

## Abstract

F18<sup>+</sup>*Escherichia coli* infections causing post-weaning diarrhoea and/or oedema disease are a major cause of economic losses in pig industry. To date, no preventive strategy can protect pigs from F18<sup>+</sup>*E. coli* infections. One of the most attractive approaches to eliminate F18<sup>+</sup>*E. coli* infections is the selection for pigs that are resistant to F18<sup>+</sup>*E. coli* infections. However, this strategy was not believed to be favourable because of reports of genetic association with the stress-susceptibility gene in the Swiss Landrace. To investigate this potential association more thoroughly, 131 randomly selected Belgian hybrid pigs were genotyped for both the F18<sup>+</sup>*E. coli* resistance alleles (*FUT1*<sup>A</sup>) and the stress-susceptibility alleles (*RYR1*<sup>T</sup>) and their association was investigated by determining the linkage disequilibrium. This linkage disequilibrium (LD = -0.0149) is close to zero and does not differ significantly from 0 (likelihood ratio test  $\chi^2_1=1.123$ ,  $P = 0.29$ ), demonstrating no association between the *FUT1*<sup>A</sup> and *RYR1*<sup>T</sup> alleles. Furthermore, only a small fraction (4.6%) of the Belgian pigs was found to be resistant to F18<sup>+</sup>*E. coli* infections. Our results suggest that selection for F18<sup>+</sup>*E. coli* resistant pigs might be an attractive approach to prevent pigs from F18<sup>+</sup>*E. coli* infections, unlike to what has previously been postulated.