Appendix 1. Theoretical Predictions for the change in G caused by autopolyploidy

Here we explore how genome duplication caused by autopolyploidy alters the genetic variance and covariance between two traits (z_1 and z_2) in the absence of linkage disequilibrium. Our model assumes that phenotypes are determined additively and that traits are perfectly heritable (**G**=**P**). Specifically, we assume that an individual's phenotype for trait *i* is determined additively by *n* diallelic loci such that:

$$z_i = \sum_{j=1}^{n} \sum_{k=1}^{P} b_{i,j} X_{j,k} \tag{1}$$

where $b_{i,j}$ is the contribution made by a "1" allele at locus *j* to phenotype *i*, $X_{j,k}$ is the individual's allelic status (0 or 1) at position *k* within locus *i*, *n* is the number of loci, and *P* is the individual's ploidy. This basic phenotypic model allows genetic correlations to emerge as a consequence of pleiotropy. Specifically, positive pleiotropy occurs when the signs of $b_{1,i}$ and $b_{2,i}$ are the same for locus *i*; negative pleiotropy occurs when the signs are different.

Assuming all loci are at Hardy-Weinberg Equilibrium and that linkage disequilibrium is absent, the trait means in the diploid and autotetraploid population are:

$$\bar{z}_{i,D} = \sum_{j=1}^{n} \left(2b_{i,j} p_j^2 + 2b_{i,j} p_j \left(1 - p_j\right)\right) \tag{2a}$$

$$\bar{z}_{i,T} = \sum_{j=1}^{n} \left(4b_{i,j} p_j^4 + 12b_{i,j} p_j^3 \left(1 - p_j\right) + 12b_{i,j} p_j^2 \left(1 - p_j\right)^2 + 4b_{i,j} p_j \left(1 - p_j\right)^3 \right) \tag{2b}$$

where the allele frequencies, p_j, are assumed to be equal in diploid (D) and autotetraploid (T) populations as would be the case in a newly formed autopolyploid population. Equations (2) can be easily used to study the effect of autopolyploidy on trait means. Specifically, if the phenotypic contribution of each locus is strictly additive and thus depends on the sum of the "1" alleles (i.e., $b_{i,j}=1$) for all loci j, the mean of the autotetraploid population will always exceed that of the diploid population simply because the autotetraploid expresses more copies of the "1" allele at each locus. If, in contrast, gene expression is regulated such that the phenotypic contribution of each locus depends on the proportion of "1" alleles rather than the sum (i.e., $b_{i,j}=1/P$), the population mean phenotypes of the diploid and autotetraploid populations will be equal. This result demonstrates that key to whether autopolyploidy has immediate effects on trait means is the extent to which it produces immediate changes in patterns of gene regulation.

Again assuming linkage equilibrium and Hardy-Weinberg Equilibrium, it is possible to write down expressions for the genetic variances in diploids and autotetraploids:

$$V_{i,D} = \sum_{j=1}^{n}\left[\left(4b_{i,j}^{2}p_{j}^{2} + 2b_{i,j}^{2} + p_{j}\left(1-p_{j}\right)\right) - \left(2b_{i,j}^{2}p_{j}^{2} + 2b_{i,j}p_{j}\left(1-p_{j}\right)\right)^{2}\right] \tag{3a}$$

$$V_{i,T} = \sum_{j=1}^{n}\left[\begin{array}{l}\left(16b_{i,j}^{2}p_{j}^{4} + 36b_{i,j}^{2} + p_{j}^{3}\left(1-p_{j}\right) + 24b_{i,j}^{2}p_{j}^{2}\left(1-p_{j}\right)^{2} + 4b_{i,j}^{2}p_{j}\left(1-p_{j}\right)^{3}\right) \\ -\left(4b_{i,j}^{2}p_{j}^{4} + 12b_{i,j}p_{j}^{3}\left(1-p_{j}\right) + 12b_{i,j}p_{j}^{2}\left(1-p_{j}\right)^{2} + 4b_{i,j}p_{j}\left(1-p_{j}\right)^{3}\right)^{2}\end{array}\right] \tag{3b}$$

Comparison of (3a) and (3b) reveals that the magnitude and direction of any change in genetic variance caused by genomic duplication depends on the extent to which autopolyploidy alters patterns of gene regulation. Specifically, if the phenotypic contribution of each locus is strictly additive and thus depends on the sum of the “1” alleles (i.e., $b_{i,j}=1$) for all loci j, numerical investigation suggests that the genetic variance of the autotetraploid population will always exceed that of the diploid population. In contrast, if gene expression is regulated such that the phenotypic contribution of each locus depends on the proportion of “1” alleles rather than the sum (i.e., $b_{i,j}=1/P$), numerical investigation suggests that the genetic variance of the autotetraploid population will always be less than that of the diploid population.

Finally, we write down expressions for the covariance between traits z_1 and z_2 in diploids and tetraploids again assuming linkage equilibrium and Hardy-Weinberg Equilibrium:

$$C_D[z_1,z_2]=\sum_{j=1}^{n}\left[\begin{array}{l}\left(4b_{1,j}b_{2,j}p_j^2+2b_{1,j}b_{2,j}p_j(1-p_j)\right)-\\ \left(2b_{1,j}p_j^2+2b_{1,j}p_j(1-p_j)\right)\left(2b_{2,j}p_j^2+2b_{2,j}p_j(1-p_j)\right)\end{array}\right] \tag{4a}$$

$$C_T[z_1,z_2]=\sum_{j=1}^{n}\left[\begin{array}{l}\left(16b_{1,j}b_{2,j}p_j^4+36b_{1,j}b_{2,j}p_j^3(1-p_j)+24b_{1,j}b_{2,j}p_j^2(1-p_j)^2+4b_{1,j}b_{2,j}p_j(1-p_j)^3\right)-\\ \left(4b_{1,j}p_j^4+12b_{1,j}p_j^3(1-p_j)+12b_{1,j}p_j^2(1-p_j)^2+4b_{1,j}p_j(1-p_j)^3\right)\\ \left(4b_{2,j}p_j^4+12b_{2,j}p_j^3(1-p_j)+12b_{2,j}p_j^2(1-p_j)^2+4b_{2,j}p_j(1-p_j)^3\right)\end{array}\right] \tag{4b}$$

Because the genetic covariance is confounded by the genetic variance of the underlying traits, we used (4) in conjunction with (3) to study the effect of autopolyploidy on the genetic correlation ($\rho = C[z_1,z_2]/\left(\sqrt{V_1}\sqrt{V_2}\right)$) rather than on the covariance. Numerical investigation of the correlation suggests that as long as genomic duplication does not alter the pattern of pleiotropy (i.e., the sign of $b_{i,j}$ is identical in diploid and autotetraploid populations and the relative expression of each locus does not change), **G** is unaffected. In conjunction with our results for genetic variances, this result demonstrates that whether or not autopolyploidization causes changes **G** depends on the extent to which genomic duplication alters underlying patterns of gene regulation and pleiotropy.