**Table 1.** Means, medians, and 95% equal tail posterior probability intervals (95% ETPPIs) of hyperparameters estimated from the Bayesian sparse linear mixed model (BSLMM) in phenological trait **FPD**, **VPD**, **BOF** and **BOS**.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Trait | **Hyperparameter** | **Mean** | **Median** | **2.5%** | **97.5%** |
| FPD | h |  0.3244  |  0.3128  |  0.0316  |  0.6830  |
|  | PVE |  0.2026  |  0.1798  |  0.0171  |  0.5215  |
|  | rho |  0.5220  |  0.5315  |  0.0275  |  0.9799  |
|  | PGE |  0.4722  |  0.4776  |  -  |  0.9671  |
|  | pi | 3.23 × 10-2 | 1.06 × 10-2 | 6.40 × 10-4 | 1.42 × 10-1 |
|  | n.gamma | 60.67 | 20.00 | - | 267.00 |
| VPD | h |  0.8224  |  0.8305  |  0.6667  |  0.9312  |
|  | PVE |  0.8695  |  0.8717  |  0.7803  |  0.9451  |
|  | rho |  0.6511  |  0.6902  |  0.1185  |  0.9872  |
|  | PGE |  0.6572  |  0.7720  |  0.0553  |  0.9947  |
|  | pi | 5.86 × 10-2 | 4.62 × 10-2 | 2.18 × 10-3 | 1.55 × 10-1 |
|  | n.gamma | 111.28 | 88.00 | 4.00 | 290.00 |
| BOF | h |  0.7046  |  0.7164  |  0.4483  |  0.8934  |
|  | PVE |  0.6603  |  0.6622  |  0.4659  |  0.8455  |
|  | rho |  0.3267  |  0.2735  |  0.0118  |  0.8882  |
|  | PGE |  0.2586  |  0.1556  |  -  |  0.9121  |
|  | pi | 2.52 × 10-2 | 1.07 × 10-2 | 6.14 × 10-4 | 1.11 × 10-1 |
|  | n.gamma | 47.29 | 20.00 | 0.00 | 207.00 |
| BOS | h | 0.7319 | 0.7414 | 0.5371 | 0.8738 |
|  | PVE | 0.7605 | 0.7616 | 0.6332 | 0.8829 |
|  | rho | 0.6346 | 0.6475 | 0.2029 | 0.9796 |
|  | PGE | 0.6319 | 0.6870 | 0.1598 | 0.9888 |
|  | pi | 3.05 × 10-2 | 2.25 × 10-2 | 2.87 × 10-3 | 1.09 × 10-1 |
|  | n.gamma | 52.58 | 39.00 | 5.00 | 189.00 |

BSLMM was fitted on 23,315 SNPs. BOF, Beginning of Flowering; BOS, Beginning of Sprouting; FPD, Flowering Period Duration; h, approximation to the proportion of phenotypic variance explained by variants; n.gamma, number of variants with major effect; PGE, Proportion of Genetic variance explained by variants with major effect; pi, proportion of variants with non-zero effects; PVE, proportion of phenotypic variance explained by variants; rho, approximation to the proportion of genetic variance explained by variants with major effect; VPD, Vegetation Period Duration.