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| --- | --- | --- |
| Model¥ | Animal Models | Sire and Dam Models |
|  | σ2w >0 | σ2w =0 | σ2w >0 | σ2w =0 |
| σ2u | 0.0072 (0.0016) | 0.0113 (0.0017) |  |  |
| σ2s |  |  | 0.0018 (0.0005) | 0.0018 (0.0005) |
| σ2d |  |  | 0.0016 (0.0006) | 0.0033 (0.0006) |
| σ2v | 0.0064 (0.0005) | 0.0071 (0.0005) | 0.0063 (0.0005) | 0.0069 (0.0005) |
| σ2w | 0.0017 (0.0005) |  | 0.0019 (0.0006) |  |
| σ2p | 0.0594 (0.0009) | 0.0605 (0.0010) | 0.0592 (0.0009) | 0.0596 (0.0009) |
| h2u | 0.12 (0.03) | 0.19 (0.03) | 0.11 (0.03) | 0.17 (0.02) |
| σ2v/σ2p | 0.11 (0.01) | 0.12 (0.01) | 0.11 (0.01) | 0.12 (0.01) |
| σ2w/σ2p | 0.03 (0.01) |  | 0.03 (0.01) |  |
| h2L liability scale | 0.46 | 0.72 | 0.44 | 0.65 |
| LogL | 8215.64 | 8201.21 | 8257.89 | 8241.54 |

¥ - σ2u, σ2v and σ2w are variances due to the additive genetic effects, litter and maternal environment effects. σ2p is phenotypic variance. h2u is estimated heritability on observed scale, and σ2v/σ2p  and σ2w/σ2p are the proportion of phenotypic variance explained by the litter and maternal environment effects respectively. h2L is theheritabilitytransformed to an underlying scale, and LogL is log likelihood.