

Figure 1 displays the accuracy of structure-corrected RDA prediction for the temperature trait across three levels of polygenicity: oligogenic, mod. polygenic, and highly polygenic. The y-axis represents the accuracy, ranging from -1.0 to 1.0, with a dashed line at 0.0 indicating the baseline. The x-axis represents the number of random loci from the genome, ranging from 0 to 20,000. The legend indicates the strength of stabilizing selection: Strong  $\sigma_K = 0.5$  (red line) and Weak  $\sigma_K = 4.0$  (teal line). The accuracy is generally higher for the oligogenic trait and decreases as the number of loci increases for the highly polygenic trait.

Figure 1 consists of three panels showing the accuracy of RDA prediction for the Env2 trait as a function of the number of random loci from the genome (0 to 20,000). The y-axis represents the accuracy, ranging from -1.0 to 1.0, with a label 'worse <<--->> better' indicating that higher values are better. The panels are labeled 'oligogenic', 'mod. polygenic', and 'highly polygenic' from left to right. In all panels, the accuracy increases rapidly from 0 to 5,000 loci and then plateaus. The 'oligogenic' panel shows the highest accuracy, reaching approximately 0.8. The 'mod. polygenic' panel shows intermediate accuracy, reaching approximately 0.7. The 'highly polygenic' panel shows the lowest accuracy, reaching approximately 0.6. Shaded regions around the lines indicate confidence intervals.