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| **Table S1** Analysis of variance for agro-morphological traits and summer dormancy index in parental genotypes (G) and half-sib families (F) of tall fescue assessed during four years (2016-2019)  |
| Mean square |
| SDI | FLO | NS | CD | PH | ADFY | AUDFY | SUDFY | SPDFY | Degree of freedom | Source of variation |
|  **Parental genotypes** |
| 0.92ns | 4.58ns | 32.78ns | 14.76ns | 314.95\*\* | 375050.59\*\* | 8845.93\* | 16864.85\* | 107278.88\*\* | 2 | Rep |
| 5.04\*\* | 81.55\*\* | 2868.00\*\* | 88.29\*\* | 309.17\*\* | 20350.61\*\* | 5378.65\*\* | 19528.58\*\* | 40800.20\*\* | 15 | G |
| 1.15 | 8.91 |  102.16 | 7.29 | 52.24 | 7580.08 | 1593.43 | 4130.76 | 20800.65 | 30 | Rep (G) |
| 15.68\*\* | 3208.37\*\* | 81931.23\*\* | 3023.32\*\* | 5422.46\*\* | 268154.52\*\* | 280209.88\*\* | 320142.49\*\* | 1455050.26\*\* | 3 | Y |
| 13.00\* | 53.54\*\* | 1414.82\*\* | 11.43\*\* | 66.63\*\* | 4541.39\*\* | 2465.00\*\* | 2765.03\*\* | 12654.14\* | 45 | Y × G |
| 12.00\* | 7.00ns | 132.60ns | 47.15\*\* | 564.99\*\* | 13249.33\*\* | 5350.44\*\* | 6471.39\*\* | 30992.44\*\* | 6 | Rep × Y |
| 2.02 | 7.84 | 417.40 | 2.59 | 23.49 | 2335.57 | 822.68 | 1283.31 | 7310.32 | 90 | Error |
| **Half-sib families** |
| 4.45\*\* | 19.19ns | 3098.73\*\* | 126.55\*\* | 748.50\*\* | 25307.87ns | 19901.27\*\* | 9856.03\*\* | 24162.21\*\* | 2 | Rep |
| 3.12\*\* | 130.20\* | 3990.97\*\* | 75.19\*\* | 451.59\*\* | 56688.69\*\* | 9174.76\*\* | 9482.56\*\* | 18393.00\*\* | 15 | F |
| 0.30 | 30.60 | 507.90 | 10.19 | 16.63 | 17773.69 | 1313.19 | 1917.85 | 4945.77 | 30 | Rep (F) |
| 41.03\*\* | 3225.74\*\* | 229539.17\*\* | 4982.63\*\* | 2377.15\*\* | 4244153.74\*\* | 318203.76\*\* | 142245.19\*\* | 1378884.31\*\* | 3 | Y |
| 1.00\*\* | 46.99\* | 1185.47\*\* | 12.52\*\* | 142.33\*\* | 19350.39\* | 4158.00\*\* | 3477.41\*\* | 9028.29\*\* | 45 | Y × F |
| 1.62\*\* | 20.95ns | 2630.92\*\* | 37.51\*\* | 295.14\*\* | 26771.99\*\* | 31295.53\*\* | 11486.82\*\* | 23886.31\*\* | 6 | Rep × Y |
| 0.15 | 25.65 | 434.09 | 2.76 | 15.35 | 10850.21 | 830.86 | 931.31 | 4779.09 | 90 | Error |
| \*: Significant at the 0.05 probability level, \*\*: Significant at the 0.01 probability level, ns: non-significant.Rep: replication, Y: year, G: parental genotypes, F: half-sib familiesSPDFY: spring dry forage yield, SUDFY: summer dry forage yield, AUDFY: autumn dry forage yield, ADFY: annual dry forage yield, PH: plant height, CD: crown diameter, NS: number of stems per plant, FLO: flowering time, SDI: summer dormancy index (summer yield of dormant control cultivar/summer yield) |

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| **Table S2** General combining ability (GCA) of measured traits in tall fescue genotypes |
| Genotypes | ADFY | PH | CD | NS | FLO | SDI | Persis |
| 21M | 261.60 | 15.82 | 7.45 | 14.00 | 6.90 | -2.12 | 18.75 |
| 20L | 86.80 | 11.67 | 4.45 | 10.52 | 3.99 | -1.29 | -178.38 |
| 14E | 11.08 | 6.22 | -1.01 | 2.06 | 2.07 | -0.89 | -271.21 |
| 23M | -10.36 | 6.14 | -1.93 | 5.36 | 2.99 | -0.66 | -31.63 |
| 6L | -121.34 | -7.94 | -4.73 | -8.98 | -1.09 | 0.99 | 43.34 |
| 3M | -42.95 | -8.95 | -1.99 | -2.37 | 2.45 | -0.11 | 108.55 |
| 22M | -22.13 | 8.26 | 2.29 | -4.55 | -3.97 | -0.43 | 18.73 |
| 12L | 59.37 | 2.06 | 1.57 | 9.30 | 7.86 | -0.98 | -95.38 |
| 9E | -105.03 | -3.32 | -0.90 | 1.01 | 2.10 | 0.21 | -65.36 |
| 11M | 157.83 | 13.12 | 5.50 | 12.50 | 5.20 | -1.61 | -266.93 |
| 3E | -35.57 | -1.36 | -0.35 | -11.50 | 2.14 | -0.24 | 92.60 |
| 1M | -123.90 | -10.31 | -2.05 | 0.88 | 1.06 | 1.65 | 71.20 |
| 10E | -2.91 | -3.32 | -0.47 | -4.18 | -3.11 | -0.34 | -16.59 |
| 1E | 310.87 | 22.45 | 9.73 | 16.48 | -1.51 | -2.14 | 10.90 |
| 17M | -203.65 | -15.22 | -6.09 | -22.19 | -12.90 | 3.58 | 228.88 |
| 4E | -219.55 | -14.51 | -5.30 | -22.71 | -10.12 | 4.56 | 332.70 |
| LSD | 49.98 | 1.97 | 0.83 | 2.14 | 1.01 | 0.50 | 24.11 |
| ADFY: annual dry forage yield,, PH: plant height, CD: crown diameter, NS: number of stems per plant, FLO: flowering time, SDI: summer dormancy index (summer yield of dormant control cultivar/summer yield) Persis: persistence |

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| **Table S3** Correlation coefficients among traits in parental genotypes (above diagonal) and half sib families of tall fescue (below diagonal) |
|  | SPDFY | SUDFY | AUDFY | ADFY | PH | CD | NS | FLO | SDI | Persis |
| SPDFY | 1 | 0.92\*\* | 0.94\*\* | 0.97\*\* | 0.82\*\* | 0.84\*\* | 0.82\*\* | 0.21ns | -0.90\*\* | 0.89\*\* |
| SUDFY | 0.97\*\* | 1 | 0.97\*\* | 0.98\*\* | 0.89\*\* | 0.74\*\* | 0.75\*\* | 0.28ns | -0.92\*\* | 0.53\* |
| AUDFY | 0.96\*\* | 0.98\*\* | 1 | 0.99\*\* | 0.88\*\* | 0.75\*\* | 0.77\*\* | 0.32ns | -0.92\*\* | 0.76\*\* |
| ADFY | 0.98\*\* | 0.99\*\* | 0.99\*\* | 1 | 0.88\*\* | 0.79\*\* | 0.79\*\* | 0.28ns | -0.93\*\* | 0.72\*\* |
| PH | 0.89\*\* | 0.93\*\* | 0.91\*\* | 0.92\*\* | 1 | 0.83\*\* | 0.75\*\* | 0.18ns | -0.86\*\* | 0.52\* |
| CD | 0.90\*\* | 0.94\*\* | 0.94\*\* | 0.95\*\* | 0.94\*\* | 1 | 0.77\*\* | 0.03ns | -0.78\*\* | 0.50\* |
| NS | 0.91\*\* | 0.95\*\* | 0.88\*\* | 0.91\*\* | 0.87\*\* | 0.89\*\* | 1 | 0.13ns | -0.76\*\* | 0.50\* |
| FLO | 0.44ns | 0.41ns | 0.37ns | 0.41ns | 0.34ns | 0.33ns | 0.58\*\* | 1 | -0.29ns | -0.41ns |
| SDI | -0.88\*\* | -0.88\*\* | -0.84\*\* | -0.87\*\* | -0.91\*\* | -0.81\*\* | -0.86\*\* | -0.51\* | 1 | -0.38ns |
| Persis | 0.10ns | -0.12ns | 0.11ns | 0.12ns | -0.21ns | -0.06ns | -0.23ns | -0.50\* | 0.50\* | 1 |
| SPDFY: spring dry forage yield, SUDFY: summer dry forage yield, AUDFY: autumn dry forage yield, ADFY: annual dry forage yield, PH: plant height, CD: crown diameter, NS: number of stems per plant, FLO: flowering time, SDI: summer dormancy index, Persis: persistencens: non-significant, \*: and \*\* Significant at 5 and 1 % level of level probability, respectively  |