



FUT1 Genotyping in Weaned Pigs: Guiding Selection for F18 Enterotoxigenic *E. coli* Research Models and Practical Implications

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TAKE HOME MESSAGES:

1. Fucosyltransferase (FUT1) genotype at the M307 position strongly predicts susceptibility to F18 enterotoxigenic *E. coli*.
2. FUT1 AA animals exhibit reduced receptor expression and F18 lesion risk.
3. Genotyping enables targeted selection of resistant or susceptible pigs for controlled *E. coli* challenge studies as well as for companies trying to reduce *E. coli* challenge.
4. Genotyping should be used by genetic companies to help select animals with less susceptibility to *E. coli*.

Tool for Improved Piglet Survivability

In swine production, weaning is a critical period in which piglets face significant health challenges such as enteric pathogens like F18 enterotoxigenic *Escherichia coli*. This bacterium commonly causes post-weaning diarrhea or even edema disease, both of which can result in reduced growth, heightened medication requirements, and piglet mortality. The most reliable genetic factor that determines a pig's susceptibility to F18 *E. coli* is the Fucosyltransferase 1 gene (FUT1). FUT1 controls the expression of a receptor in the pig's intestine that F18 *E. coli* must find to cause an infection.¹ However, there are genetic variants which are important to note.

A single genetic variation at the M307 position determines susceptibility.

- AA genotype = resistant; no receptor expression
- AG genotype = heterozygous
- GG genotype = fully susceptible

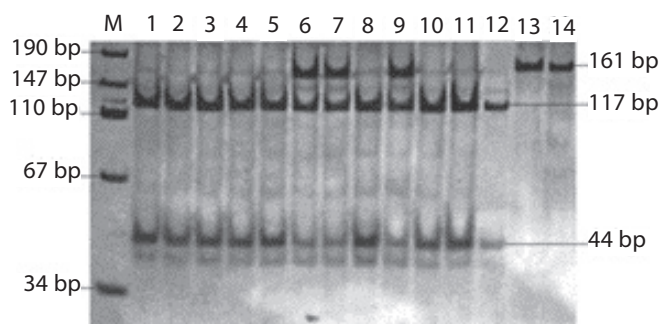


Figure 1. Genotyping Result of FUT1 Gene by PCR²

PCR products generated allele A (161 base pairs) or allele G (117 base pairs and 44 base pairs)

Lanes 1, 2, 3, 4, 5, 8, 10, 11, 12 were GG genotype; lanes 13, 14 were AA genotype; lanes 6, 7, 9 were AG genotype.²

Looking into the future, genetic suppliers could utilize this technology to select for the AA genotype within their breeding stock to ensure more complete genetic resistance to F18 related diseases. Ultimately this can reduce post-weaning health challenges, improve survivability, and lower the excess cost of antibiotics. Studies also find that western commercial lines typically have more AA genotype animals, opposed to Chinese breeds that are often found to have more GG.² In order to validate this genetic protection, it was found that in Sutan piglets, only AG and GG genotypes showed signs of post-weaning diarrhea after being exposed to *E. coli*.² Understanding genotype profiles can help guide targeted decisions to benchmark against less desirable outcomes, ultimately guiding long term decisions involved with genetic selection, health management, and swine survivability. This is especially helpful for genetic companies trying to drive health in the industry.

Genotyping Methods and Sampling

Fucosyltransferase genotyping can be performed using a few different techniques. One common approach is to use molecular techniques such as polymerase chain reaction amplification (PCR) followed up by restriction enzyme digestion or direct sequencing. Using modern, real time PCR testing, this process can be performed very quickly on several sample types. All of these methods reliably detect FUT1 polymorphism that determines the individual pig's susceptibility to F18 *E. coli*.

Appropriate sample types include whole blood, ear notches, and tissue samples from the pig's being tested. Tails docked during litter processing can serve as an excellent option (Figure 2). However, there are preferred sample types given results from ear notching have shown

to be less consistent than tails. The Iowa State University Veterinary Diagnostic Laboratory (ISU VDL) lists whole blood and tail samples as acceptable for DNA-based testing, offering several different genotyping services using validated molecular protocols.^{3,4} It's important to note that those desiring to submit samples should ensure proper identification and sterility of collections in order to maintain the integrity of the samples being submitted. The link to the VDL's website can be found below for more testing information. susceptibility to F18 *E. coli*.



Figure 2. Tail collection for Genotype Testing by KSU.

Metabolic and Microbial Impacts

Research also links the FUT1 genotype to microbiota and metabolism differences between pigs. AA pigs exhibit a heightened microbial population and metabolite profile compared to AG pigs, even without the challenge of infection present. This suggests that FUT1 impacts overall gut function in weaned pigs, only furthering the positive impacts that genetic selection can have on productivity.^{2,5}

Practical Implications

FUT1 genotyping gives the swine industry a practical, genetics-based route to improve herd health and reduce post-weaning mortality in relation to F18 *E. coli*. Because pigs with the AA genotype do not express the intestinal receptor to contract F18, they are considered resistant. This offers a variety of paths to take, both as negative controls in trials, but also as a selection opportunity to boost resistance. In contrast, those with the AG, GA, or GG genotypes are susceptible or partially susceptible, often used in enteric challenge studies.

Incorporating FUT1 genotyping into genetic selection over time increases the frequency of the resistant A allele. Although full herd conversion may currently not be practical, selecting AA or AG animals can incrementally shift the population susceptibility in a positive direction.

Many groups conducting research on piglets that are inoculated with *E. coli* use FUT1 genotyping to avoid use of AA pigs, for consistent response to F18 *E. coli*. Strict protocols ensure proper sampling and testing through the ISU VDL to determine DNA sampling and genotyping. At Kansas State University's Swine Enteric Health Research Center mapped the genotype across 790 pigs tested in EC trials, 59.7% were GG, 35.4% were AG/GA, and only 4.8% were AA (Figure 3). This highlights how uncommon natural resistance is, and the opportunity for genetic change in commercial farms. However, it's important to note these percentages and ratios differ between groups even within Kansas State University's farm. One group had a greater percentage of AG or GA genotypes while another may have more AA.

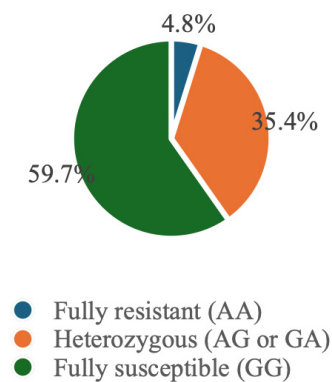


Figure 3: KSU Swine Enteric Health Research Center FUT1 genotype database results. $n = 792$ samples.

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