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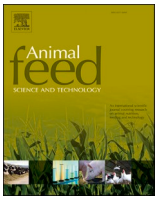

Maternal and/or direct feeding of organic acid-preserved cereal grains improves performance and digestive health of pigs from birth to slaughter

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ABSTRACT

A 2 × 2 factorial arrangement was conducted to investigate the effects of maternal and/or direct feeding of organic acid (OA)-preserved cereal grains compared to conventionally dried grains on pig growth performance to slaughter, nutrient digestibility, and carcass characteristics. On day 100 of gestation, 80 sows were blocked by parity, body weight (BW), and back-fat thickness and assigned to one of two diets (dried or preserved grain) until weaning. From day 10 postpartum, their progeny were assigned to one of two diets (dried or preserved grain) resulting in four dietary treatments: (1) dried (sow)-dried (progeny), (2) dried-preserved, (3) preserved-dried, and (4) preserved-preserved (n = 20 litters per treatment). Pigs remained in these groups post-weaning (PW) and were monitored until slaughter at 142 days PW (n = 10 pens per treatment). Additionally, faecal samples from pigs in the dried-dried and preserved-preserved groups were collected for microbial analysis throughout production. Progeny from sows fed preserved grain had improved gain-to-feed ratio (G:F) between days 0–14 and 62–142 PW, with enhanced coefficients of apparent total tract digestibility (CATTD) of dry matter (DM), organic matter (OM), and gross energy (GE) on day 30 PW and CATTD of nitrogen (N) at slaughter compared to those from sows fed dried grain ($P < 0.05$). Pigs directly fed preserved grain exhibited higher daily gain from weaning to slaughter, improved G:F from day 14 PW, and greater BW from day 30 PW compared to those directly fed dried grain ($P < 0.05$). Pigs fed preserved grain showed increased CATTD of DM, OM, N, and GE on day 30 PW and at slaughter ($P < 0.01$). Additionally, these pigs had higher carcass weight, kill-out percentage, and muscle depth at slaughter ($P < 0.01$). Pigs in the preserved-preserved group had higher microbial diversity at weaning and on day 30 PW, with beneficial taxa such as *Ruminococcus*, *Propionibacterium,* and *Faecalibacterium* enriched at key

Abbreviations: ADF, acid detergent fibre; ADFI, average daily feed intake; ADG, average daily gain; AIA, acid-insoluble ash; BF, back-fat thickness; BW, body weight; CATTD, coefficient of apparent total tract digestibility; CP, crude protein; DE, digestible energy; DM, dry matter; DON, deoxynivalenol; GE, gross energy; G:F, gain-to-feed ratio; N, nitrogen; aNDF, neutral detergent fibre assayed with thermal-stable amylase and expressed inclusive of residual ash; NE, net energy; OA, organic acid; OM, organic matter; OTA, ochratoxin A; PW, post-weaning; SID, standard ileal digestible; TMC, total mould count; ZEN, zearalenone.

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production stages compared to those in the dried-dried group ($P < 0.05$). In conclusion, maternal feeding of preserved grain improved progeny feed efficiency and CATTD of nutrients, while direct feeding enhanced pig growth performance, CATTD of nutrients, and carcass characteristics. Combined maternal and direct feeding of preserved grain also improved microbial health throughout production.

1. Introduction

Feed represents the largest financial and environmental burden in pig production, with energy being the most expensive component (McAuliffe et al., 2017; Andretta et al., 2021; Noblet et al., 2022). Cereal grains are the primary energy source in pig diets, and their quality directly affects feed palatability and digestibility (Guerre, 2016; Clarke et al., 2018a; 2018b). Storage is a critical stage in the supply chain for maintaining grain integrity and preventing spoilage (Ziegler et al., 2021). In temperate climates, cereals are commonly harvested at moisture levels exceeding the safe threshold for long-term storage, necessitating effective preservation methods (Jouany, 2007). While mechanical drying is the conventional approach, it is energy intensive, increasing production costs and greenhouse gas emissions (Chojnacka et al., 2021; Mondal and Sarker, 2024). Additionally, high-temperature drying can cause structural and compositional damage to grains, reducing nutritional value and digestibility (Jokiniemi and Ahokas, 2014; Coradi et al., 2020). These challenges have driven the search for more sustainable, cost-effective preservation alternatives.

Topical application of organic acids (OA) offers an energy-efficient solution by lowering pH and suppressing microbial activity, thereby reducing bacterial, mould, and mycotoxin contamination (Koyuncu et al., 2013; Kholif et al., 2025). Among these OA, propionic acid is widely used due to its competitive cost and potent antifungal properties (Dijksterhuis et al., 2019; Villa et al., 2024). However, concerns over equipment corrosion, volatility, palatability, and antimicrobial resistance have led to the development of stabilised formulations incorporating other OA and salts for improved efficacy (Rutenberg et al., 2018; Nowak et al., 2021). Beyond preservation, dietary OA supplementation in pigs can enhance nutrient digestibility and intestinal health, potentially reducing reliance on in-feed antimicrobials (Tugnoli et al., 2020). These benefits are primarily linked to enhanced enzymatic activity, improved mineral utilisation, pathogen inhibition, and modulation of beneficial intestinal bacteria (Pearlin et al., 2020; Nguyen et al., 2020). While research on dietary propionic acid supplementation in pigs remains limited, studies have reported beneficial shifts in gastrointestinal microbial populations (Bolduan et al., 1988; Matthew et al., 1991), improved amino acid digestibility (Mosenthin et al., 1992), and reduced diarrhoea incidence (Tsiloyiannis et al., 2001).

Recent findings from our group have demonstrated that preserving grain with a propionic acid-based mould inhibitor not only improved grain quality, but also enhanced pig growth performance, nutrient digestibility, and intestinal health during the post-weaning (PW) period (Maher et al., 2024; Connolly et al., 2025). Given the well-documented challenges of weaning, most research on dietary OA inclusion has focused on this critical stage of production (Suiryanrayna and Ramana, 2015). However, emerging evidence suggests that OA benefits extend to other production stages, including the grow-finisher period and lactation (Lan and Kim, 2018; Wang et al., 2022).

Dietary OA supplementation in sows during late gestation and lactation has been shown to improve nutrient digestibility, modulate the microbiota, and enhance progeny growth (Liu et al., 2014; Devi et al., 2016; Sampath et al., 2022). Manipulating maternal nutrition can positively influence piglet health and performance by supporting gastrointestinal tract development, enhancing nutrient absoprtion capacity, and shaping microbial colonisation (Lu et al., 2012; Gormley et al., 2024). Additionally, direct OA supplementation pre-weaning has been reported to stimulate growth and improve nutrient digestibility PW (Le Gall et al., 2009). Thus, feeding OA-preserved grain from pre-weaning throughout production may further enhance growth, nutrient digestibility, and carcass characteristics. However, the current literature is primarily focused on short-term outcomes, particularly during the PW period, with no studies evaluating the potential long-term impacts to slaughter.

Thus, the objective of this study was to investigate the effects of maternal and/or direct feeding of OA-preserved grain compared to dried grain on pig performance to slaughter, nutrient digestibility, and carcass characteristics. Additionally, the study examined the effects of the combined maternal and direct feeding of dried or OA-preserved grain on the faecal microbiota of pigs at key production stages. It was hypothesised that maternal and direct feeding of OA-preserved grain would enhance pig performance, nutrient digestibility and carcass characteristics at slaughter, while their combined feeding would further improve these parameters, as well as the microbial health of pigs throughout production.

2. Material and methods

Ethical approval was granted by the University College Dublin Animal Research Ethics Committee (AREC-20–22-O'Doherty) and all procedures were conducted in accordance with Irish legislation (SI no. 534/2012) and the EU directive 2010/63/EU for animal experimentation.

2.1. Grain management and quality assessment

The winter wheat (cv. *JB Diego*) and spring barley (cv. *SY Errigal*) grains used in this study were established in Ireland during the 2022 growing season and were sourced from Platin Grain (Drogheda, Co. Louth, Ireland). The wheat was sown in October 2021 and

received a 3-spray fungicide programme and a 3-split nitrogen (N) application rate of 180 kg N/ha. The barley was sown in February 2022 and received a 2-spray fungicide programme and a 2-split N application rate of 140 kg/ha. The wheat and barley were harvested in August 2022 at a moisture content of 179.7 g/kg and 182.1 g/kg, respectively. Prior to storage, both cereals were divided into two batches: one batch was mechanically dried using a continuous flow-type dryer (Cimbria, Thisted, Denmark) for 3 hours (h), followed by a 2-h cooling period, while the other was preserved with an organic acid liquid surfactant mould inhibitor as described by Maher et al. (2024). The OA blend (MycoCURB ES Liquid; propionic acid (650 g/kg), ammonium propionate (70 g/kg), glycerol polyethyleneglycol ricinoleate (17.5 g/kg) and a carrier), was sourced from Adesco Nutricines (Dungarvan, Waterford, Ireland), and was applied at 4 g/kg via spray action using a mixing auger for uniform distribution. All grains were ventilated and stored for at least 120 days.

At harvest, the moisture content of the wheat and barley was determined using a DICKEY-john GAC 2500-UGMA electronic moisture metre (Auburn, IL, USA). Grain density was measured using a Pfeuffer Chondrometer and bulk density calibration chart and the thousand grain weight was measured by recording the weight of 1000 grains using a Pfeuffer Contador seed counter (Kitzingen, Germany). Before feed manufacture, representative grain samples were collected and analysed for dry matter (DM), ash, gross energy (GE), crude protein, crude fibre, starch, ether extract, pH, total mould count, and mycotoxins. The pH of the grain was measured using a pH probe (Mettler-Toledo FiveEasy Plus; Greifensee, Switzerland), calibrated using certified pH 4 and pH 7 buffer solutions. Mould count was determined using the colony count technique (ISO21527–2:2008) as described by Laca et al. (2006). The mycotoxin presence of aflatoxin B1, B2, G1 and G2, fumonisin B1 and B2, deoxynivalenol (DON), T-2 Toxin, HT-2 Toxin, zearalenone (ZEN) and ochratoxin A (OTA) were quantified by liquid chromatography-mass spectrometry as previously described by Soleimany et al. (2012). The chemical and mycotoxin analyses of the wheat and barley after storage are presented in Table 1.

2.2. Experimental design and animal management

A total of 80 Large White × Landrace sows (Hermitage, Kilkenny, Ireland) were selected on day 100 of gestation and blocked according to parity (mean ± SD; 3.3 ± 0.3), body weight (BW; 270.4 kg ± 5.5), and back-fat thickness (BF; 15.9 mm ± 0.3). Within each block, sows were assigned to one of two dietary groups: a dried grain lactation diet and a preserved grain lactation diet (n = 40 sows per treatment) until weaning (26 days postpartum). During gestation, sows were housed in dynamic groups of 20 with fully slatted floors and insulated concrete lying bays. The temperature was maintained at 20°C throughout gestation. On day 100 of gestation, sows were housed in groups of 10 according to their assigned diets. On day 110 of gestation, sows were moved into individual farrowing pens (2.2 × 2.4 m) across four different farrowing rooms. The dietary groups were evenly distributed across the rooms and the temperature was maintained at approximately 24°C, gradually decreasing to 20°C by day 7 of lactation. Sows had free access to water throughout the experiment via single-bite drinkers.

At farrowing, litter data, including total-born, live-born, stillborn, and mummified piglets, was recorded. Litters were standardised to 17 piglets per sow within 24 h postpartum by cross-fostering within dietary groups. Piglets had access to a water-heated floor pad in each farrowing pen which remained at 32°C throughout the suckling period. Within the first 5 days postpartum, piglets had their tails docked, teeth clipped, and received an intramuscular injection of iron (Gleptosil, Ceva Sante Animale; Lisbourne, France). On day 10 postpartum, within maternal block, litters were assigned to one of two starter diets: a dried grain starter diet and a preserved grain starter diet (n = 20 litters per treatment). The experiment was arranged in a 2 × 2 factorial, resulting in four dietary treatment groups: (1) dried grain for both sows and progeny (dried-dried), (2) dried grain for sows and preserved grain for progeny (dried-preserved), (3) preserved grain for sows and dried grain for progeny (preserved-dried), and (4) preserved grain for both (preserved-preserved; Fig. 1).

All feed offered to piglets during lactation was recorded daily to calculate litter feed intake from day 10 postpartum until weaning. Litter size and litter weight were recorded after cross-fostering, before the starter diet was introduced (day 10) and at weaning (day 26). Subsequently, mean piglet BW, mean piglet gain, and pre-weaning litter mortality were calculated. Faecal scoring of piglets during

Table 1
The chemical analysis of experimental wheat and barley after storage on a dry matter basis (g/kg DM, unless otherwise indicated).

Cereal crop type	Wheat		Barley	
Grain preservation	Dried	Preserved	Dried	Preserved
Chemical composition (g/kg DM)				
Dry matter (g/kg)	868.4	820.3	872.1	817.9
Ash	17.5	17.3	22.7	21.6
Gross energy (MJ/kg)	18.0	18.0	17.4	17.3
Ether extract	16.9	16.8	21.8	20.8
Crude protein	112.9	112.7	106.6	107.3
Crude fibre	27.1	26.2	57.9	55.6
Starch	670.9	666.8	612.5	610.0
pH	6.0	5.7	5.8	5.6
Total mould count (cfu/g)[a]	2.2	0.9	3.3	1.2

[a] These values were log-transformed.
All mycotoxins analysed were below the detectable levels: Aflatoxin B1, B2, G1 and G2 (<1 μg/kg); fumonisin B1 (<125 μg/kg) and fumonisin B2 (<50 μg/kg) deoxynivalenol (<75.0 μg/kg), HT-2 Toxin (<4.0 μg/kg), T-2 Toxin (<4.0μg/kg), zearalenone (<10.0 μg/kg) and ochratoxin A (<1.0 μg/kg)

lactation was carried out on days 7, 14, 21, and 26 postpartum. Each pen was scored by the same individual using a scale from 1 to 5 where; 1 = hard, firm faeces; 2 = slightly soft faeces; 3 = soft, partially formed faeces; 4 = loose, semi-liquid faeces and 5 = watery, mucous-like faeces as described by Walsh et al. (2013). Diarrhoea incidence was characterised by a faecal score greater than 3.

At weaning, a total of 1120 pigs were selected and housed in mixed-sex groups of 28 animals according to their pre-weaning dietary treatments. Each pen consisted of piglets from two different sow litters (n = 10 pens per treatment). They were housed sequentially in first and second-stage weaner accommodations (days 0–30 and days 30–62 PW) and finisher accommodations (days 62–142 PW). Using an electronic scale (Avery, Smethwick, UK), pen weight was recorded at weaning, day 14 PW, day 30 PW, day 62 PW and day 142 PW (slaughter). Feed consumption was recorded fortnightly to calculate average daily feed intake and gain-to-feed ratio (G:F). The weaner accommodation temperature was maintained at 28°C during the first week PW, reducing by 2°C each week until 22°C was reached by day 30 PW. The temperature was maintained at 20°C thereafter. Ventilation for all houses was via a punched ceiling with air exhausted through a variable speed fan linked to a computer-controlled thermostat (Big Dutchman 135, Vechta, Germany). Pigs were monitored twice daily, and any pig showing signs of ill health was recorded and treated according to veterinarian recommendations. No mixing of pigs occurred throughout the experiment. Any pigs removed were documented, and their feed intake was adjusted based on the duration they remained in the pens to ensure accurate growth performance calculations. All accommodation was illuminated by daylight and artificial light. Pigs had free access to water via drinker bowls throughout the experiment.

2.3. Diets and feeding

The diets were manufactured by Kiernan Milling (Granard, Longford, Ireland) and were formulated to meet or exceed the NRC (2012) recommendations for pigs at the relevant stages of production. From days 0–100 of gestation, sows were offered 2.4 kg/day of a standard gestation diet in meal form via a 20-space feeding trough. The gestation diet contained 150 g/kg of crude protein (CP)/kg, 12.2 MJ of digestible energy (DE)/kg, 8.6 MJ of net energy (NE)/kg and 6 g of standardised ileal digestible (SID) lysine/kg. From day 100 of gestation to farrowing, sows were allocated 2.7 kg/day of their assigned experimental diets in meal form via individual feeding crates. The lactation diet was formulated to contain 170 g of CP/kg, 14.2 MJ of DE/kg, 10.0 MJ of NE/kg and 10 g of SID lysine/kg. Post-farrowing, feed supply increased by 1.0 kg/day from days 1–3 post-farrowing and by 0.5 kg/day from days 4–6 post-farrowing. In the farrowing house, sows were fed four times daily through a computerised feed delivery system (HydroAir, Big Dutchman, Vechta, Germany), and feed curves were individually adjusted throughout lactation, to prevent feed wastage.

From day 10 postpartum to weaning, the starter diet (2 mm diameter pellets) was offered to piglets in frequent small quantities throughout the day using circular hopper creep feeders (Mini Hopper Creep Feeder, Rotecna, Spain). The starter diet was formulated to contain 190 g of CP/kg, 17.0 MJ of DE/kg, 12.0 MJ of NE/kg and 12.5 g/kg of SID lysine. During all stages from weaning until slaughter, pigs had free access to feed via 4-space feeders (Verba, Sint-Oedenrode, Netherlands). During the first 14 days PW, pigs remained on their starter diets and an additional creep hopper (Complete Maxi Pan w/Hopper, Rotecna, Spain) was placed in the pens to encourage feed intake. Pigs were subsequently offered the following sequence of pelleted diets (3 mm diameter): two-stage weaner diet from day 14–30 PW (192 g CP/kg, 16.0 MJ DE/kg, 11.3 MJ NE/kg and 12.5 g SID lysine/kg), and day 30–62 PW (189 g CP/kg, 15.0 MJ DE/kg, 10.6 MJ NE/kg and 11 g/kg SID lysine) and two-stage finisher diet from day 62–102 PW (160 g CP/kg, 14.0 MJ DE/kg, 9.9 MJ NE/kg and 10 g SID lysine/kg) and day 102–142 PW (155 g CP/kg, 13.8 MJ DE/kg, 9.7 MJ NE/kg and 8.5 g SID lysine/kg). The ingredient composition and chemical analyses of all diets are presented in Tables 2 and 3.

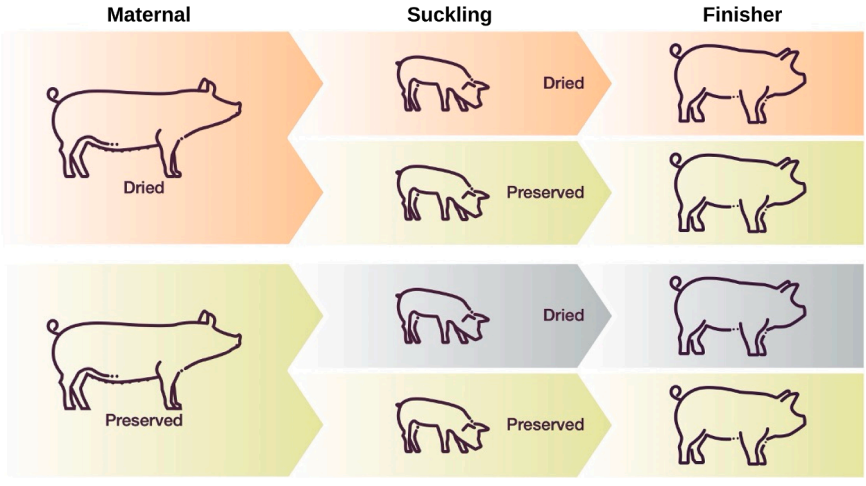

Fig. 1. The feeding strategy across production stages, including maternal (late gestation to weaning) and direct (suckling to finisher) feeding of dried or preserved grain.

2.4. Coefficient of apparent total tract digestibility

Thirty piglets from 10 litters per treatment were selected based on average birth weight and tagged on day 10 postpartum. A pooled faecal sample was collected from these pigs on day 30 PW and at slaughter for the determination of the coefficient of apparent total tract digestibility (CATTD) of nutrients (n = 10 samples per treatment). The CATTD was calculated using the acid-insoluble ash (AIA) technique according to McCarthy et al. (1977), using the following equation: CATTD of nutrient (g/kg) = [1 – (nutrient in faeces/nutrient in diet) × (AIA-diet/AIA-faeces)], where nutrient in faeces and nutrient in diet represent the nutrient concentration (g/kg) in the faeces and diet DM, respectively and AIA-diet and AIA-faeces represent the marker concentrations (g/kg) in the diet and faeces DM, respectively (Clarke et al., 2018c). Before analysis, faecal samples were dried at 55°C for 72 h.

2.5. Chemical analysis

Representative feed samples were collected throughout the experiment and retained for chemical and mycotoxin analyses. The feed and dried faeces were milled through a 1 mm screen (Christy and Norris Hammer Mill, Chelmsford, UK). The crude ash content was determined after ignition of a weighted sample in a muffle furnace (Nabertherm, Breman, Germany) at 550°C for 6 h. The GE content was determined using an adiabatic bomb calorimeter (Parr Instruments, Moline, IL, USA). The N content was determined using the

Table 2
The ingredient composition of the experimental diets (g/kg).

Production stage	Lactation	Starter	Weaner 1	Weaner 2	Finisher 1	Finisher 2
Ingredients (g/kg)						
Wheat[a]	380.0	300.0	300.0	400.0	400.0	400.0
Barley[a]	250.0	135.0	224.0	260.0	200.0	200.0
Maize	0.0	0.0	0.0	0.0	148.0	148.0
Soya bean meal	170.0	30.0	150.0	150.0	150.0	100.0
Rapeseed meal	0.0	0.0	0.0	0.0	15.0	45.0
Full-fat soya	80.0	110.0	100.0	100.0	0.0	0.0
Soya protein concentrate	0.0	50.0	40.0	0.0	0.0	0.0
Whey protein	0.0	70.0	30.0	0.0	0.0	0.0
Whey	0.0	180.0	100.0	0.0	0.0	0.0
Potato protein	0.0	30.0	0.0	0.0	0.0	0.0
Soya hulls	10.0	0.0	0.0	22.0	10.0	10.0
Soya oil	25.0	5.0	10.0	20.0	5.0	5.0
Starch	0.0	38.0	0.0	0.0	0.0	0.0
Pollard	40.0	20.0	20.0	20.0	50.0	70.0
Beet pulp	10.0	0.0	0.0	0.0	0.0	0.0
Vitamin and mineral premix	1.5[b]	3.0[c]	3.0[d]	3.0[d]	1.0[e]	1.0[e]
Salt	5.0	3.0	3.0	3.0	3.0	3.0
Monocalcium phosphate	8.0	9.0	5.0	3.0	1.0	1.0
Calcium carbonate (limestone)	12.0	6.0	6.0	10.0	10.0	10.0
L-lysine HCl, 78.8 %	4.0	6.0	5.0	5.0	4.0	4.0
DL-Methionine	1.3	2.5	1.5	1.5	1.0	1.0
L-Threonine	2.5	2.5	2.1	2.2	1.8	1.8
L-Tryptophan	0.7	1.0	0.4	0.3	0.2	0.2

[a] Grain was either mechanically dried to 140 g/kg moisture content or preserved with an organic acid mould inhibitor (650 g/kg propionic acid) at an inclusion rate of 4 g/kg and remained at 180 g/kg moisture content.

[b] Vitamin and mineral premix (per kg lactation diet): 70 mg of Fe as $FeSO_4$; 60 mg of Mn as MnO; 80 mg of Zn as ZnO; 15 mg of Cu as $CuSO_4$; 0.6 mg of I as calcium iodate on a calcium sulphate/calcium carbonate carrier; 0.2 mg Se as sodium selenite; 3.4 mg of vitamin A as retinyl acetate; 0.025 mg of vitamin D_3 as cholecalciferol; 100 mg of vitamin E as DL-α-tocopheryl acetate; 2 mg of vitamin K as phytylmenaquinone, 2 mg of vitamin B_1 as thiamine, 5 mg of vitamin B_2 as riboflavin, 3 mg of vitamin B_6 as pyridoxine, 0.015 mg of vitamin B_{12} as cyanocobalamin, 12 mg of nicotinic acid; 10 mg of pantothenic acid; 500 mg of choline chloride; 0.02 mg of biotin, 5 mg of folic acid.

[c] Vitamin and mineral premix (per kg starter diet): 250 mg of Fe as $FeSO_4$; 60 mg of Mn as MnO; 275 mg of Zn as ZnO; 340 mg of Cu as $CuSO_4$; 3 mg of I as calcium iodate on a calcium sulphate/calcium carbonate carrier; 0.3 mg Se as sodium selenite; 4 mg of vitamin A as retinyl acetate; 0.025 mg of vitamin D_3 as cholecalciferol; 376 mg of vitamin E as DL-α-tocopheryl acetate; 5 mg of vitamin K as phytylmenaquinone, 5 mg of vitamin B_1 as thiamine, 10 mg of vitamin B_2 as riboflavin, 7.5 mg of vitamin B_6 as pyridoxine, 0.06 mg of vitamin B_{12} as cyanocobalamin, 75 mg of nicotinic acid; 40 mg of pantothenic acid; 500 mg of choline chloride, 0.04 of biotin, 5 mg of folic acid

[d] Vitamin and mineral premix (per kg weaner diet): 100 mg of Fe as $FeSO_4$; 40 mg of Mn as MnO; 110 mg of Zn as ZnO; 135 mg of Cu as $CuSO_4$; 1 mg of I as calcium iodate on a calcium sulphate/calcium carbonate carrier; 0.4 mg Se as sodium selenite; 1.6 mg of vitamin A as retinyl acetate; 0.01 mg of vitamin D_3 as cholecalciferol; 150 mg of vitamin E as DL-α-tocopheryl acetate; 2 mg of vitamin K as phytylmenaquinone, 4 mg of vitamin B_1 as thiamine, 4 mg of vitamin B_2 as riboflavin, 3 mg of vitamin B_6 as pyridoxine, 0.03 mg of vitamin B_{12} as cyanocobalamin, 30 mg of nicotinic acid; 20 mg of pantothenic acid; 250 mg of choline chloride, 0.02 mg of biotin, 2 mg of folic acid

[e] Vitamin and mineral premix (per kg finisher diet): 24 mg of Fe as $FeSO_4$; 30 mg of Mn as MnO; 80 mg of Zn as ZnO; 15 mg of Cu as $CuSO_4$; 0.5 mg of I as calcium iodate on a calcium sulphate/calcium carbonate carrier; 0.2 mg Se as sodium selenite; 0.7 mg of vitamin A as retinyl acetate; 0.01 mg of vitamin D_3 as cholecalciferol; 40 mg of vitamin E as DL-α-tocopheryl acetate; 2 mg of vitamin K as phytylmenaquinone, 2 mg of vitamin B_1 as thiamine, 2 mg of vitamin B_2 as riboflavin, 3 mg of vitamin B_6 as pyridoxine, 0.015 mg of vitamin B_{12} as cyanocobalamin, 12 mg of nicotinic acid; 10 mg of pantothenic acid; 250 mg of choline chloride

Table 3
The chemical analysis of the experimental diets on an as-fed basis (g/kg, unless otherwise indicated).

Production stage	Lactation		Starter		Weaner 1		Weaner 2		Finisher 1		Finisher 2	
Grain preservation	Dried	Preserved	Dried	Preserved	Dried	Preserved	Dried	Preserved	Dried	Preserved	Dried	Preserved
Chemical composition												
Dry matter	885.3	867.2	885.1	881.7	873.5	863.7	871.2	855.3	877.0	862.4	876.0	859.1
Ash	52.6	50.8	52.1	49.7	46.1	45.2	44.5	42.2	40.1	39.4	38.0	37.5
Gross energy (MJ/kg)	16.1	15.9	16.7	16.4	16.4	16.2	16.4	16.1	15.5	15.3	15.2	15.0
Ether extract	51.0	49.0	60.0	59.5	47.0	45.5	52.0	48.0	22.0	19.0	21.0	18.5
Crude protein	170.0	168.0	196.0	195.0	192.0	190.8	188.0	186.0	160.0	158.0	141.0	140.0
Crude fibre	52.0	47.0	39.5	38.0	38.0	37.0	33.0	31.0	42.0	40.0	43.0	41.0
aNDF	140.0	135.0	117.0	112.5	109.0	106.0	99.0	97.0	140.0	137.0	140.0	137.0
ADF	57.0	51.5	48.5	47.5	45.0	45.0	41.0	40.0	59.0	61.0	59.0	61.0
Starch	375.5	362.5	347.3	325.5	377.2	367.7	414.4	400.1	463.0	441.3	458.6	438.5
TMC (cfu/g)[a]	< 100	< 100	< 100	< 100	< 100	< 100	< 100	< 100	< 100	< 100	< 100	< 100
Mycotoxins (μg/kg)[b]												
Deoxynivalenol	< 75.0	< 75.0	< 75.0	< 75.0	< 75.0	< 75.0	< 75.0	< 75.0	120	110	170	150
Zearalenone	< 10.0	< 10.0	< 10.0	< 10.0	< 10.0	< 10.0	< 10.0	< 10.0	22	19	26	20
Essential amino acids												
Arginine	11.0	11.0	11.4	11.3	11.7	11.7	11.5	11.4	8.0	7.9	8.3	8.1
Histidine	4.1	4.1	4.3	4.2	4.1	4.2	4.4	4.3	3.1	3.2	3.0	3.1
Isoleucine	7.2	7.1	7.9	7.8	7.8	7.8	7.5	7.6	5.2	5.3	5.0	5.0
Leucine	12.6	12.8	14.9	15.0	14.3	14.2	13.6	13.7	10.3	10.2	10.0	10.0
Lysine	11.3	11.2	15.5	15.4	14.2	14.3	12.7	12.7	10.2	10.1	9.8	9.7
Methionine	2.5	2.6	4.5	4.9	4.3	4.1	3.2	3.1	2.1	2.1	2.1	2.1
Phenylalanine	8.0	8.0	8.9	8.7	8.6	8.6	8.6	8.6	6.0	6.0	5.6	5.8
Threonine	6.9	6.8	8.7	8.9	9.0	8.9	7.8	8.0	5.7	5.6	5.5	5.5
Tryptophan	2.2	2.3	2.8	2.8	2.9	2.9	2.4	2.4	1.6	1.7	1.7	1.7
Valine	7.9	7.7	9.2	9.3	9.0	8.9	8.1	8.0	5.7	5.8	5.5	5.5

aNDF, neutral detergent fibre (assayed with thermal-stable amylase and expressed inclusive of residual ash); ADF, acid detergent fibre; TMC, total mould count.
[a] These values were log-transformed. [b] The following mycotoxins were below the listed detectable levels: Aflatoxin B1, B2, G1 and G2 (<1 μg/kg); fumonisin B1 (<125 μg/kg) and fumonisin B2 (<50 μg/kg); T-2 Toxin and HT-2 Toxin (<4 μg/kg) and ochratoxin A (<1 μg/kg).

LECO FP 528 instrument (Leco Instruments, Stockport, UK). The ANKOM 220 Fibre Analyser (Ankom Technology, NY, USA) was used to determine the crude fibre content according to AOAC (2005) (method 962.09), the neutral detergent fibre (assayed with thermal-stable amylase and expressed inclusive of residual ash; aNDF) and acid detergent fibre (ADF) were determined according to Mertens (2002) (AOAC method, (2002).04). The chemical analysis of the diets is presented in Table 3.

2.6. Carcass characteristics

At slaughter, pigs were transported to a commercial abattoir (Rosderra Irish Meats, Roscrea, Tipperary, Ireland) and were killed by exsanguination after carbon dioxide stunning. Pigs were fasted for 12 h pre-slaughter. Hot carcass weight was recorded 45 minutes after stunning, and a Hennessy Grading Probe (Hennessy and Chong, Auckland, New Zealand) was used to determine the BF and muscle depth at 6 cm from the edge of the split back at the level of the third and fourth last rib (Dowley et al., 2022). Lean meat content was estimated using the following equation: Estimated lean meat content (g/kg) = (600.3 – 8.47x + 1.47 y), where x = BF (mm); y = muscle depth (mm; O' Meara et al., 2020). Cold carcass weight (kg) was calculated by multiplying hot carcass weight by 0.98 and kill-out proportion (g/kg) was determined by dividing cold carcass weight by final BW before slaughter.

2.7. Microbiological analysis

For microbial analysis, faecal samples were collected from pigs in the dried-dried and preserved-preserved groups at weaning, day 30 PW, and at slaughter. The same tagged piglets, as outlined in Section 2.4, were used for sample collection in these selected treatments (n = 10 samples per treatment). To maintain sample integrity, only faeces that had not come into contact with the floor were collected. Samples were placed in sterile containers (Sarstedt, Wexford, Ireland) and stored at – 80 °C for 16S rRNA sequencing.

2.7.1. Microbial DNA extraction and Illumina sequencing

Microbial DNA was extracted from faecal samples using a QIAamp PowerFecal Pro DNA Kit (Qiagen, West Sussex, UK). The quality and quantity of DNA were assessed using a Nanodrop ND-1000 Spectrophotometer (Thermo Scientific, Wilmington, DE, USA). High throughput sequencing of the V3-V5 hypervariable region of the bacterial 16S rRNA gene was conducted using an Illumina MiSeq platform according to standard protocol (Eurofins Genomics, Ebersberg, Germany). The V3-V5 region was PCR-amplified using universal primers containing adapter overhang nucleotide sequences for forward and reverse index primers. Amplicons were purified using AMPure XP beads (Beckman Coulter, Indianapolis, IN) and set up for the index PCR using Nextera XT index primers (Illumina, San Diego, CA). The indexed samples were purified using AMPure XP beads before quantification using a fragment analyser (Agilent, Santa Clara, CA). Equal quantities from each sample were pooled and the resulting library was quantified using the Bioanalyser 7500 DNA kit (Agilent, Santa Clara, CA) and sequenced using the v3 chemistry (2 × 300 bp paired-end reads).

2.7.2. Bioinformatics

The bioinformatic analysis of the sequences was conducted by Eurofins Genomics (Eberberg, Germany) using the open-source package Quantitative Insights into Microbial Ecology (Version 1.9.1; Caporaso et al., 2010). Raw reads that passed the standard Illumina chastity filter were demultiplexed in accordance with their index sequences (read quality score >30). The primer sequences were clipped from the start of the raw forward and reverse reads. Where primer sequences were not perfectly matched, read pairs were removed to retain only high-quality reads. Paired-end reads were merged to form a single, longer read that covered the entire target region using the software FLASH 2.200 (Magoč and Salzberg, 2011). The pairs were then merged with a minimum overlap size of 10 bp to minimise false-positive merges. Forward reads were only retained for the subsequent assessment steps when merging was not possible. Quality filtration of merged reads was then conducted according to the expected and known length variations in the V3-V5 region. The ends of retained forward reads were cut to a total read length of 285 bp to eliminate low-quality bases. Merged and retained reads with ambiguous bases were removed. These filtered reads were used to generate the microbiome profile. Chimeric reads were detected and discarded based on the de-novo algorithm of UCHIME (Edgar et al., 2011) as implemented in the VSEARCH package (Rognes et al., 2016). The remaining set of high-quality reads was processed using minimum entropy decomposition to partition reads into operational taxonomic units (Eren et al., 2015, 2013). The DC-MEGABLAST alignments of cluster representative sequences to the NCBI nucleotide sequence database were conducted for the taxonomic assignment of every operational taxonomic unit. A sequence similarity of 70 % across a minimum of 80 % of the representative sequence was the minimal requirement for considering reference sequences. Abundances of bacterial taxonomic units were normalised using linear-specific copy numbers of the appropriate marker genes to enhance estimates (Angly et al., 2014). The normalised operational taxonomic units table combined with the phenotype metadata and phylogenetic tree comprised the data matrix. The data matrix was loaded into the phyloseq package in R (Version 3.5.0, accessed on 14/4/24). Differential abundance analysis was carried out on tables extracted from the phyloseq object at phylum, family, and genus levels. The dynamics of richness and diversity were computed using the Observed, Shannon, Simpson, Inverse Simpson and Fisher indices. Additionally, beta diversity was determined by normalizing the data so the taxonomic feature counts could be compared across samples. Several distance metrics were considered and the non-phylogenetic distance metric Bray Curtis was selected using phyloseq in R as previously described by Dowley et al. (2021).

2.8. Statistical analysis

All data was initially checked for normality of scaled residuals using PROC UNIVARIATE of SAS® version 9.4 (SAS Institute Inc.

Cary, USA). Pre-weaning growth performance (BW, ADG, and litter feed intake) was analysed as a 2 × 2 factorial using PROC GLM of SAS. The model examined the effects of maternal diet, progeny diet, and their associated two-way interactions, using sow parity and litter size as covariates. Litter diarrhoea incidence during lactation was analysed using PROC GENMOD of SAS. Post-weaning growth performance (BW, ADFI, ADG, and G:F) and carcass characteristics at slaughter were also analysed as a 2 × 2 factorial using PROC GLM. The statistical model included the effects of maternal diet, progeny diet, and their associated two-way interactions. The pen was the experimental unit for growth performance and carcass characteristics. The data is presented as least-square means with their standard error of the mean (SEM). Faecal microbial populations in the dried-dried and preserved-preserved groups were analysed using PROC GLIMMIX for nonparametric data, with the results presented as least-square means, using Benjamini-Hochberg adjusted P-values. The model examined the effect of diet on the pooled samples, as described in Section 2.7. The probability level that denoted significance was $P < 0.05$, while P values between 0.05 and 0.10 were considered tendencies.

3. Results

3.1. Grain and feed quality

Before grain preservation, the moisture content, hectolitre weight, and thousand-grain weight of the wheat were determined to be 179.7 g/kg, 71 kg/hL, and 47.4 g, respectively. The moisture, hectolitre weight, and thousand-grain weight of the barley were determined to be 182.1 g/kg, 62 kg/hL, and 53.1 g, respectively.

Wheat and barley preserved with the OA mould inhibitor maintained lower DM content, grain pH, and total mould counts after storage, compared to dried grain. However, all other nutrients remained similar on a DM basis (Table 1). The levels of mycotoxins (aflatoxin B1, B2, G1 and G2, fumonisins B1 and B2, DON, T-2 and HT-2 Toxins, ZEN and OTA) were all below the detectable levels in the dried and preserved wheat and barley. Similarly, the DM content was reduced in the preserved grain diets and mycotoxins remained undetected except for the finisher diets. Detectable limits of DON and ZEN were found in both the dried and preserved grain finisher diets but remained below the EU guidance levels for finisher pigs.

3.2. Pre-weaning growth performance

The effect of treatment on pre-weaning piglet growth performance is presented in Table 4. There was no effect of treatment on mean piglet BW on days 0, 10, or 26. Similarly, piglet ADG was not affected by treatment during lactation. Pre-weaning litter feed intake, diarrhoea incidence, and mortality during lactation were similar between dietary groups.

3.3. Post-weaning growth performance

The effect of treatment on pig growth performance (BW, ADG, ADFI, and G:F) PW are presented in Table 5. There were no interactions observed between maternal and progeny dietary treatments on performance. Pigs from sows fed the preserved grain diet had reduced ADFI during days 0–14 PW, and improved G:F during days 0–14 and days 62–142 compared to pigs from sows fed the dried grain diet ($P < 0.05$). Pigs directly fed the preserved grain diet had increased ADG during days 0–14, 14–30, 30–62, and 62–142 PW compared to pigs fed the dried grain diet ($P < 0.05$). Subsequently, pigs fed preserved grain had increased BW on days 30, 62, and 142 PW ($P < 0.05$), and enhanced G:F during days 14–30, 30–62, and 62–142 PW ($P < 0.05$).

Table 4
The effect of dietary treatments on pre-weaning growth performance, litter feed intake, litter diarrhoea incidence, and litter mortality (Least square means with their standard error of the mean).

	Treatments				P-value*			
Maternal diet **Progeny diet**	Dried Dried	Dried Preserved	Preserved Dried	Preserved Preserved	SEM	Maternal	Progeny	Maternal × Progeny
No of replicates	20	20	20	20				
BW, kg								
Day 0	1.40	1.33	1.35	1.33	0.050	0.500	0.339	0.660
Day 10	3.29	3.24	3.12	3.24	0.111	0.384	0.729	0.455
Day 26[a]	7.03	7.22	7.22	7.15	0.177	0.752	0.740	0.444
ADG, kg/day								
Day 0	0.19	0.20	0.18	0.19	8.326	0.678	0.312	0.885
Day 10–26	0.23	0.25	0.26	0.24	9.071	0.299	0.873	0.133
Day 0–26	0.22	0.23	0.23	0.23	7.145	0.445	0.617	0.219
Litter feed intake, kg	3.97	3.87	3.84	3.73	0.227	0.173	0.234	0.482
Diarrhoea incidence, %	15.00	8.75	8.68	5.00	3.992	0.133	0.143	0.990
Litter mortality, %	8.96	9.82	7.77	7.36	1.941	0.316	0.894	0.744

BW, body weight; ADG, average daily gain
*Maternal = the effect of maternal dietary treatment; Progeny = the effect of progeny dietary treatment; Maternal × Progeny = the two-way interaction between maternal and progeny dietary treatment

Table 5
The effect of dietary treatments on post-weaning growth performance and carcass characteristics (Least square means with their standard error of the mean).

	Treatments				P-value*			
Maternal diet **Progeny diet**	Dried Dried	Dried Preserved	Preserved Dried	Preserved Preserved	SEM	Maternal	Progeny	Maternal × Progeny
No of replicates	10	10	10	10				
BW, kg								
Day 0	7.0	7.2	7.2	7.2	0.177	0.752	0.740	0.444
Day 14	9.6	10.0	9.5	9.6	0.398	0.539	0.513	0.745
Day 30	15.0	16.7	15.8	17.1	0.658	0.947	**0.037**	0.505
Day 62	31.4	35.3	33.8	36.2	1.120	0.141	**0.007**	0.492
Day 142	117.6	126.0	123.2	127.7	2.524	0.158	**0.014**	0.453
ADFI, kg/day								
Day 0–14	0.26	0.27	0.25	0.25	0.007	**0.003**	0.758	0.224
Day 14–30	0.58	0.54	0.56	0.56	0.014	0.905	0.277	0.128
Day 30–62	1.15	1.16	1.17	1.14	0.031	0.958	0.813	0.556
Day 62–142	2.88	2.89	2.85	2.86	0.025	0.224	0.603	0.976
ADG, kg/day								
Day 0–14	0.15	0.17	0.15	0.16	0.005	0.464	**0.045**	0.882
Day 14–30	0.36	0.44	0.39	0.45	0.025	0.639	**0.029**	0.324
Day 30–62	0.52	0.59	0.56	0.60	0.019	0.118	**0.008**	0.326
Day 62–142	1.07	1.12	1.11	1.14	0.018	0.159	**0.034**	0.504
G:F, kg/kg								
Day 0–14	0.57	0.61	0.61	0.66	0.022	**0.035**	0.151	0.377
Day 14–30	0.62	0.81	0.71	0.80	0.044	0.823	**0.022**	0.113
Day 30–62	0.45	0.51	0.49	0.54	0.019	0.138	**0.006**	0.864
Day 62–142	0.37	0.39	0.39	0.41	0.007	**0.040**	**0.045**	0.359
Carcass characteristics								
Carcass weight, kg	88.1	95.2	92.2	96.4	2.010	0.185	**0.008**	0.484
Kill out, g/kg	748.5	754.6	748.5	754.6	0.524	0.912	**< 0.001**	0.951
Lean meat, g/kg	570.9	565.0	570.5	565.5	0.543	0.951	**< 0.001**	0.941
Muscle depth, mm	58.9	60.3	58.2	60.0	0.513	0.894	**< 0.001**	0.920
BF, mm	15.1	15.0	15.1	14.9	0.053	0.980	0.072	0.894

BW, body weight; ADFI, average daily feed intake; ADG, average daily gain; G:F, gain-to-feed ratio; BF, back-fat thickness.
* Maternal = the effect of maternal dietary treatment; Progeny = the effect of progeny dietary treatment; Maternal × Progeny = the two-way interaction between maternal and progeny dietary treatment.

3.4. Coefficient of apparent total tract digestibility

The effects of treatment on the CATTD of nutrients are presented in Table 6. Pigs from sows fed the preserved grain diet had increased CATTD of DM, OM and GE on day 30 PW and increased CATTD of N at slaughter compared to pigs from sows fed the dried grain diet ($P < 0.05$). Pigs from preserved grain-fed sows also tended to have higher CATTD of DM at slaughter ($P = 0.052$). Pigs directly fed preserved grain had increased CATTD of DM, OM, N and GE on day 30 PW and increased CATTD of DM, OM, ash, N and GE at slaughter compared to those fed dried grain ($P < 0.001$). Pigs fed preserved grain also tended to have increased CATTD of ash on day

Table 6
The effect of dietary treatment on the coefficient of apparent total tract digestibility of dry matter (DM), organic matter (OM), ash, nitrogen (N), and gross energy (GE; least square means with their standard error of the mean).

	Treatments				P-value*			
Maternal diet **Progeny diet**	Dried Dried	Dried Preserved	Preserved Dried	Preserved Preserved	SEM	Maternal	Progeny	Maternal × Progeny
Day 30 PW								
DM	0.801	0.833	0.821	0.840	0.006	**0.041**	**< 0.001**	0.246
OM	0.814	0.845	0.834	0.853	0.005	**0.026**	**< 0.001**	0.284
Ash	0.570	0.622	0.601	0.619	0.018	0.444	0.077	0.370
N	0.734	0.774	0.745	0.776	0.011	0.562	**0.009**	0.730
GE	0.785	0.813	0.806	0.832	0.005	**0.003**	**< 0.001**	0.800
Slaughter								
DM	0.827	0.843	0.831	0.852	0.003	0.052	**< 0.001**	0.405
OM	0.844	0.858	0.846	0.866	0.004	0.175	**< 0.001**	0.461
Ash	0.439	0.484	0.447	0.509	0.015	0.284	**0.001**	0.563
N	0.765	0.784	0.778	0.810	0.007	**0.009**	**< 0.001**	0.380
GE	0.809	0.823	0.812	0.831	0.004	0.135	**< 0.001**	0.411

*Maternal = the effect of maternal dietary treatment; Progeny = the effect of progeny dietary treatment; Maternal × Progeny = the two-way interaction between maternal and progeny dietary treatment.

30 PW (P = 0.077).

3.5. Carcass characteristics

The effects of treatment on carcass characteristics at slaughter are presented in Table 5. There was no maternal effect observed on carcass characteristics at slaughter. Pigs directly fed preserved grain had higher carcass weight, kill-out percentage, and muscle depth at slaughter compared to those fed dried grain (P < 0.001). Pigs fed dried grain had increased lean meat percentage compared to those fed preserved grain (P < 0.001). Pigs fed preserved grain tended to have lower BF compared to those fed dried grain (P = 0.072).

3.6. Microbiological analysis

3.6.1. Bacterial richness and diversity

The alpha microbial diversity of pigs in the dried-dried and preserved-preserved groups is presented in Table 7. The Shannon, Simpson, and Inverse Simpson indices of diversity showed that pigs in the preserved-preserved group harboured a higher microbial diversity at weaning compared to pigs in the dried-dried group (P < 0.05). Additionally, the Observed, Shannon, Simpson, Inverse Simpson, and Fisher diversity indices were higher in pigs from the preserved-preserved group on day 30 PW compared to the dried-dried group (P < 0.05). There was no effect of treatment on alpha diversity between pigs in the dried-dried and preserved-preserved groups at slaughter. There was no difference in beta microbial diversity between groups based on PERMANOVA analysis, through visualisation using the Bray-Curtis distance matrix and multi-dimensional scaling (not presented).

3.6.2. Differential bacterial abundance analysis

The bacterial abundance at phylum, family, and genus level in pigs from the dried-dried and preserved-preserved groups at weaning, day 30 PW, and slaughter are presented in Tables 8–10.

3.6.2.1. Weaning. Phylum (Table 8): At weaning, four bacterial phyla above 1 % relative abundance were identified with Firmicutes representing the dominant phyla (~60.2 %), followed by Bacteroidetes (~35.4 %), Actinobacteria (~1.9 %) and Proteobacteria (~1.4 %). The relative abundance of Firmicutes was increased, while the abundance of Bacteroidetes was decreased in the preserved-preserved group compared to the dried-dried group (P < 0.05). Pigs in the preserved-preserved group tended to have lower Actinobacteria compared to those in the dried-dried group (P = 0.062).

Family (Table 9): Within the phylum Firmicutes, the abundance of *Ruminococcaceae, Clostridiaceae,* and *Erysipelotrichaceae* were increased in the preserved-preserved group compared to the dried-dried group (P < 0.05). Within the phylum Bacteroidetes, the abundance of *Rikenellaceae* was decreased, while the abundance of *Bacteridaceae* and *Tannerellaceae* were increased in the preserved-preserved group compared to the dried-dried group (P < 0.05).

Genus (Table 10): Within the phylum Firmicutes, the abundance of *Ruminococcus, Clostridium, Pseudoflavonifractor, Sporobacter, Holdemania* and *Turicibacter* were increased in the preserved-preserved group compared to the dried-dried group (P < 0.05). Within the phylum Bacteroidetes, the abundance of *Alistipes, Paramuribaculum,* and *Propionibacterium* were decreased, while the abundance of *Bacteroides* and *Parabacteroides* were increased in the preserved-preserved group compared to the dried-dried group (P < 0.05).

Table 7
The effect of combined maternal and direct feeding of dried or preserved grain on measures of alpha diversity in pigs at weaning, day 30 post-weaning, and slaughter (least square means with their standard error of the mean).

Maternal diet **Progeny diet**	Dried Dried	Preserved Preserved	SEM	P-value
Alpha diversity				
Weaning				
Observed	54.88	53.78	2.022	0.699
Shannon	3.26	3.44	0.076	**0.025**
Simpson	0.91	0.95	0.014	**0.046**
Inverse Simpson	15.55	21.78	1.358	**0.034**
Fisher	9.81	9.57	0.440	0.692
Day 30 PW				
Observed	56.25	64.25	2.620	**< 0.001**
Shannon	3.57	3.92	0.046	**< 0.001**
Simpson	0.96	0.97	0.002	**0.036**
Inverse Simpson	26.23	32.13	1.817	**0.038**
Fisher	10.14	16.60	0.584	**< 0.001**
Slaughter				
Observed	66.00	67.25	2.975	0.771
Shannon	3.66	3.69	0.073	0.769
Simpson	0.96	0.96	0.004	0.712
Inverse Simpson	26.02	27.08	2.500	0.764
Fisher	12.32	12.57	0.678	0.794

Table 8
The effect of combined maternal and direct feeding of dried or preserved grain on the bacterial abundance at phylum level (%) in pigs at weaning, day 30 post-weaning, and slaughter (least square means with their standard error of the mean).

Maternal diet **Progeny diet**	Dried Dried	Preserved Preserved	SEM	P-value
Phylum				
Weaning				
Firmicutes	53.04	67.36	2.770	**0.003**
Bacteroidetes	42.79	27.93	2.077	**< 0.001**
Actinobacteria	2.65	1.21	0.539	0.062
Proteobacteria	1.34	1.54	0.424	0.746
Day 30 PW				
Firmicutes	78.56	72.16	3.002	0.160
Bacteroidetes	14.82	16.14	1.420	0.516
Actinobacteria	3.15	8.10	1.006	**0.001**
Spirochaetes	2.88	0.04	0.601	**0.028**
Slaughter				
Firmicutes	70.66	70.22	2.967	0.919
Bacteroidetes	15.98	14.95	1.390	0.610
Actinobacteria	12.27	11.60	1.179	0.701

Table 9
The effect of combined maternal and direct feeding of dried or preserved grain on the bacterial abundance at family level (%) in pigs at weaning, day 30 post-weaning, and slaughter (least square means with their standard error of the mean).

Maternal diet **Progeny diet**		Dried Dried	Preserved Preserved	SEM	P-value
Phylum	**Family**				
Weaning					
Firmicutes	*Ruminococcaceae*	15.30	26.22	1.597	**< 0.001**
	Clostridiaceae	1.44	5.09	0.798	**0.002**
	Erysipelotrichaceae	1.74	3.65	0.675	**0.039**
Bacteroidetes	*Rikenellaceae*	24.40	9.22	1.410	**< 0.001**
	Bacteroidaceae	0.66	4.41	0.515	**0.001**
	Tannerellaceae	0.10	1.27	0.255	**0.046**
Day 30 PW					
Bacteroidetes	*Muribaculaceae*	0.15	2.16	0.327	**0.014**
Actinobacteria	*Propionibacteriaceae*	2.98	8.02	0.806	**0.001**
Slaughter					
Firmicutes	*Ruminococcaceae*	7.29	15.97	1.183	**< 0.001**
	Oscillospiraceae	7.38	4.03	0.835	**0.015**
	Lachnospiraceae	7.58	1.90	0.730	**< 0.001**

3.6.2.2. Day 30 PW. Phylum (Table 8): Four bacterial phyla above 1 % relative abundance were identified with Firmicutes representing the dominant phyla (~74.6 %), followed by Bacteroidetes (~15.0 %), Actinobacteria (~7.2 %) and Spirochaetes (1.2 %). The preserved-preserved group had higher abundance of Actinobacteria and lower Spirochaetes compared to the dried-dried group ($P < 0.05$).

Family (Table 9): Two families were identified as more abundant in the preserved-preserved group compared to the dried-dried group. Within the phylum Bacteroidetes, *Muribaculaceae* was increased, while within the phylum Actinobacteria, *Propionbacteriaceae* was more abundant ($P < 0.05$).

Genus (Table 10): Within the phylum Firmicutes, the abundance of *Lactobacillus*, *Butyricicoccus* and *Agathobacter* decreased, while the abundance of *Clostridium* increased in the preserved-preserved group compared to the dried-dried group ($P < 0.05$). Within the phyla Bacteroidetes and Actinobacteria, the genera *Paramuribaculum* and *Propionibacterium* were more abundant in the preserved-preserved group compared to the dried-dried group, respectively ($P < 0.05$).

3.6.2.3. Slaughter. Phylum (Table 8): Three bacterial phyla above 1 % relative abundance were identified with Firmicutes representing the dominant phyla (~70.4 %), followed by Bacteroidetes (~15.5 %) and Actinobacteria (~11.9 %). There was no effect of treatment at the phylum level at slaughter.

Family (Table 9): Within the phylum Firmicutes, the abundance of *Ruminococcaceae* was increased while *Oscillospiraceae* and *Lachnospiraceae* were decreased in the preserved-preserved group compared to the dried-dried group ($P < 0.05$).

Genus (Table 10): Within the phylum Firmicutes, the abundance of *Faecalibacterium* and *Ruminococcus* was increased, while the abundance of *Coprococcus* was decreased in the preserved-preserved group compared to the dried-dried group ($P < 0.05$).

Table 10
The effect of combined maternal and direct feeding of dried or preserved grain on the bacterial abundance at genus level (%) in pigs at weaning, day 30 post-weaning, and slaughter (least square means with their standard error of the mean).

Maternal diet **Progeny diet**			Dried Dried	Preserved Preserved	SEM	P-value
Phylum	**Family**	**Genus**				
Weaning						
Firmicutes	*Ruminococcaceae*	*Ruminococcus*	6.49	13.15	1.091	**0.001**
	Ruminococcaceae	*Pseudoflavonifractor*	1.49	3.84	0.563	**0.015**
	Ruminococcaceae	*Sporobacter*	0.35	3.11	0.623	**0.004**
	Clostridiaceae	*Clostridium*	1.37	5.23	0.809	**0.001**
	Erysipelotrichaceae	*Holdemania*	0.80	2.27	0.424	**0.039**
	Erysipelotrichaceae	*Turicibacter*	0.41	1.82	0.352	**0.029**
Bacteroidetes	*Rikenellaceae*	*Alistipes*	16.05	0.00	1.417	**< 0.001**
	Muribaculaceae	*Paramuribaculum*	3.92	1.48	0.699	**0.013**
	Bacteroidaceae	*Bacteroides*	0.66	4.37	0.514	**0.001**
	Tannerellaceae	*Parabacteroides*	0.09	1.27	0.252	**0.048**
Actinobacteria	*Propionibacteriaceae*	*Propionibacterium*	2.89	1.62	0.526	**0.012**
Day 30 PW						
Firmicutes	*Lactobacillaceae*	*Lactobacillus*	11.27	6.34	1.017	**0.020**
	Clostridiaceae	*Butyricicoccus*	5.29	3.04	0.715	**0.047**
	Clostridiaceae	*Clostridium*	2.15	5.00	0.654	**0.011**
	Lachnospiraceae	*Agathobacter*	1.63	0.38	0.335	**0.038**
Bacteroidetes	*Muribaculaceae*	*Paramuribaculum*	0.15	1.87	0.309	**0.019**
Actinobacteria	*Propionibacteriaceae*	*Propionibacterium*	2.97	7.99	0.804	**0.001**
Slaughter						
Firmicutes	*Ruminococcaceae*	*Faecalibacterium*	3.66	6.15	0.776	**0.043**
	Ruminococcaceae	*Ruminococcus*	0.39	3.06	0.420	**0.004**
	Lachnospiraceae	*Coprococcus*	4.36	0.46	0.489	**0.001**

4. Discussion

This study hypothesised that maternal and direct feeding of OA-preserved grain would improve pig growth performance, nutrient digestibility at key production stages, and carcass characteristics at slaughter. While no synergistic effects were observed, both maternal and direct feeding independently improved performance from weaning to slaughter, demonstrating the long-term benefits of preserved grain. Progeny from sows fed preserved grain exhibited enhanced feed efficiency during the first two weeks PW and the finisher stage compared to those from sows fed dried grain. However, no maternal effects on carcass characteristics were observed. Pigs directly fed preserved grain consistently outperformed those fed dried grain from weaning to slaughter, with growth rate improvements evident as early as the first two weeks PW, despite similar feed intake between treatments. This early advantage contributed to enhanced feed efficiency from day 14 PW, increased BW from day 30 PW, and ultimately a higher carcass weight and kill out percentage at slaughter. Given these benefits, it was essential to assess whether differences in grain preservation influenced feed quality and composition.

Consistent with previous research, the OA mould inhibitor effectively preserved wheat and barley at higher moisture levels compared to drying (Maher et al., 2024; Connolly et al., 2025). Despite expected DM differences after storage, both methods produced grains with comparable quality and chemical composition. Notably, preserved grain had lower mould levels, likely due to the OA antifungal properties, reinforcing its viability as an efficient alternative to drying. However, despite successful preservation, DON and ZEN mycotoxins were detected in both dried and preserved grain finisher diets, suggesting wheat and barley were unlikely sources of contamination. Instead, the inclusion of maize may be responsible, as it was not used in any other diets. Fusarium mycotoxins, which produce both DON and ZEN, are commonly associated with maize and its inclusion may have introduced low levels of co-contamination (Carvajal-Moreno, 2022). Although mycotoxin exposure can impair nutrient digestibility and growth (Jo et al., 2016; Mwaniki et al., 2021; Tolosa et al., 2021), the levels detected remined below the EU guidance levels and were consistent across dietary groups, suggesting minimal impacts on the findings of this study.

Although preserved grain has demonstrated benefits during the PW period (Xu et al., 2016; Maher et al., 2024; Connolly et al., 2025), its effects pre-weaning remains largely unexplored. In this study, piglet growth during lactation was unaffected, potentially due to several factors. The lactose in sow milk may have attenuated the effects of preserved grain, as lactose fermentation in the stomach has been shown to interfere with the beneficial effects of OA in weaner pigs (Giesting et al., 1991; Partanen and Mroz, 1999; Pierce et al., 2004). Additionally, total feed intake during lactation was lower than in previous studies reporting growth responses from pelleted starter diets over similar supplementation periods (Bruininx et al., 2002; Lee and Kim., 2018; Arnaud et al., 2024). Furthermore, although the starter diet was introduced from day 10 postpartum to maximise pre-weaning feed intake, it is well-recognised that not all piglets within the litter actively consume creep before weaning (Huting et al., 2021), with the proportion of eaters ranging from 40 % to 60 % (Pluske et al., 2007; Sulabo et al., 2010). As individual feed intake was not quantified in this study, future studies could address this limitation by utilising markers to measure individual feed consumption for a more accurate assessment of the pre-weaning effects of preserved grain. The improved growth and feed efficiency in pigs fed preserved grain from weaning

to slaughter suggests its benefits became more pronounced once sow milk was no longer available, and ADFI increased.

Progeny from sows fed preserved grain had increased CATTD of DM, OM, and GE on day 30 PW and N at slaughter compared to those from sows fed dried grain, indicating enhanced digestive function. These improvements in nutrient digestibility partially explain the better feed efficiency observed in these pigs during the first two weeks PW and the finisher stage. Despite an initial reduction in feed intake PW, progeny from sows fed preserved grain maintained similar growth rates compared to those from sows fed dried grain, potentially due to improved nutrient utilisation. Maternal OA supplementation has been shown to enhance digestive health and performance of progeny through several pathways. Lu et al. (2012) reported that pigs from OA-supplemented sows exhibited enhanced growth performance PW, attributed to metabolic adaptations that improved nutrient utilisation and energy metabolism. These effects were linked to the upregulation of oxidative genes involved in fatty acid oxidation and mitochondrial function, promoting more efficient use of dietary energy (Lu et al., 2012). Improved energy metabolism may allow for greater utilisation of nutrients for maintenance and growth, thereby enhancing feed efficiency. Additionally, maternal OA supplementation has been associated with increased immunoglobulin concentrations in colostrum and milk, as well as modulation of the sow's microbiota (Liu et al., 2014; Devi et al., 2016; Lin et al., 2023), which may further support nutrient utilisation in progeny. However, further research is needed to delve deeper into these effects.

Pigs directly fed preserved grain showed increased CATTD of DM, OM, GE, and N on day 30 PW and at slaughter compared to those fed dried grain. These findings align with previous research, which demonstrated that preserved grain enhanced the ileal digestibility of nutrients on day 35 PW (Maher et al., 2024). The acidification potential of OA is often proposed as the primary mechanism for enhancing nutrient digestibility, especially in weaned pigs with immature gastric acid secretion (Suiryanrayna and Ramana, 2015). However, OA blends have shown inconsistent effects on gastric pH modulation (Grecco et al., 2018; Li et al., 2018), particularly in older pigs with established gastric acid secretion (Partanen and Mroz, 1999). Despite this, OA may still optimise nutrient digestibility through mechanisms beyond acidification, including enhanced enzyme activity, increased digesta retention time, improved mineral utilisation, and modulation of the intestinal microbiota (Tung and Pettigrew, 2006; Tugnoli et al., 2020). Accordingly, various OA combinations have been shown to improve feed efficiency and nutrient digestibility in grower-finisher pigs (Mroz et al., 2000; Upadhaya et al., 2014; Wang et al., 2022), consistent with the findings of this study. Feeding pigs preserved grain increased carcass weight, kill-out percentage, and muscle depth, whereas pigs fed dried grain had a higher lean meat percentage. These results suggest that feed type influences carcass composition by impacting both muscle development and fat deposition. This aligns with previous research demonstrating a positive correlation between BW, BF, and muscle depth, indicating that as pigs gain weight, they tend to accumulate more muscle and fat mass (Hoque et al., 2009).

A key factor underlying these improvements may be the impact of OA on the intestinal microbiota. At weaning, pigs in the preserved-preserved group harboured higher microbial diversity compared to pigs in the dried-dried group. Greater microbial diversity is typically associated with intestinal stability and resilience, promoting resistance to shifts in microbial composition (Han et al., 2019; St-Pierre et al., 2023). The preserved-preserved group had a higher abundance of Firmicutes, coinciding with increased *Ruminococcaceae*, a key fibre-degrading bacterial family that enhances volatile fatty acid production, particularly butyrate (Yang et al., 2018). Increases in *Ruminococcaceae* during lactation have been associated with improved growth (Morissette et al., 2018) and reduced risk of diarrhoea PW (Dou et al., 2017). Although no significant pre-weaning differences were observed, the preserved-preserved group had 10 % lower diarrhoea during lactation compared to the dried-dried group. The higher abundance of *Ruminococcaceae* at weaning may have primed the intestine for plant-based carbohydrate digestion and facilitated adaptation to dietary substrates PW (Gaukroger et al., 2020). Conversely, the dried-dried group had a higher abundance of Bacteroidetes, particularly *Rikenellaceae,* which have been associated with oxidative stress in weaned piglets (Correa et al., 2023). *Alistipes*, the most abundant genus in the dried-dried group at weaning, was remarkably undetectable in the preserved-preserved group. This genus has been linked to intestinal inflammation, gastrointestinal disorders, and disrupted intestinal homeostasis (Fenner et al., 2007; Saulnier et al., 2011; Parker et al., 2020), suggesting that its absence in the preserved-preserved group may have further contributed to improved intestinal health.

By day 30 PW, microbial diversity remained higher in the preserved-preserved group, which may have contributed to greater resilience, promoting ADG and enhancing G:F (Thompson et al., 2008). Although the abundance of *Propionibacterium* was initially lower in the preserved-preserved group at weaning, it increased markedly by day 30 PW. As propionic acid was the active ingredient in the mould inhibitor, this may have supported the proliferation of *Propionibacterium*, as feed intake increased PW. This genus is known to have promising probiotic effects, as it modulates the intestinal microbiota (Cousin et al., 2012) and supports mucosal development (Martínez et al., 2016). Additionally, its lactose-fermenting capacity contributes to volatile fatty acid production, potentially explaining the reduced abundance of *Lactobacillus* in the preserved-preserved group on day 30 PW. While this reduction of *Lactobacillus* could be negatively interpreted, it may represent an adaptive microbial shift favouring *Propionibacterium*, potentially contributing to performance and digestive health benefits.

At slaughter, the preserved-preserved group maintained increased abundance of *Ruminococcaceae,* potentially highlighting their role in fibre degradation and butyrate production during later growth stages. Interestingly, *Lachnospiraceae* was more abundant in the dried-dried group at slaughter, which has been negatively correlated with butyrate production (Zhong et al., 2019). Conversely, the increased abundance of *Faecalibacterium* in the preserved-preserved group suggests a beneficial microbial shift, as it is well recognised for its strong anti-inflammatory and immunomodulatory properties (Sokol et al., 2008; Lopez-Siles et al., 2018). These findings align with previous research, where preserved grain increased the abundance of *Faecalibacterium* and growth in pigs during the PW period (Maher et al., 2024; Connolly et al., 2025). However, since this study did not include a full factorial comparison of all four dietary treatments, further research is required to investigate the individual effects of maternal and progeny feeding of preserved grain on the microbiota throughout production.

5. Conclusion

In conclusion, maternal feeding of preserved cereal grains during late gestation and lactation improved progeny feed efficiency and CATTD of nutrients, while direct feeding of preserved grain further enhanced pig growth performance to slaughter, CATTD of nutrients throughout production, and carcass characteristics at slaughter. Combined maternal and direct feeding of preserved grain increased microbial diversity at weaning and on day 30 PW, which may have contributed to improved resilience. Additionally, the increased abundance of beneficial taxa, such as *Ruminococcus*, *Propionibacterium,* and *Faecalibacterium* at key production stages may have improved intestinal health and digestive function. These findings demonstrate the long-term potential of preserved grain to enhance pig performance and digestive health, offering a sustainable feeding strategy that supports economic viability for producers while promoting a more resilient swine population.

CRediT authorship contribution statement

Maher Shane: Writing – review & editing, Writing – original draft, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Sweeney Torres:** Writing – review & editing. **Vigors Stafford:** Writing – review & editing, Formal analysis. **O'Doherty John V:** Writing – review & editing, Supervision, Methodology, Funding acquisition, Formal analysis, Conceptualization.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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