified. Previous work has begun to characterize physiological contributors to this phenomenon. Specifically, differences in inflammatory biomarkers and analytes in circulation have been identified in sows at varying POP risk. The objective of the current study was to utilize metabolomics to further evaluate differences in circulating metabolites between late gestation sows with presumed high or low risk for POP as well as between sows that did or did not subsequently experience POP. We hypothesized that metabolites would differ between sows at varying risk for POP. During late gestation (days 110-115), sows (n = 106) from two farms were evaluated for POP risk using a 3-point perineal scoring system. Briefly, a perineal score (PS) of 1 (PS1) presumes little to no risk of POP, a PS of 2 (PS2) presumes moderate risk of POP, and a PS of 3 (PS3) presumes high risk of POP. Blood samples were collected from PS3 sows (n = 56) and parity matched PS1 sows (n = 50). Out of these 106 sows, 29 subsequently experienced POP and 77 did not, all sows that prolapsed were assigned PS3. Serum metabolites were evaluated via gas chromatography mass-spectrometry (GC-MS) with a non-targeted approach. Metabolite comparisons were evaluated between PS3 sows and PS1 sows, sows that subsequently experienced POP versus sows that did not, and PS3 sows that subsequently did or did not experience POP. When comparing PS3 and PS1 sows, 14 metabolites were observed to be significantly different ($P \leq 0.05$), and five metabolites tended to be different ($0.05 < P \leq 0.10$). Of these 19 metabolites, 15 are known and four are unknown. When comparing sows that did or did not subsequently experience POP, six metabolites were significantly different ($P \leq 0.05$), and seven metabolites tended to be different ($0.05 < P \leq 0.10$). Of these 13 metabolites, 10 are known and three are unknown. Differences in 2-hydroxybutyric acid, erythritol, lysine, ornithine, phenylalanine, proline, tyrosine, and valine were observed ($P \leq 0.10$) in both the PS and POP comparisons. When evaluating the PS3 assigned sows that did or did not experience POP, three metabolites were significantly different ($P \leq 0.05$) and two metabolites tended to be different ($0.05 < P \leq 0.10$). Of these metabolites, four are known and one is unknown. The comparison of POP outcome demonstrated differences in 5-Oxoproline. 9-Octadecenoic acid was observed to be different in the PS3 POP outcome comparison and different based on PS. No metabolites were observed to be different across all three comparisons. Collectively, these data indicate sows at high risk for POP have differences in serum metabolites compared to sows at low risk, and differences exist between sows that did or did not subsequently experience POP. Focusing on metabolites that differ between high and low risk sows as well as between sows that did or did not experience POP can lead to a better understanding of what contributes to POP risk. This project was supported by the National Pork Board and the Foundation for Food and Agriculture Research.