**Identifying the Genetic Basis for Resistance to Avian Influenza in Commercial Egg Layer Chickens**

W. Drobik-Czwarno, A. Wolc, J.E. Fulton, J. Arango, T. Jankowski, P. Settar, N.P. O'Sullivan, J.C.M. Dekkers

**Supplementary material**

***Supplementary Table S1.*** *Significant SNPs (Adjusted p-value ≤ 0.01) after Bonferroni correction based on the case-control frequency test for the Mexico/H7N3 and Iowa/H5N2 outbreak.*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Chr | SNP  rs | Position  [Mb] | P-value | Adjusted p-value | Allele frequency | | Closest  genes | | Location  [kbp] |
| Surv | Con |
| *Mexico/H7N3 outbreak* | | | | | | | | | |
| 1 | 315546485 | 126.028 | 4.17e-15 | 1.93e-08 | 0.025 | 0.163 | PUDP | | - 96 |
| NLGN4X,  mir-1397 | | + 262 + 290 |
| 1 | 317720887 | 82.299 | 1.15E-07 | 1.48E-03 | 0.417 | 0.628 | GAP43 | | - 565 |
| ZBTB20 | | +26 |
| 1 | 317988017 | 82.282 | 1.78E-07 | 2.30E-03 | 0.420 | 0.628 | GAP43 | - 548 | |
| ZBTB20 | +43 | |
| 10 | 314005397 | 18.245 | 5.38E-07 | 6.96E-03 | 0.220 | 0.394 | SMAD6 | | -43 |
| SMAD3 | | +37 |
| 1 | 14850450 | 82.250 | 6.63E-07 | 8.57E-03 | 0.349 | 0.543 | GAP43 | - 516 | |
| ZBTB20 | +75 | |
| *Iowa/H5N2 outbreak* | | | | | | | | | |
| 1 | 13970962 | 167.900 | 1.64E-10 | 2.12e-06 | 0.671 | 0.362 | SUCLA2 | | - 42 |
| HTR2A | | + 227 |
| 4 | 316133278 | 31.501 | 1.04E-08 | 1.34e-04 | 0.462 | 0.209 | ARHGAP10 | | overlap |
| 4 | 16385164 | 31.524 | 1.89E-08 | 2.44e-04 | 0.456 | 0.209 | ARHGAP10 | | overlap |
| 1 | 315387479 | 173.176 | 4.14E-07 | 5.35e-03 | 0.532 | 0.292 | RFC3 | | - 15 |
| STARD13 | | + 318 |
| 28 | 313249231 | 0.158 | 4.38E-07 | 5.66e-03 | 0.405 | 0.190 | ENSGALG00000026177 | | - 3 |
| FBN3 | | + 114 |
| 1 | 317232433 | 176.040 | 4.45E-07 | 5.75E-03 | 0.481 | 0.252 | ATP8A2 | | overlap |
| 7 | 16605877 | 28.707 | 6.58E-07 | 8.51E-03 | 0.261 | 0.085 | DPP10 | | overlap |
| 15 | 316781487 | 0.554 | 6.82E-07 | 8.82E-03 | 0.620 | 0.380 | KDM2B | | overlap |

*Chr = Chromosome; SNP = reference SNP ID (rs); Position = Position in Mb according to build 4;* Adjusted p-value *= p-value adjusted for multiple testing with Bonfferoni correction; Surv = survivors; Con = Controls; Location = Location of the closest gene, + SNP is located X kbp upstream, - SNP is located X kbp downstream.*

** ***Supplementary Figure S1.*** *Manhattan plot for results based on the basic case-control association model for the (a) Mexico/H7N3 and (b) Iowa/H5N2 outbreaks. The blue line represents the 5% significance threshold after Bonfferoni correction.*