**Table A. The partial production performance of Tibetan and 7 lowland chicken breeds.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Breed | Body weight (g) | | Eviscerated yield (%) | | Age at first egg (d) | Egg weight (g) |
|  | male | female | male | female |  |  |
| Tibetan | 1585 | 860 | 73.4 | 67.3 | 270 | 42 |
| Emei | 2622 | 1904 | 79.65 | 70.9 | 186 | 54 |
| Shimian | 3650 | 3060 | 69.5 | 65.2 | 216 | 55 |
| Jiuyuan | 2616 | 1763 | 79.7 | 67 | 181 | 55 |
| Pengxian | 3950 | 1880 | 79.1 | 72.12 | 216 | 54 |
| Blue-shelled | 1650 | 1300 | 64.5 | 71.25 | 152 | 50 |
| Muchuan black-bone | 2680 | 2290 | 79 | 69 | 225 | 54 |
| Wenchang | 1800 | 1500 | 75 | 70.3 | 145 | 49 |

The production performance data of 8 breeds of chicken is based on poultry genetic resources in China[[1](#_ENREF_1)] .

**Table B. Allele and genotype frequencies of the SNP1 rs315040213 and SNP2 rs14330062 in the *EPAS1.***

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Breed | SNP1 rs315040213 | | | | | SNP2 rs14330062 | | | | |
| Genotype | | | Allele | | Genotype | | | Allele | |
| C C | C T | T T | C | T | C C | C T | T T | C | T |
| RKZ(30) | 16(0.53) | 12(0.4) | 2(0.07) | 44(0.73) | 16(0.27) | 30(1) | 0(0) | 0(0) | 60(1) | 0(0) |
| SN(17) | 4(0.24) | 12(0.71) | 1(0.06) | 20(0.59) | 14(0.41) | 16(0.94) | 1(0.06) | 0(0) | 33(0.97) | 1(0.03) |
| LS(24) | 5(0.21) | 13(0.54) | 6(0.25) | 23(0.48) | 25(0.52) | 22(0.92) | 2(0.08) | 0(0) | 46(0.96) | 2(0.04) |
| GZ(16) | 13(0.81) | 3(0.19) | 0(0) | 29(0.91) | 3(0.09) | 16(1) | 0(0) | 0(0) | 32(1) | 0(0) |
| AB(24) | 14(0.58) | 9(0.38) | 1(0.04) | 37(0.77) | 11(0.23) | 24(1) | 0(0) | 0(0) | 48(1) | 0(0) |
| DQ(12) | 3(0.25) | 8(0.67) | 1(0.08) | 14(0.58) | 10(0.42) | 12(1) | 0(0) | 0(0) | 24(1) | 0(0) |
| QH(15) | 5(0.33) | 8(0.53) | 2(0.13) | 18(0.6) | 12(0.4) | 15(1) | 0(0) | 0(0) | 30(1) | 0(0) |
| LZ(19) | 14(0.74) | 5(0.26) | 0(0) | 33(0.87) | 5(0.13) | 17(0.89) | 2(0.11) | 0(0) | 36(0.95) | 2(0.05) |
| EM(23) | 16(0.7) | 6(0.26) | 1(0.04) | 38(0.83) | 8(0.17) | 23(1) | 0(0) | 0(0) | 46(1) | 0(0) |
| SM(14) | 7(0.5) | 3(0.21) | 4(0.29) | 17(0.61) | 11(0.39) | 14(1) | 0(0) | 0(0) | 28(1) | 0(0) |
| JY(25) | 10(0.4) | 12(0.48) | 3(0.12) | 32(0.64) | 18(0.36) | 25(1) | 0(0) | 0(0) | 50(1) | 0(0) |
| PX(12) | 9(0.75) | 3(0.25) | 0(0) | 21(0.88) | 3(0.13) | 12(1) | 0(0) | 0(0) | 24(1) | 0(0) |
| LK(14) | 9(0.64) | 5(0.36) | 0(0) | 23(0.82) | 5(0.18) | 14(1) | 0(0) | 0(0) | 28(1) | 0(0) |
| MC(20) | 15(0.75) | 5(0.25) | 0(0) | 35(0.875) | 5(0.125) | 20(1) | 0(0) | 0(0) | 40(1) | 0(0) |
| WC(31) | 28(0.9) | 2(0.06) | 1(0.03) | 58(0.94) | 4(0.06) | 31(1) | 0(0) | 0(0) | 62(1) | 0(0) |

“C” represents the reference allele and “T” represents the mutant allele. Numbers represent allele/genotype frequency, with the figures in brackets representing the number of individuals with each genotype.

**Table C. Allele and genotype frequencies of the SNP3 rs316126786 and SNP4 rs739281102 in the *EPAS1*.**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Breed | SNP3 rs316126786 | | | | | SNP4 rs739281102 | | | | |
| Genotype | | | Allele | | Genotype | | | Allele | |
| A A | A G | G G | A | G | A A | A G | G G | A | G |
| RKZ(30) | 30(1) | 0(0) | 0(0) | 60(1) | 0(0) | 22(0.73) | 6(0.2) | 2(0.07) | 50(0.83) | 10(0.17) |
| SN(17) | 17(1) | 0(0) | 0(0) | 34(1) | 0(0) | 15(0.88) | 1(0.06) | 1(0.06) | 31(0.91) | 3(0.09) |
| LS(24) | 24(1) | 0(0) | 0(0) | 48(1) | 0(0) | 21(0.88) | 2(0.08) | 1(0.04) | 44(0.92) | 4(0.08) |
| GZ(16) | 16(1) | 0(0) | 0(0) | 32(1) | 0(0) | 12(0.75) | 3(0.19) | 1(0.06) | 27(0.84) | 5(0.16) |
| AB(24) | 18(0.75) | 6(0.25) | 0(0) | 42(0.88) | 6(0.13) | 14(0.58) | 8(0.33) | 2(0.08) | 36(0.75) | 12(0.25) |
| DQ(12) | 10(0.83) | 2(0.17) | 0(0) | 22(0.92) | 2(0.08) | 11(0.92) | 1(0.08) | 0(0) | 23(0.96) | 1(0.04) |
| QH(15) | 13(0.87) | 2(0.13) | 0(0) | 28(0.93) | 2(0.07) | 14(0.93) | 1(0.07) | 0(0) | 29(0.97) | 1(0.03) |
| LZ(19) | 14(0.74) | 4(0.21) | 1(0.05) | 32(0.84) | 6(0.16) | 10(0.53) | 8(0.42) | 1(0.05) | 28(0.74) | 10(0.26) |
| EM(23) | 19(0.83) | 4(0.17) | 0(0) | 42(0.91) | 4(0.09) | 14(0.61) | 7(0.3) | 2(0.09) | 35(0.76) | 11(0.24) |
| SM(14) | 11(0.79) | 3(0.21) | 0(0) | 25(0.89) | 3(0.11) | 9(0.64) | 5(0.36) | 0(0) | 23(0.82) | 5(0.18) |
| JY(25) | 18(0.72) | 7(0.28) | 0(0) | 43(0.86) | 7(0.14) | 16(0.64) | 4(0.16) | 5(0.2) | 36(0.72) | 14(0.28) |
| PX(12) | 7(0.58) | 5(0.42) | 0(0) | 19(0.79) | 5(0.21) | 8(0.67) | 2(0.17) | 2(0.17) | 18(0.75) | 6(0.25) |
| LK(14) | 7(0.5) | 7(0.5) | 0(0) | 21(0.75) | 7(0.25) | 8(0.57) | 5(0.36) | 1(0.07) | 21(0.75) | 7(0.25) |
| MC(20) | 15(0.75) | 5(0.25) | 0(0) | 35(0.875) | 5(0.125) | 10(0.5) | 9(0.45) | 1(0.05) | 29(0.725) | 11(0.275) |
| WC(31) | 17(0.55) | 11(0.35) | 3(0.1) | 45(0.73) | 17(0.27) | 25(0.81) | 6(0.19) | 0(0) | 56(0.9) | 6(0.1) |

“A” represents the reference allele and “G” represents the mutant allele. Numbers represent allele/genotype frequency, with the figures in brackets representing the number of individuals with each genotype.

**Table D. Allele and genotype frequencies of the SNP5 rs740389732 and SNP6 rs739010166 in the *EPAS1*.**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Breed | SNP5 rs740389732 | | | | | SNP6 rs739010166 | | | | |
| Genotype | | | Allele | | Genotype | | | Allele | |
| A A | A G | G G | A | G | C C | C T | T T | C | T |
| RKZ(30) | 23(0.77) | 4(0.13) | 3(0.1) | 50(0.83) | 10(0.17) | 30(1) | 0(0) | 0(0) | 60(1) | 0(0) |
| SN(17) | 14(0.82) | 2(0.12) | 1(0.06) | 30(0.88) | 4(0.12) | 16(0.94) | 1(0.06) | 0(0) | 33(0.97) | 1(0.03) |
| LS(24) | 22(0.92) | 1(0.04) | 1(0.04) | 45(0.94) | 3(0.06) | 23(0.96) | 1(0.04) | 0(0) | 47(0.98) | 1(0.02) |
| GZ(16) | 12(0.75) | 3(0.19) | 1(0.06) | 27(0.84) | 5(0.16) | 16(1) | 0(0) | 0(0) | 32(1) | 0(0) |
| AB(24) | 15(0.63) | 7(0.29) | 2(0.08) | 37(0.77) | 11(0.23) | 18(0.75) | 6(0.25) | 0(0) | 42(0.88) | 6(0.13) |
| DQ(12) | 11(0.92) | 1(0.08) | 0(0) | 23(0.96) | 1(0.04) | 10(0.83) | 2(0.17) | 0(0) | 22(0.92) | 2(0.08) |
| QH(15) | 14(0.93) | 1(0.07) | 0(0) | 29(0.97) | 1(0.03) | 13(0.87) | 2(0.13) | 0(0) | 28(0.93) | 2(0.07) |
| LZ(19) | 11(0.58) | 7(0.37) | 1(0.05) | 29(0.76) | 9(0.24) | 15(0.79) | 3(0.16) | 1(0.05) | 33(0.87) | 5(0.13) |
| EM(23) | 14(0.61) | 7(0.3) | 2(0.09) | 35(0.76) | 11(0.24) | 16(0.7) | 7(0.3) | 0(0) | 39(0.85) | 7(0.15) |
| SM(14) | 9(0.64) | 5(0.36) | 0(0) | 23(0.82) | 5(0.18) | 8(0.57) | 5(0.36) | 1(0.07) | 21(0.75) | 7(0.25) |
| JY(25) | 17(0.68) | 7(0.28) | 1(0.04) | 41(0.82) | 9(0.18) | 17(0.68) | 8(0.32) | 0(0) | 42(0.84) | 8(0.16) |
| PX(12) | 9(0.75) | 1(0.08) | 2(0.17) | 19(0.79) | 5(0.21) | 9(0.75) | 2(0.17) | 1(0.08) | 20(0.83) | 4(0.17) |
| LK(14) | 9(0.64) | 2(0.14) | 3(0.21) | 20(0.71) | 8(0.29) | 12(0.86) | 2(0.14) | 0(0) | 26(0.93) | 2(0.07) |
| MC(20) | 10(0.5) | 9(0.45) | 1(0.05) | 29(0.725) | 11(0.275) | 15(0.75) | 4(0.2) | 1(0.05) | 34(0.85) | 6(0.15) |
| WC(31) | 26(0.84) | 5(0.16) | 0(0) | 57(0.92) | 5(0.08) | 14(0.45) | 9(0.29) | 8(0.26) | 37(0.6) | 25(0.4) |

“A” represents the reference allele and “G” represents the mutant allele. Numbers represent allele/genotype frequency, with the figures in brackets representing the number of individuals with each genotype.

“C” represents the reference allele and “T” represents the mutant allele. Numbers represent allele/genotype frequency, with the figures in brackets representing the number of individuals with each genotype.

**Table E. Nucleotide diversities of EPAS1 gene in Tibetan chicken and Lowland chicken.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Population | Sample size | SNP sites | Pi1 | K2 |
| TC3 | 157 | 6 | 0.00188 | 1.150 |
| LC4 | 139 | 5 | 0.00295 | 1.590 |
| P-value | NA | 0.058 | 0.139 | 0.101 |

1 Pi is the abbreviation of nucleotide diversity.

2 K is the abbreviation of average number of nucleotide differences.

3 TC means Tibetan chicken.

4 LC means Lowland chicken.

**Figure A. The LD block of Tibetan chicken.**

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TC means Tibetan chicken.

Genbank Sequence access number.

Gene pool sequence number: grp 5894795.

Gallus\_gallus\_endothelial\_PAS\_domain\_protein.sqn: KY572133

Individual sequence number: grp 5894798.

Gallus\_gallus\_endothelial\_PAS\_domain\_protein\_1\_gene\_partial\_CDS\_exon1.sqn: KY570949 - KY571244

Gallus\_gallus\_endothelial\_PAS\_domain\_protein\_1\_gene\_partial\_CDS\_exon7.sqn: KY571245 - KY571540

Gallus\_gallus\_endothelial\_PAS\_domain\_protein\_1\_gene\_partial\_CDS\_exon12.sqn: KY571541 - KY571836

Gallus\_gallus\_endothelial\_PAS\_domain\_protein\_1\_gene\_partial\_CDS\_exon14.sqn: KY571837 - KY572132

**Reference**

1. Chen G-H, Wang K-H, Wang J-Y, Ding C, Yang N, Dai G, et al. Poultry genetic resources in China. Shanghai Scientific and Technological Press, Shanghai, China. 2004.