**Effect and mode of action of the Texel Muscling QTL (TM-QTL) on carcass traits in purebred Texel lambs**

J.M. Macfarlane1, N.R. Lambe1, O. Matika2, P.L. Johnson3, B.T. Wolf4, W. Haresign4, S.C. Bishop2 and L. Bünger1

Supplementary tables

Supplementary table S1. Carcass composition: Least squares means† for lean meat yield (LMY), fat trim and bone weights measured from butchery of a half carcass and proportion of each of these of total carcass side weight (LMY\_p, Fat trim\_p, Bone\_p) (all adjusted for cold carcass weight) for the four TM-QTL genotype groups and the p-values for the tests of different modes of action for the QTL

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | LMY1 | Fat trim2 | Bone | LMY\_p | Fat trim\_p | Bone\_p3 |
| +/+ | 4205ab | 389b | 2178 | 0.618 | 0.057 | 0.325ab |
| +/TM | 4150b | 365ab | 2195 | 0.617 | 0.054 | 0.329ab |
| TM/+ | 4215ab | 346a | 2206 | 0.620 | 0.051 | 0.330a |
| TM/TM | 4280a | 363ab | 2170 | 0.627 | 0.054 | 0.320b |
| ave s.ed. | 43.7 | 25.5 | 34.3 | 0.0052 | 0.0036 | 0.0055 |
| min s.e.d. | 34.4 | 20.6 | 27.8 | 0.0042 | 0.0029 | 0.0044 |
| max s.e.d. | 51.1 | 30.0 | 40.3 | 0.0061 | 0.0043 | 0.0064 |
| P values for: |  |  |  |  |  |  |
| Additive effect | 0.09 | 0.09 | 0.53 | 0.39 | 0.13 | 0.53 |
| Dominance effect | 0.33 | 0.06 | 0.12 | 0.098 | 0.07 | 0.04 |
| Reciprocal heterozygote effect | 0.80 | 0.73 | 0.73 | 0.99 | 0.73 | 0.64 |
| Maternal dominance effect | 0.42 | 0.15 | 0.22 | 0.27 | 0.15 | 0.10 |
| Paternal polar overdominance | 0.69 | 0.35 | 0.49 | 0.25 | 0.37 | 0.34 |

† LS means with common letters in their superscripts are not significantly different (P > 0.05), where differences were significant, p-values are shown in the numbered footnote corresponding to that trait. Average, minimum and maximum s.e.d. are shown for information only.

1 LMY: TM/TM vs. +/TM = 0.012

2 Fat trim: TM/+ vs. +/+ = 0.036

3 Bone%: TM/+ vs. TM/TM = 0.045

Supplementary table S2. Weight of carcass regions and distribution of weight across carcass: Least squares means† for weight of leg (LEGwt), saddle (SADwt) and shoulder (SHLDwt) regions from a half carcass and proportion of each of these of total carcass weight (LEGp, SADp, SHLDp) (all adjusted for cold carcass weight) for the four TM-QTL genotype groups and the p-values for the tests of different modes of action for the QTL

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | SHLDwt | SADwt | LEGwt | SHLDp | SADp | LEGp |
| +/+ | 2804 | 1694 | 2650 | 0.195 | 0.115 | 0.183 |
| +/TM | 2768 | 1704 | 2637 | 0.192 | 0.116 | 0.182 |
| TM/+ | 2791 | 1694 | 2666 | 0.194 | 0.115 | 0.184 |
| TM/TM | 2808 | 1718 | 2645 | 0.194 | 0.117 | 0.183 |
| ave s.e.d. | 28.65 | 28.29 | 21.37 | 0.0020 | 0.0019 | 0.0016 |
| min s.e.d. | 22.82 | 22.85 | 17.76 | 0.0016 | 0.0015 | 0.0013 |
| max s.e.d. | 33.76 | 33.34 | 25.11 | 0.0024 | 0.0022 | 0.0018 |
| P values for: |  |  |  |  |  |  |
| Additive effect | 0.33 | 0.71 | 0.91 | 0.57 | 0.40 | 0.91 |
| Dominance effect | 0.42 | 0.82 | 0.70 | 0.43 | 0.76 | 0.50 |
| Reciprocal heterozygote effect | 0.43 | 0.88 | 0.14 | 0.37 | 0.90 | 0.13 |
| Maternal dominance effect | 0.89 | 0.82 | 0.62 | 0.95 | 0.78 | 0.73 |
| Paternal polar overdominance | 0.17 | 0.997 | 0.07 | 0.14 | 0.93 | 0.04 |

† LS means with common letters in their superscripts, within column, are not significantly different (P > 0.05), where differences were significant, p-values are shown in the numbered footnote corresponding to that trait. Average, minimum and maximum s.e.d. are shown for information only

.

Supplementary table S3. Composition of carcass regions measured by carcass CT scanning: Least squares means† for weight of muscle (Musc), fat and bone in each region of the carcass (leg, saddle, shoulder) (all adjusted for cold carcass weight) for the four TM-QTL genotype groups and the p-values for the tests of different modes of action for the QTL

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Leg | | | Saddle | | | Shoulder | | |
|  | Muscle1 | Fat | Bone2 | Muscle | Fat | Bone | Muscle | Fat | Bone |
| +/+ | 3894a | 525a | 793 | 1899a | 569ab | 391 | 3622 | 935 | 956 |
| +/TM | 3763b | 497ab | 761 | 2035b | 626a | 408 | 3615 | 914 | 935 |
| TM/+ | 3893a | 498b | 784 | 1985b | 542b | 402 | 3655 | 875 | 952 |
| TM/TM | 3907a | 510ab | 771 | 1957ab | 559ab | 394 | 3631 | 907 | 926 |
| ave s.e.d. | 51.8 | 16.2 | 15.4 | 45.0 | 39.2 | 11.8 | 55.1 | 40.6 | 21.1 |
| min s.e.d. | 42.3 | 13.0 | 12.4 | 35.4 | 30.8 | 9.40 | 43.8 | 32.3 | 16.8 |
| max s.e.d. | 60.8 | 19.1 | 18.2 | 52.6 | 45.9 | 13.9 | 65.0 | 47.9 | 24.9 |
| P values for: |  |  |  |  |  |  |  |  |  |
| Additive effect | 0.81 | 0.10 | 0.23 | 0.15 | 0.30 | 0.77 | 0.25 | 0.35 | 0.51 |
| Dominance effect | 0.11 | 0.01 | 0.96 | 0.01 | 0.83 | 0.02 | 0.31 | 0.045 | 0.25 |
| Reciprocal heterozygote effect | 0.02 | 0.54 | 0.80 | 0.74 | 0.42 | 0.13 | 0.45 | 0.63 | 0.34 |
| Maternal dominance effect | 0.02 | 0.047 | 0.87 | 0.050 | 0.79 | 0.02 | 0.28 | 0.27 | 0.20 |
| Paternal polar overdominance | 0.16 | 0.29 | 0.82 | 0.14 | 0.32 | 0.98 | 0.93 | 0.06 | 0.84 |

† LS means with common letters in their superscripts, within column, are not significantly different (P > 0.05), where differences were significant, p-values are shown in the numbered footnote corresponding to that trait. Average, minimum and maximum s.e.d. are shown for information only.

1 Leg muscle: +/+ vs. +/TM P = 0.017, TM/+ vs. +/TM P = 0.029, TM/TM vs. +/TM P = 0.011

2 Leg fat: TM/+ vs. +/+ P = 0.04

3 Saddle muscle: +/+ vs. +/TM P = 0.009, +/+ vs. TM/+ P = 0.016

4 Saddle fat: TM/+ vs. +/TM P = 0.049

Supplementary table S4. Composition of carcass regions: Least squares means† for weight of lean meat yield (LMY), fat trim and bone in each region of a half carcass (leg, saddle, shoulder) measured by butchery (all adjusted for cold carcass weight) for the four TM-QTL genotype groups and the p-values for the tests of different modes of action for the QTL

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Leg | | | Saddle | | | Shoulder | | |
|  | LMY1 | Fat trim | Bone2 | LMY | Fat trim | Bone | LMY | Fat trim | Bone |
| +/+ | 1409ab | 187 | 698b | 1085 | 92.8 | 519 | 1735 | 104 | 962 |
| +/TM | 1351b | 181 | 704b | 1077 | 91.8 | 550 | 1722 | 97.7 | 940 |
| TM/+ | 1428a | 175 | 703b | 1093 | 76.5 | 526 | 1725 | 89.4 | 976 |
| TM/TM | 1429a | 188 | 676a | 1112 | 84.4 | 537 | 1759 | 88.1 | 955 |
| ave s.e.d. | 29.9 | 11.5 | 11.1 | 21.5 | 15.8 | 15.2 | 24.8 | 9.77 | 24.3 |
| min s.e.d. | 24.5 | 9.30 | 9.00 | 17.8 | 12.4 | 12.2 | 19.5 | 7.90 | 19.5 |
| max s.e.d. | 34.8 | 13.6 | 13.3 | 25.1 | 18.4 | 17.9 | 29.0 | 11.5 | 28.7 |
| P values for: |  |  |  |  |  |  |  |  |  |
| Additive effect | 0.59 | 0.81 | 0.30 | 0.38 | 0.13 | 0.17 | 0.03 | 0.04 | 0.98 |
| Dominance effect | 0.13 | 0.11 | 0.03 | 0.66 | 0.17 | 0.22 | 0.48 | 0.22 | 0.62 |
| Reciprocal heterozygote effect | 0.02 | 0.86 | 0.86 | 0.70 | 0.65 | 0.118 | 0.16 | 0.97 | 0.60 |
| Maternal dominance effect | 0.03 | 0.24 | 0.12 | 0.62 | 0.24 | 0.10 | 0.80 | 0.40 | 0.95 |
| Paternal polar overdominance | 0.16 | 0.36 | 0.20 | 0.92 | 0.65 | 0.40 | 0.05 | 0.43 | 0.38 |

† LS means with common letters in their superscripts, within column, are not significantly different (P > 0.05), where differences were significant, p-values are shown in the numbered footnote corresponding to that trait. Average, minimum and maximum s.e.d. are shown for information only.

1 Leg LMY: TM/TM vs. +/TM = 0.026, TM/+ vs. +/TM = 0.019

2 Leg Bone: TM/TM vs. +/+ = 0.013, TM/TM vs. +/TM = 0.028, TM/TM vs. TM/+ = 0.008