Table 1 Main advantages and pitfalls[1] for GS in science and breeding (Adopted from Miedaner et al., 2020)

Advantages	Pitfalls[1]
No special population structure or segregating generations necessary	Same environments for testing training and validation sets
Usage of the full genome for trait association including small QTLs that might not surpass the significance level in mapping	Creating training and validation set from the same base population or having a high degree of relatedness between both sets
GS data can directly be used for selection without phenotyping	Inclusion of non-related populations can cause severe changes in allele frequencies

Note: [1] leading to an incorrect estimation of prediction accuracies (over-/underestimation)