Antimicrobial resistance in pigs has been under scrutiny for many years. However, many questions remain unanswered, including whether the initial antimicrobial resistance level of a pig will influence the antimicrobial resistance found at slaughter. Faecal samples from finishers pigs from 681 farms and from sows from 82 farms were collected, and levels of seven antimicrobial resistance genes, ermB, ermF, sulI, sulII, tet(M), tet(O), and tet(W), were quantified by high-capacity qPCR. There were 40 pairs of observations where the finishers were born in the farms of the sows. The objective of this study was to evaluate whether the levels of AMR genes found in finisher pigs at slaughter were associated with the levels in the farm where the finishers were born, and whether the levels of the AMR genes were equal in the sow and finisher pig populations. We found a significant positive correlation between the levels of AMR genes in finishers and the sows in the farms where the pigs were born for some of the genes (ermB (ρ = 0.47, p-value = 0.002), ermF (ρ = 0.41, p-value = 0.03), and tet(O) (ρ = 0.33, p-value = 0.04)). Furthermore, there were significant differences between AMR gene levels for the sow and finisher populations for ermB, ermF, sulI, sulII, tet(O), and tet(W), though not for tet(M).