GWAS model extensions

- Polyploid Species -

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Polyploidy

- 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.

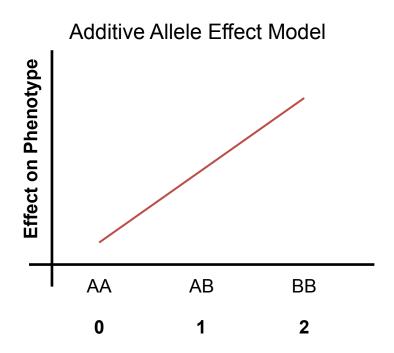
Autopolyploidy occurs when a polyploid offspring is derived from a single parental species.

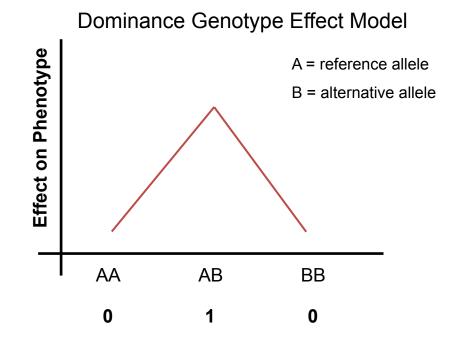
Genome duplication

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

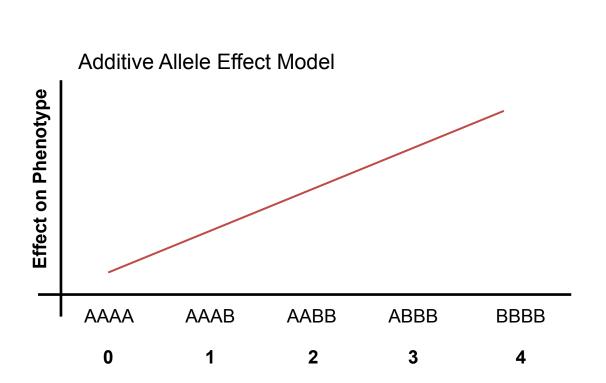
Genome hybridization (diploid-like behavior)

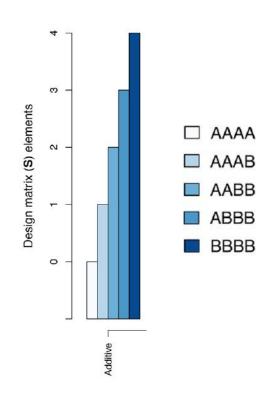
Diploid Species – Additive + Dominance Model





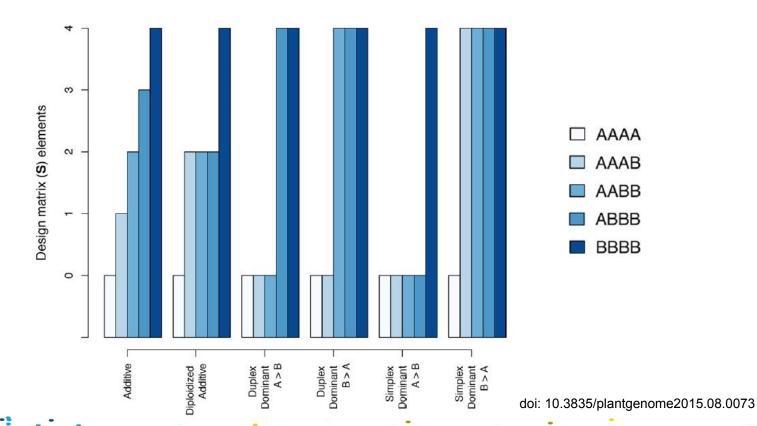
Tetraploid Species – Additive Model



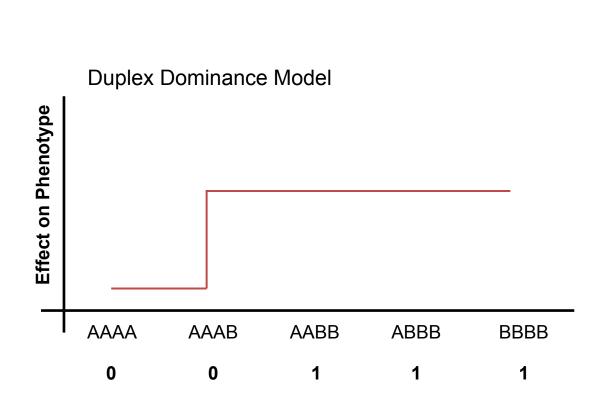


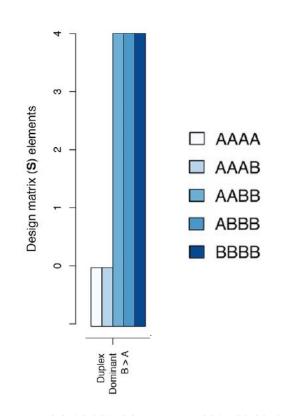
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Tetraploid Species – How to include non-additive gene action?



Tetraploid Species – Duplex Dominance (non-linear regression)





doi: 10.3835/plantgenome2015.08.0073

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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