

GWAS model **extensions**

- Polyploid Species -

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Ployploidy

- Heritable condition of possessing more than two complete sets of chromosomes.
- Common among plants, certain groups of fish and amphibians.
- For instance, some salamanders, frogs, and leeches are polyploids.

Autopolyploidy occurs when a polyploid offspring is derived from a single parental species.

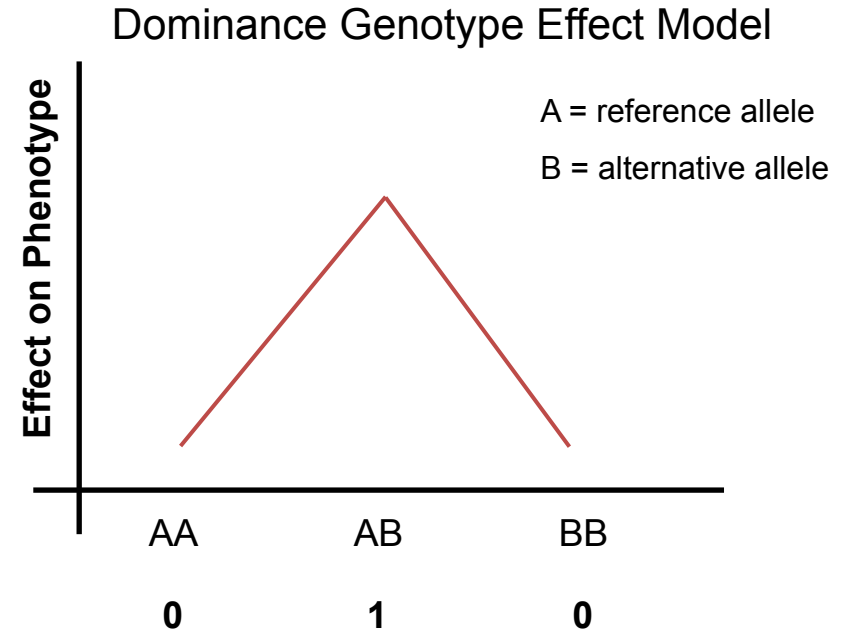
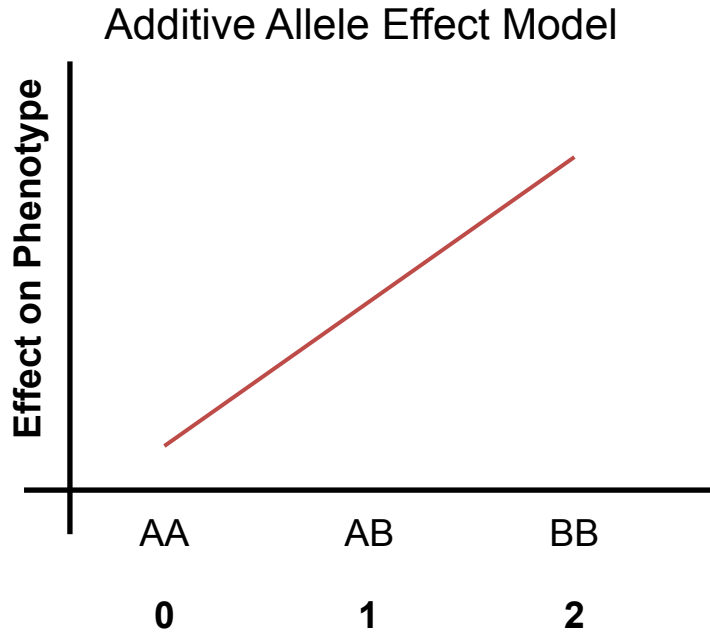
- Genome duplication

Allopolyploidy occurs when a polyploid offspring is derived from two distinct parental species.

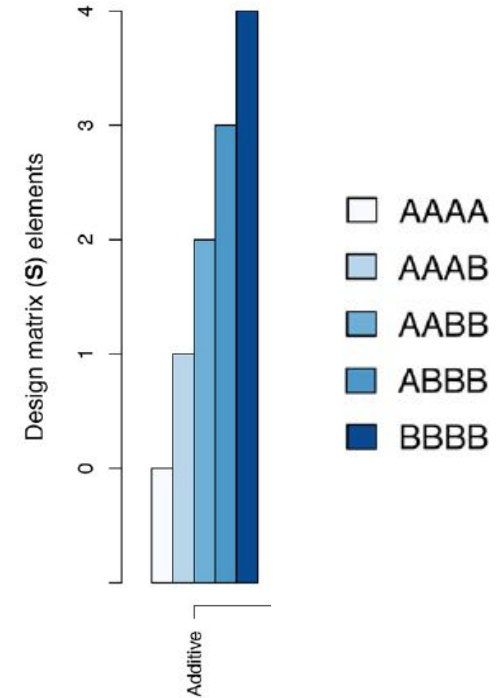
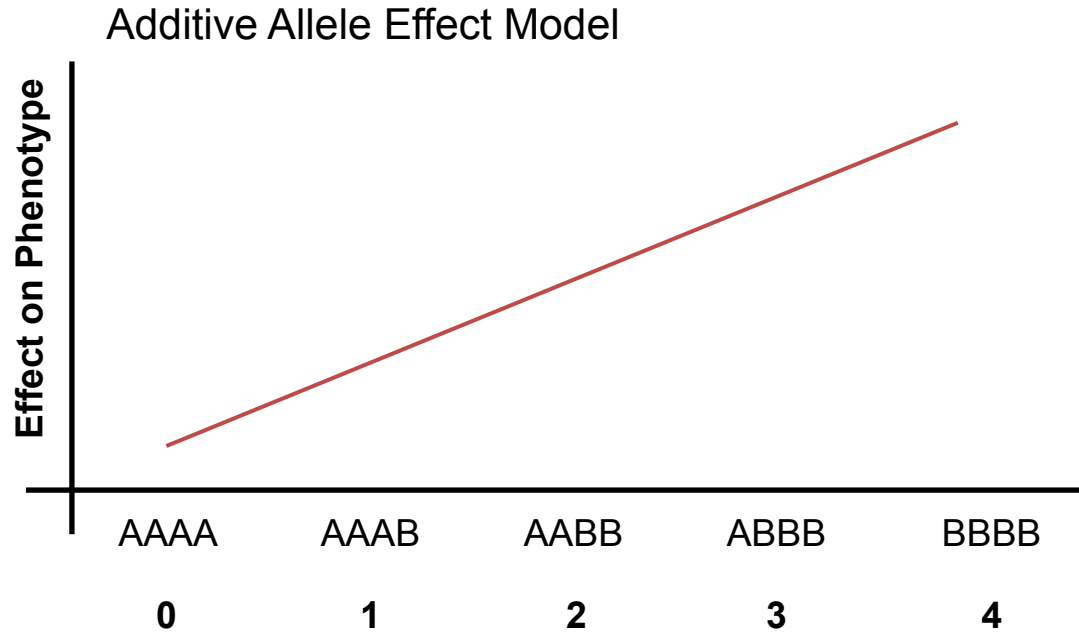
- Genome hybridization (diploid-like behavior)



Diploid Species – Additive + Dominance Model

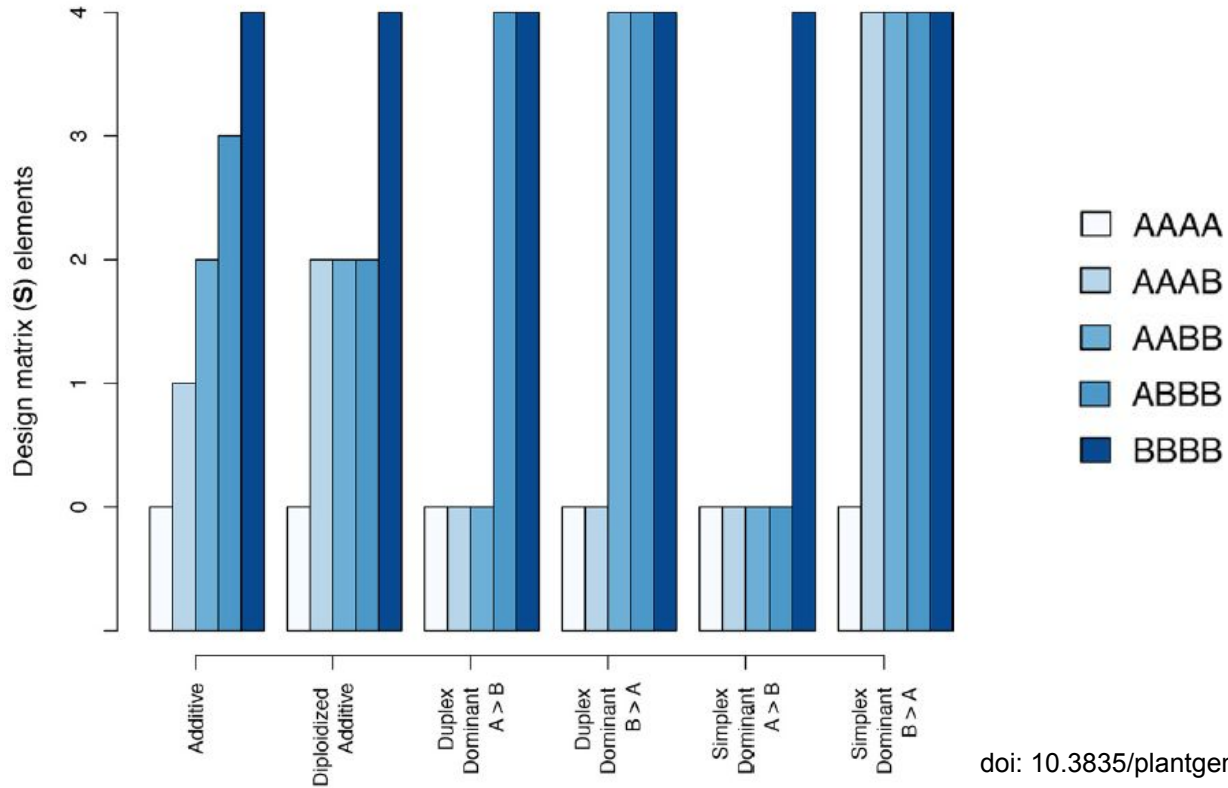


Tetraploid Species – Additive Model



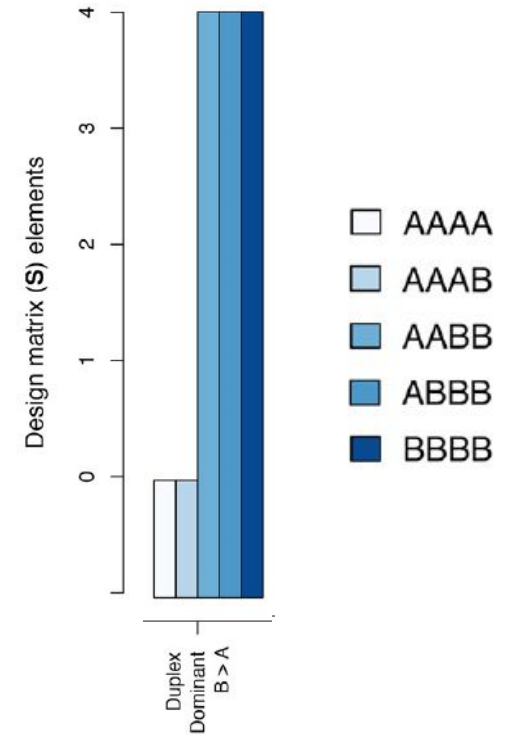
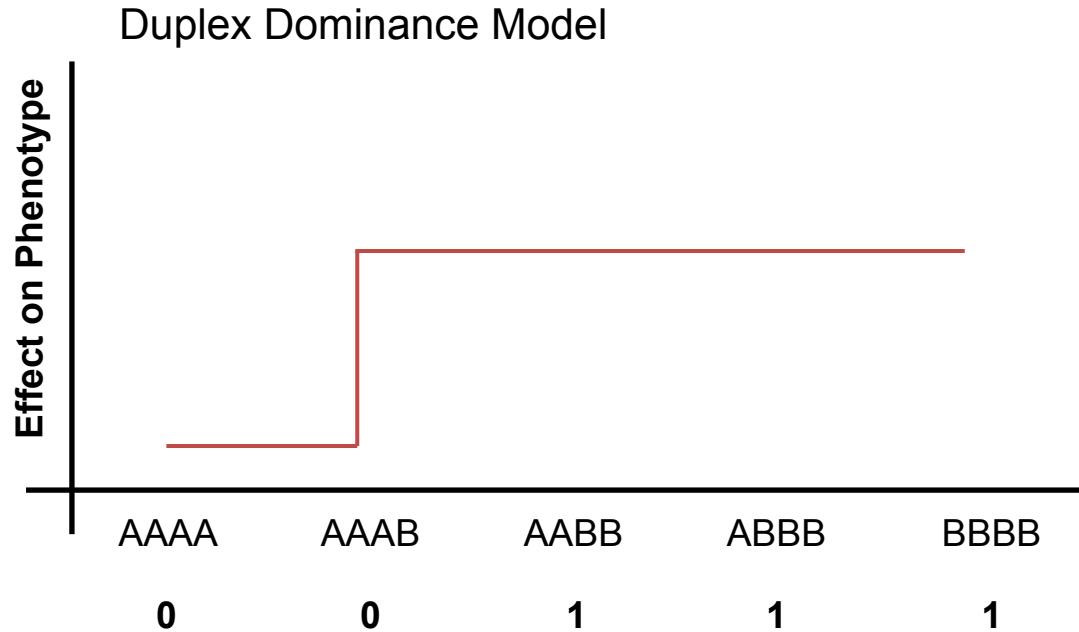
doi: 10.3835/plantgenome2015.08.0073

Tetraploid Species – How to include non-additive gene action?



doi: 10.3835/plantgenome2015.08.0073

Tetraploid Species – Duplex Dominance (non-linear regression)



<https://github.com/jendelman/GWASpoly>

README.md

R Package GWASpoly

This package was designed for genome-wide association studies in autopolyploids but also works for diploids. A [vignette is available](#) to illustrate the basic workflow using the potato dataset that comes with the package. More detailed information is available in the [package reference manual](#).

If you use the package in a publication, please cite [Rosyara et al. \(2016\)](#).

The original development of the package was supported by the USDA NIFA SCRI (Award No. 2011-51181-30629) and Hatch (Accession No. 1002731) programs. Beginning Fall 2020, new features are being added as part of the SCRI Project "Tools for Genomics-Assisted Breeding in Polyploids" (Award No. 2020-51181-32156).

To install and load the package:

```
install.packages("devtools")
devtools::install_github("jendelman/GWASpoly", build_vignettes=FALSE)
library(GWASpoly)
```

Software for Genome-Wide Association Studies in Autopolyploids and Its Application to Potato

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