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Original Polyploidy as a Contributor to Diversification

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Abstract

Plant life is incredibly diverse, with many plant families consisting of thousands or even tens of thousands of species. This extensive diversity must be explained within a creation model of origins. If, as is generally assumed, the taxonomic family is roughly the classification level of the created kinds, then many plant kinds are incredibly diverse. One way to account for this diversity may be created polyploidy. Created polyploidy would allow for an increased number of created alleles, thereby increasing the potential diversity of the original baramins. This increased diversity would enable created polyploids to diversify to the levels we see today within a creationist paradigm. A computer model of the differences in genetic diversity maintained by polyploid and diploid lineages was written in Python, a general-purpose, high-level, programming language. The model found that polyploids consistently maintained greater diversity than diploids. As such, created polyploidy should be considered as a potential explanation for genetic diversity. This article will propose a unique explanation for the origins of the diversity of many angiosperms as well as some gymnosperms where polyploidy is common.

Key Words: allopolyploidy, autopolyploidy, creation, genetic diversity, polyploidy

Introduction

Baraminology has largely been focused on animals, and with good reason. One of the common skeptical questions is "How do you fit millions of species on the Ark of Noah?" While species were not the taxonomic unit taken on the Ark, identifying kinds is crucial to answering the skeptic's question. Plants have largely, though not completely, been overlooked compared to vertebrate organisms. The question of the origin of plant diversity has largely also been overlooked. This article will overview plant polyploidy (i.e., the genetic condition of having more than two sets of replicated chromosomes) and examine the differences in genetic diversity among plants of various ploidy levels.

The Problem

Some plant groups have incredibly large numbers of species. For example, Asteraceae contains more than 32,000

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species of plants and Orchidaceae has over 28,000 (WCSP, 2021). The grasses of Poaceae, representing 12,000 species, were tentatively placed in a holobaramin by Wood (2002). Data from a subsection of the Grammitidaceae ferns, which have over 700 species, was also used to claim they were a holobaramin (Wood, 2008). All these baramins are quite large. If a Flood year of 2348 BC is assumed, Poaceae had to form new species at the rate 2.75 species per year. Even if the Flood date is moved back to the oldest possible date under a young-Earth model, this rate of rapid speciation does not get much better. Note that this rate is almost certainly too high as it is likely more than a single grass seed survived the Flood. If more than one seed survived the Flood, as is probable, there may have been more than one founding species of grass post-Flood, hence lowering the number of species required to arise since the Flood. However, since the real rate cannot be known with certainty, 2.75 species per year serves as an upper boundary for what is required.

However, it is not just that new species form. Some of these proposed baramins are widely morphologically disparate. For example, Poaceae contains both woody and herbaceous grasses. Different members of the family have widely different life cycles, with both annuals and perennials present in the family. Further, both C3 and C4 photosynthesis occurs within the group, in one instance even in the same species! (Lundgren et al., 2016). If the actual baramin is as large as is claimed, a lot of diversity needs to be accounted for, and in a relatively short time compared to an evolutionary scenario.

To account for the staggering diversity of life, Jeanson and Lisle (2016) proposed the "created heterozygosity and natural processes" (CHNP) model which is the best model of diversification proposed so far. They showed that mutations are insufficient to account for genetic diversity across all life, but importantly for the purposes of this paper, especially for plants. However, while mutations are insufficient, is created diploid heterozygosity sufficient? This paper will propose extending the CHNP model to include created polyploids in plants to account for their greater diversity.

Survey of Current Thought in Polyploidy

Secular research in polyploidy has been ongoing for a long time. It is far beyond the scope of this paper to even attempt to cover over 100 years of research. Instead, it will provide a short overview of relevant secular polyploidy literature.

Many species are polyploid, limited largely to plants but including some animals and fungi as well. Evolutionists have proposed that up to 70% of angiosperms have polyploidy in their lineage at least once (Soltis and Soltis, 1999). However, the estimate assumes universal common ancestry, often based on duplicated genes (Blanc and Wolfe, 2004). Therefore, it is important when discussing polyploidy to distinguish between paleopolyploids and extant ones, distinctions evolutionists are not always careful to make. However, even discounting the proposed paleopolyploids, many species of extant plants are polyploid. A 2009 paper estimated that about 34.5% of plants were polyploid when compared to the lowest chromosome counts in the genus (Wood et al., 2009). In 2015, a separate paper estimated polyploids were roughly 24% of vascular plants (Barker et al., 2016). Returning to the Poaceae example, more than 60% of known species are considered polyploid (Levy and Feldman, 2002.) Since polyploid plants are common, it is important to account for them within the creation model.

It is important to note that polyploidy is a relative term. It is contextually dependent. The problem is that we do not know how many chromosomes the original kinds had. Generally, evolutionists select a chromosome base number for a taxonomic group and, from that number, evaluate the rest of the taxonomic group's ploidy status (Parris et al., 2010; Contreras et al., 2016). If the original base number is incorrect, the rest of the taxonomic group (usually a genus) may have improper ploidy classification. The only certain ploidy levels are those determined by observation of chromosome pairing during meiosis. Simply counting the number of chromosomes is not enough because it assumes a potentially inaccurate base number (Bennett, 2004.) It also ignores chromosomal pairings that might reveal a polyploid heritage when it has been lost due to diploidization. While specific species currently thought polyploid may or may not actually be polyploid, polyploidy itself is a real and common phenomenon as, within genera and other taxonomic groups, plants vary widely in chromosome number, often in multiples of the selected base number.

There are two main forms of polyploidy: allo and autopolyploidy. Allopolyploidy results from the cross of two different plant lineages. As a result, the offspring carry two divergent genomes (Wendel et al., 2008). The two genomes, referred to as subgenomes of the polyploid genome, are commonly thought to be differentially expressed, with a dominant genome often containing more genes and remaining dominant even if another whole genome duplication (WGD) occurs (Freeling et al., 2014). The genome shock associated with combining two disparate genomes often causes rapid genomic changes through multiple pathways to permit the two genomes to cohabitate, usually by allowing one genome to become dominant at

the expense of the other (Edger et al., 2018). This consensus about genome dominance has recently been challenged, with the suggestion that differences between the genomes are tied to their progenitor genomes rather than post-polyploidy changes (Liu and Wang, 2022). Importantly, however, the rapid genomic changes associated with allopolyploidy are not in dispute, even by those challenging the genome dominance hypothesis.

Autopolyploids may comprise most polyploids (Barker et al., 2016). In autopolyploids, the parental genomes are homologs (due to shared ancestry) instead of having two separate parental genomes. As such, genome dominance may be unnecessary, as the genomes are already compatible. Thus, allopolyploids' rapid genomic changes likely do not occur in autopolyploids (Spoelhof et al., 2017).

Newly formed auto and allopolyploids both suffer from minority cytotype exclusion (MCE) during establishment. The higher the frequency of a particular cytotype in a population, the easier it will be to breed with a compatible mate, and therefore the more reproductively successful it would likely be (Levin, 1975). Because polyploids, according to the conventional model, begin at low population frequencies, founding a new lineage in the presence of their diploid progenitors is predicted to be difficult, something confirmed in experimental studies (Husband, 2000; Baack, 2005). Thus, the minority cytotype often occupies slightly different niches or entirely different habitats than their parental population (Felber-Girard et al., 1996; Baack, 2004; Scopece et al., 2016). Often there is little overlap between the cytotypes, because of differences in mode of life (Johnson et al., 2003), because hybridization either fails (Castro et al., 2012), or because triploids are less successful than their parents (Burton and Husband, 2000).

There are, however, ways around MCE. One is selfing. By pollinating itself, a neopolyploid can avoid MCE and reproduce, but at a potential long-term cost. Allopolyploids tend to self at a higher rate than diploids, but autopolyploids self at a lower rate (Husband et al., 2002). However, a large-scale meta-analysis found that there was no association between the ability to self and the number of polyploid taxa in a taxonomic group (Mable, 2004). More recent work has found that in at least some taxa, self-incompatibility breaks down over time in polyploid lineages (Horandl, 2008; Sutherland et al., 2018), and close association between polyploidy and self-compatibility has been found in certain groups (Barringer, 2007; Robertson et al., 2010; Gao et al., 2016). The question of polyploidy's association with selfing remains open, but the evidence seems to indicate that at least allopolyploid lineages may survive in part through selfing.

The problem with selfing is, it reduces reproductive success compared to outcrossing populations (Siopa et al., 2020). Over time, this can reduce a population's viability. Asexual reproduction is another way to deal with MCE, while avoiding the loss of reproductive success. Data suggests that polyploidy does not cause an increase in asexual behavior, but instead exploits existing asexuality to survive (Schwander et al., 2014). Where asexuality already exists, however, evidence suggests it might be important in promoting the survival of polyploid lineages (Kao, 2007). Asexuals, however, are subject to Muller's ratchet, which means that they are subject to mutational meltdown from a build-up of deleterious mutations (Muller, 1964), a phenomenon akin to genetic entropy (Sanford, 2014). While there is no escape from genetic entropy, asexual polyploids can slow the ratchet by periodically outcrossing (Hojsgaard and Horandl, 2015).

Genomic Changes Associated with Polyploidy

When polyploids arise, changes occur in the genome as a result. In an autopolyploid scenario, each allele is doubled, leading to an increased dosage of the allele. This may also be the case for some of the alleles under allopolyploidy as well. In some cases, this may not matter, but for many genes, an exact dosage balance is required for the gene products to work correctly. For example, many X-Y genes show dosage compensation (Muyle et al., 2017; Filatov et al., 2019). In hexaploid *Tritium*, deletion of an arm of one copy of the chromosome containing genes for glutenins and gliadins resulted in the other chromosomes increasing production of the protein to compensate (Galili et al., 1986). In an examination of almost 3100 transcripts in wheat, 60 changed because of allotetraploidy, with 80% being silenced (Kashkush et al., 2002). In *Leucanthemum*, two genes for subunits of a specialized protein are increasingly expressed with higher ploidy, but two other genes for photosystem II show no difference in expression intensity (Oberprieler et al., 2019). In maize, rRNA showed a rough 1:1 ratio of dosage effects, but not for every gene, and only 5 genes showed consistent dosage effects across the four ploidy levels studied (Guo et al., 1996). An examination of roughly 9,000 potato gene expressions found that few were linearly associated with changes in ploidy level (Stupar et al., 2007).

The contradictory nature of the evidence seems to indicate that dosage compensation varies from plant to plant and gene to gene. There is also a difference between allo- and autopolyploids. Around 1400 genes were dosage-compensated in a comparison of an *Arabidopsis* hybrid tetraploid with its diploid progenitors (making up slightly more than 5% of the studied genes) (Wang et al., 2006). A much smaller study in *Helianthus* autopoly-

ploids showed no changes in gene expression due to polyploidy (Church and Spaulding, 2009). A larger study of autotetraploids versus diploids of over 21,000 genes showed differences in expression in just over 600 (<3%) (Tang et al., 2015). Polyploidy does seem to influence gene expression, but the effect seems limited to a small section of genes, and the exact number varies depending on the type of polyploidy involved.

Sometimes when dosage is increased, the resultant polyploid reacts by undergoing diploidization. Diploidization is the process of a polyploid losing redundant duplicate genes and becoming more diploid in nature. The product is termed a "paleopolyploid": a current diploid with a polyploid ancestor (Wolfe, 2001). Diploidization is believed to have made large-scale contributions to the evolution of angiosperms (Dodsworth et al., 2016) While this idea assumes deep time and multiple rounds of gene duplications in the history of life and the history of flowering plants (Conant et al., 2014), diploidization can begin to occur very quickly after the formation of a polyploid. For example, in a very recent (<100-years-old) polyploid species of *Tragopogon*, 11 of 13 analyzed loci had already lost at least one parental homeolog (Tate et al., 2009).

Transposable elements (TEs) can also be activated after a polyploid event. In tobacco allotetraploids, the polyploidization event significantly amplified retrotransposon activity (Grandbastien et al., 2010). Significant restructuring of the genome also often occurs, sometimes resulting in a reduction of discernible transposons (Ainouche et al., 2009). These deletions often take place quickly, within three generations in one study (Kashkush et al., 2010). However, other studies in different systems found no evidence for increased transposon activity (Belzile et al., 2009). In wheat allopolyploids, the additional transposons did not increase their rate of movement (Kashkush et al., 2002). Similar results were reported in cotton as well (Wendel et al., 2020). Thus, while transposon-mediated restructuring occurs, there is, as yet, no consistent pattern for when or why the restructuring will take place.

Importantly, TEs seem to preferentially insert themselves in areas of the genome that are gene-poor (i.e., near telomeres and centromeres) (Vicient and Casacuberta, 2017), though there are exceptions (Feschotte and Pritham, 2007). This fact hints at a possible structural or epigenetic effect for most TEs, rather than a directly genetic one. This is unsurprising given that TE movement is associated with significant methylation changes near the newly inserted TE (Ainouche et al. 2009; Kashkush and Yaakov, 2011). However, TEs are not usually mobile, being repressed by DNA methylation (Slotkin et al., 2016) using small noncoding RNA (sRNA) (Dubcovsky et al., 2010). Polyploidy can provide a release from the epigenetic control for TEs as discussed above, but it also can generate new epigenetic controls on other parts of the genome. Some TEs will generate short interfering RNA (siRNA) to control gene expression in either their own, or their counterpart subgenomes (Liu et al., 2021).

Interestingly, polyploid events are associated with homeologous exchanges (HE). These changes happen during meiosis, where chromosomes that are assumed to have a common ancestor but which do not normally pair or are from separate sub-genomes recombine (Pires and Gaeta, 2010). In cotton, the number of contigs (i.e., sets of *contig*uous or overlapping DNA segments) associated with HE is estimated to be roughly 2%, assuming a 1–2 mya origin of cotton (Wendel et al., 2009). Many synthetic polyploids show HE in at least a few cases (Mason and Wendel, 2020). The effect of HE is a net increase in genetic diversity in the resultant offspring (Liu et al., 2021). However, it can damage the genome, hindering normal meiosis and decreasing the fertility of the polyploid (Pires and Gaeta, 2010). This potential cost in fertility makes HE a double-edged sword for newly formed polyploids. MCE already restricts the number of possible mates, effectively reducing the likelihood of mating success. HE goes a step further, reducing fertility rates even if the newly formed polyploid can find a mate. The two compound each other, making it incredibly difficult for a newly formed polyploid to establish a population in the presence of its parents. However, if it does succeed, the increased diversity may give it an advantage in its new habitat.

Created Polyploids

If polyploids were created from the beginning, what might be expected as a result? How would such polyploids behave? If it is assumed that created polyploidy extends the CHNP model, then the created genomes would have been more like allopolyploids as this increases the amount of genetic diversity present. Mendelian rules of dominance and recessiveness would likely have been in place prior to the Fall of Genesis 3. However, genetic dominance (if it exists) in allopolyploids likely represents a post-Fall adaptation. In a perfect pre-Fall environment, existing plants would not have needed to subsume one genome to another as the two genomes would likely have been perfectly compatible within each plant. Thus, much of the genomic shock associated with allopolyploids in the present would have been absent in created polyploids, leading to their genomes functioning like autopolyploid genomes, but having the diversity of allopolyploid genomes.

However, perfect internal compatibility does not necessarily mean that each individual plant within a baramin had a genome completely compatible with every other individual plant in the baramin. Only in the Flood account are we told the number of surviving organisms and that is limited to the animal kinds that boarded the Ark (Genesis 6:19; 7:2). The creation account does not specify how many of each kind were created. From God's planting of the Garden of Eden (Gen. 2:8), it can be reasonably inferred that most plants were created with more than two organisms per baramin. The increased number of organisms per baramin increases the number of possible genomes available within the baramin, and therefore increases the amount of potential genetic diversity. Given the high potential diversity of a cross between two heterozygous tetraploids (136 possible genotypes per locus), adding additional distinct heterozygotes to the population only increases potential genetic diversity. Obviously much of this diversity was lost during the Flood, but much of it is still present today as evidenced by some of the incredibly large plant families and proposed baramins.

In a post-Fall, post-Flood environment, all organisms underwent a population bottleneck, and most would have also experienced a founder effect. Such effects may be deleterious to the genome of an organism as they tend to fix dominant (or at least increase the frequency of) deleterious mutations (Sunyaev et al., 2015). Founder events like this reduce the overall genetic diversity of the population (Shirk et al., 2014). However, polyploids are less susceptible to these effects as they have more alleles (Layman and Busch, 2018). While a founder event of equal proportion will likely remove the same number of alleles from both diploid and polyploid populations, polyploids have more alleles at the start of the process and, therefore, will retain more alleles.

Heterozygosity Changes in Model Populations

Computer modeling can demonstrate the extent of genetic diversity retained by polyploids compared to diploids. Using Python, three ploidy levels were modeled under both selfing and outcrossing systems. The code is available from the author on request. The simulation accounted for generation times, linkage, migration rate, recombination rate, environmental effects, selection strength, genetic drift, and deleterious mutations. Population sizes were assumed to be stable, and 100 generations were used for each simulation. Each model was simulated 10,000 times, and the data was exported in an Excel file. The data was then used to perform a Mann-Whitney U test, a non-parametric statistical test among two groups or samples, comparing the ploidy levels to each other in terms of median resultant heterozygosity within the selfing and outcrossing systems. Here heterozygosity means the proportion of heterozygous individuals in the simulated population for a given loci. The Mann-Whitney U test results were confirmed using histograms to determine whether the median heterozygosity was different or the distribution of heterozygosity between the two populations was different.

In the first simulation, initial heterozygosity was set to 0.5. All other parameters for each simulation can be seen in supplementary Table I. Table I shows the final heterozygosity of all simulations. Figure 1 shows the trajectory of the heterozygosity across 100 generations. A second simulation was run with slightly different parameters (found in Supplementary Table I). Figure 2 shows the trajectory of heterozygosity over 100 generations. Table II shows the results of the statistical tests for the first and second simulations. In all cases, the results are statistically significant with a p-value below 0.05. Histograms for each simulation showed comparable distributions (Supplementary Figures 1–16) except for the diploid-hexaploid comparisons. Therefore the diploid-tetraploid and tetraploid-hexaploid comparisons are interpreted as having significantly different means. The diploid-hexaploid comparisons are left uninterpreted as the diploid-tetraploid-hexaploid distributions show roughly step-wise comparable distributions, but the diploid-hexaploid distributions are not comparable.

In keeping with the CHNP model, heterozygosity was set to its maximum, 1, meaning full heterozygosity for two simulations. All other parameters can be found in supplementary Table I. Figure 3 shows the trajectory of heterozygosity across 100 generations. Interestingly, the selfed tetraploid and hexaploid maintain higher average heterozygosity than the outcrossing diploid. A second simulation for a heterozygosity of 1 with some adjusted parameters was performed as shown in Figure 4. In each case, the results were statistically significant as shown in Table III. In this instance, all histograms showed visually comparable distributions (Supplementary Figures 17–32), indicating a statistically significant difference in median between the populations.

This model makes it clear that higher ploidy maintains genetic diversity significantly better than diploids. Of course, this model is simplistic and does not account for things like genetic bottlenecks and founder effects. Both will decrease the heterozygosity either over time or during a founding event. Nor does it account for the effects of diploidization, which would drastically reduce heterozygosity. Nevertheless, initial results indicate

Table I. Average heterozygosity in multiple simulations.

Ploidy	Simulation	Breeding Method	Average Heterozygosity
Diploid	1	selfing	0.33
Tetraploid	1	selfing	0.36
Hexaploid	1	selfing	0.37
Diploid	1	outcrossing	0.351
Tetraploid	1	outcrossing	0.372
Hexaploid	1	outcrossing	0.379
Diploid	2	selfing	0.166
Tetraploid	2	selfing	0.198
Hexaploid	2	selfing	0.21
Diploid	2	outcrossing	0.224
Tetraploid	2	outcrossing	0.232
Hexaploid	2	outcrossing	0.233
Diploid	3	selfing	0.372
Tetraploid	3	selfing	0.433
Hexaploid	3	selfing	0.458
Diploid	3	outcrossing	0.413
Tetraploid	3	outcrossing	0.458
Hexaploid	3	outcrossing	0.479
Diploid	4	selfing	0.130
Tetraploid	4	selfing	0.162
Hexaploid	4	selfing	0.176
Diploid	4	outcrossing	0.191
Tetraploid	4	outcrossing	0.201
Hexaploid	4	outcrossing	0.203

that polyploid baramins would have maintained higher genetic diversity over time.

Since, within some baramins, some plants were created polyploid in this model, MCE is unlikely to be an issue and was excluded from the model. Instead, the newly formed diploids might suffer from MCE, but this would likely begin to be an issue after the Fall introduced genomic degradation. However, particularly after the Flood, niche differentiation would have allowed for a proliferation of new diploid and polyploid populations to arise quickly as seeds with different cytotypes landed in different habitats and reproduced into populations.

Post-Flood Recovery

Because the Flood completely reshaped the Earth's surface and wiped out all existing communities, the post-Flood landscape would have initially been completely bare, with many open spaces for plants to colonize. MCE would still have existed within populations, but it would have been much easier for a newly formed diploid to colonize an area that its polyploid ancestors were not utilizing. Indeed, today, many polyploid species are niche-differentiated, with cytotypes inhabiting different habitats and only occasionally overlapping (Baack, 2004; Castro et al., 2012; Kirchheimer et al., 2016; Castro et al., 2020). The Flood thus may have provided a release from MCE, allowing rapid establishments of different cytotypes in different habitats, leading to vast varieties of species and cytotypes in polyploid baramins that would further differentiate under selection and drift. This scenario would create incredibly speciose baramins in a very short period.

An additional benefit would be if selfing was possible within the baramin. Self-pollination may be a post-Fall adaptation, or it may have been built into the original creation, as the negative effects are only possible in a fallen world. In either case, self-fertilization almost certainly existed by the time of the Flood, some 1,656 years after Creation according to Genesis 5, either due to a breakdown of self-incompatibility or created design. Breaking down self-incompatibility is relatively simple, requiring the inactivation of a single locus, the *S*-locus, in many plants (Iezzoni et al., 2006; Kelly et al., 2017; Chai et al., 2022). In the nearly 1700 years prior to the Flood, it seems very unlikely that this locus suffered no mutations or that in at least a few species, the mutations did not proliferate due to its reproductive advantage. The ability to self in this way would have been a great benefit for any plant species able to do so in the post-Flood world. The nearest member of the same baramin might have been hundreds of miles away. The ability to self-fertilize, or alternatively, perform apomixis or other forms of asexual reproduction could have been a key driver of ecosystem recovery.

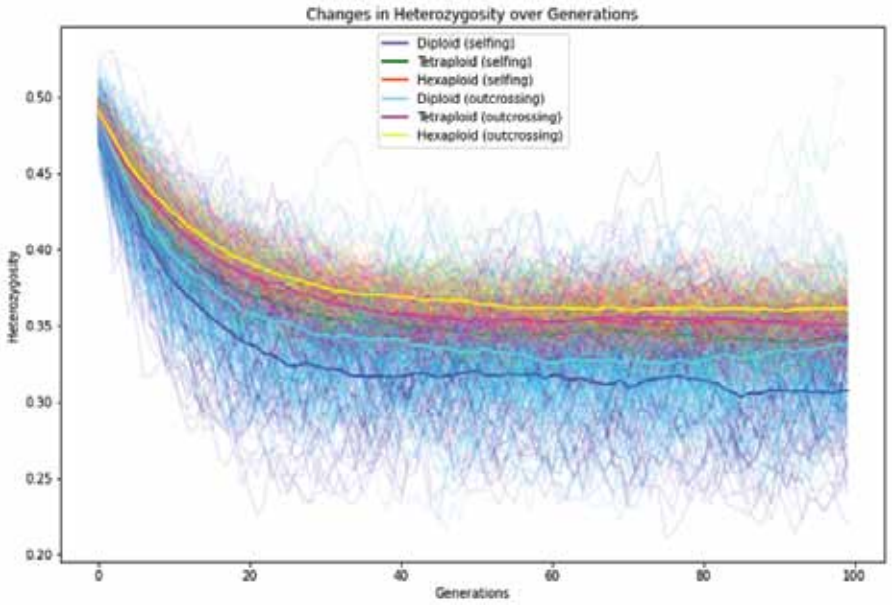

Figure 1. Trajectory of heterozygosity over 100 generations when starting with 0.5 heterozygosity.

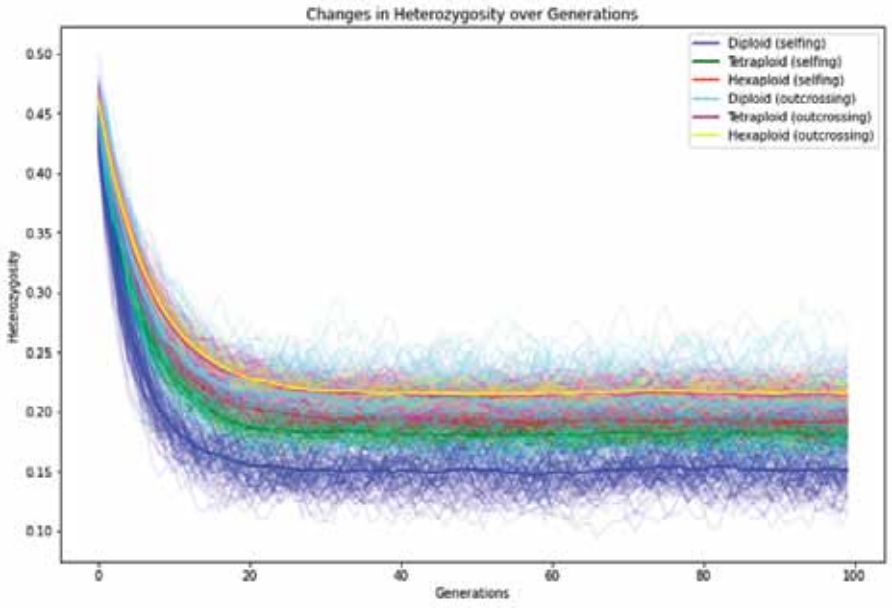

Figure 2. Trajectory of heterozygosity over 100 generations when starting with 0.5 heterozygosity and different starting parameters.

If polyploids were created as all or part of some pre-Fall baramins, we would expect that, if those baramins now contain multiple ploidy levels, some form of non-traditional sexual reproduction would be associated with that baramin. This could include vegetative reproduction, apomixis, selfing, or any other form of reproduction requiring only one plant. In some groups as noted above, selfing has been associated with polyploidy (Husband et al., 2002; Barringer, 2007; Robertson et al., 2010; Gao et al., 2016). In at least a few instances, apomixis is associated with polyploidy as well (Dickinson et al., 2007; Lo et al., 2009). In one genus of Rosaceae, diploids produced only 2% apomictic seeds while tetraploids produced 97% (Burgess et al., 2014)! In a species of Ranunculeae, 65% of the tetraploid populations were at least facultative apomicts (Horandl et al., 2016). An analysis of 940 Czech angiosperms found a similar correlation between increased vegetative reproduction and polyploidy (Herben et al., 2017). It is likely than many of these forms of reproduction, even potentially all of them, were present in the original created polyploids and were exploited in the post-Flood world to allow plants to rapidly fill niches.

Predictions of Created Polyploidy

If polyploidy was built into baramins from the beginning, what might we expect in the present? Baramins with created polyploidy would likely have multiple ploidy levels within them due to the potential for further polyploidization and diploidization (Chen et al., 2007). Due to genome degradation, it is likely that the present baramin has significantly differentiated in cytotypes. Another prediction would be a significant number of the species within the baramin would employ asexual reproduction or selfing at least part of the time. Neither of these predictions is particularly Earth-shattering and are in line with current research in polyploidy.

A corollary to the prediction that polyploids will be associated with

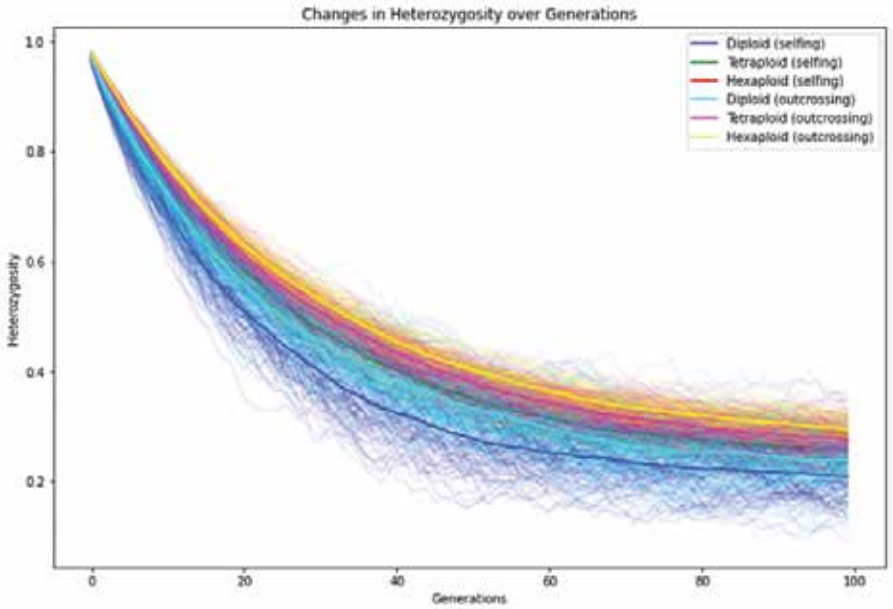

Figure 3. Trajectory of heterozygosity over 100 generations when starting with 1.0 heterozygosity.

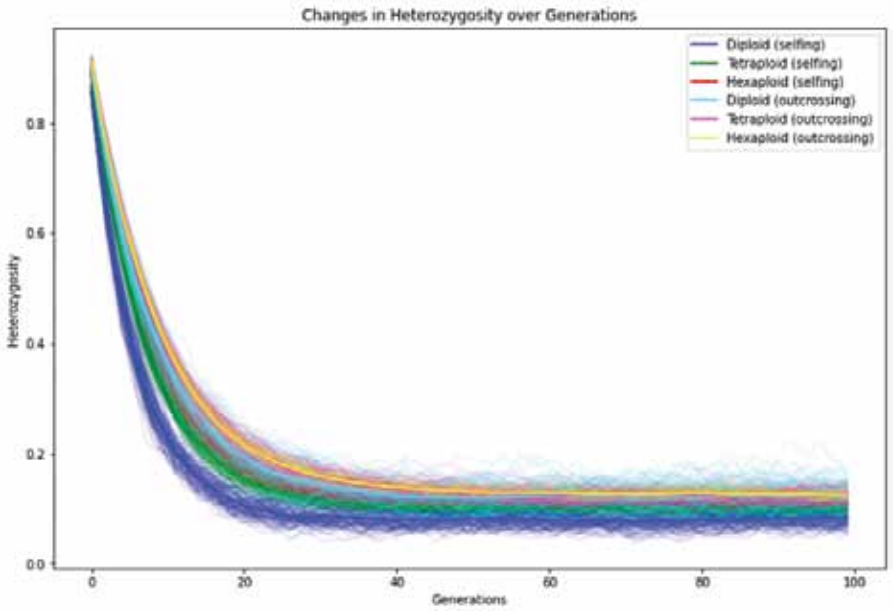

Figure 4. Trajectory of heterozygosity over 100 generations when starting with 1.0 heterozygosity and different starting parameters.

asexuals and selfing, is that polyploids are likely to be monoecious (having both gender organs on the same plant) because this would enable selfing. There is at least some evidence for this idea. The annual *Mercurialis annua* is a polyploid complex in which the diploids are dioecious (having separate male and female individuals), but the polyploids are either androdiocious (having males and hermaphrodites coexist) or completely monoecious (Pannell et al., 2004). However, in *Bryonia*, there is no association between polyploidy and sexual system (Volz and Renner, 2008) and the consensus is that dioecy is associated with polyploidy, not monoecy (Ashman et al., 2013). Dioecy is present in roughly six percent of total angiosperm species (Renner, 2014), which, given the vast number of angiosperm species presumed to have a polyploid origin (Levy and Feldman, 2002), makes a link between polyploids and dioecy seem to be a stretch. More research is needed in this area.

If polyploids were created and then diploidized later, we would expect that the polyploid members of the baramin in the present would generally have higher genetic diversity than their diploid relatives, provided they share the same mode of reproduction. By default, a change from tetraploidy to diploidy costs the plant 2 alleles of 4 at a given loci. Thus, if CHNP is true and the created polyploids were full heterozygotes, a drop in ploidy to diploid could cost the plant half (or more if it originated higher than a tetraploid) of its genetic diversity. However, if diploidy is the created state and polyploidy arises afterwards via autopolyploidy, the diploids should have higher genetic diversity. Allopolyploidy arising in a baramin not created polyploid may or may not have greater diversity than the paternal diploid species. If one species produces sexually, and the other asexually, diversity will usually be lower for the asexual species.

Because of the difficulty of determining the allele frequencies in polyploids, studies of genetic diversity are rarely done. That said, there have been a few investigations into the topic. Polyploidy has been proposed as the

Table II. Results of simulations with starting heterozygosity of 0.5.

Simulation Number	Breeding System	Comparison	p-value
1	Selfing	Diploid-Tetraploid	0 [1]
1	Selfing	Tetraploid-Hexaploid	$1.697\ e^{-206}$
1	Selfing	Diploid-Hexaploid	0
1	Outcross	Diploid-Tetraploid	0
1	Outcross	Tetraploid-Hexaploid	$5.181\ e^{-104}$
1	Outcross	Diploid-Hexaploid	0
2	Selfing	Diploid-Tetraploid	0
2	Selfing	Tetraploid-Hexaploid	0
2	Selfing	Diploid-Hexaploid	0
2	Outcross	Diploid-Tetraploid	$7.915\ e^{-103}$
2	Outcross	Tetraploid-Hexaploid	$1.273\ e^{-13}$
2	Outcross	Diploid-Hexaploid	0

[1] P values of zero are statistically impossible. They represent values too small for the software to record. In this instance it is likely due to the large (10,000 simulation) dataset. They have not been rounded.

Table III. Results of simulations with starting heterozygosity of 1.

Simulation Number	Breeding System	Comparison	p-value
3	Selfing	Diploid-Tetraploid	$3.541\ e^{-238}$
3	Selfing	Tetraploid-Hexaploid	$4.371\ e^{-57}$
3	Selfing	Diploid-Hexaploid	0 [2]
3	Outcross	Diploid-Tetraploid	$2.823\ e^{-118}$
3	Outcross	Tetraploid-Hexaploid	$1.094\ e^{-237}$
3	Outcross	Diploid-Hexaploid	$1.361\ e^{-33}$
4	Selfing	Diploid-Tetraploid	0
4	Selfing	Tetraploid-Hexaploid	$1.278\ e^{-291}$
4	Selfing	Diploid-Hexaploid	0
4	Outcross	Diploid-Tetraploid	$3.51\ e^{-52}$
4	Outcross	Tetraploid-Hexaploid	$8.39\ e^{-12}$
4	Outcross	Diploid-Hexaploid	$2.46\ e^{-90}$

[2] P values of zero are statistically impossible. They represent values too small for the software to record. In this instance it is likely due to the large (10,000 simulation) dataset. They have not been rounded.

explanation for the higher genetic diversity in the tetraploid of a diploid-tetraploid species complex (Ortiz-Dorda et al., 2005). Genetic diversity is believed to be maintained better in polyploids than in diploids (Soltis and Soltis, 2000). In a species of *Oxalis*, sexual tetraploids had higher mean genetic diversity than sexual diploids, but asexual pentaploids had lower genetic diversity than sexual tetraploids (Ferrero et al., 2015). Genetic diversity increased with increasing ploidy level in a study of Bermudagrasses (Yan et al., 2019). Obviously much more work is needed here, particularly baramin-wide analysis of genetic diversity, but early results look promising and align with the computer model presented above.

In the post-Flood world, the entire Earth would have been available for plants to colonize. Species able to reproduce quickly, and with a generalized genome that enabled them to adapt quickly, would be preferred in such an open environment. Polyploid plants fit both bills with their penchant for asexuality and their increased diversity. In a sense, the post-Flood dispersal was the ultimate invasion of foreign species, with little competition. Polyploidy has been associated with invasive species (Te Beest et al., 2012; Wani et al., 2018) through improved nutrient uptake (Qiang et al., 2019) and the potential for increased growth rate (Hahn et al., 2012). In a post-Flood environment, these traits would have likely made polyploidy a dominant factor in the landscape. Therefore, we might expect an association between polyploidy and invasiveness in at least the baramins with created polyploidy.

In addition to their invasive capabilities, there is an association between polyploid plants and perennialism across most angiosperms (Van Drunen and Husband, 2019). This association is not necessarily a prediction of the model, but it is not incongruous with created polyploidy. It is possible that created polyploids had the genes required for both an annual and perennial lifestyle, and post-Fall diploidization and diversification resulted in a prevalence of polyploid perennials

and diploid annuals. Due to this gene loss, it is conceivable that there will be differences in flowering times, lengths, and frequencies between related annuals and polyploids. Indeed, in several perennials, tetraploids flower before diploids (Petit et al., 1997; Nuismer and Cunningham, 2005; Scopece et al., 2016). Since flowering time is epigenetically regulated in some polyploids (Pires et al., 2011; Jiang et al., 2022), and epigenetics is controlled in part by TEs (Ainouche et al., 2009), there is a potentially fruitful field of research here that could find an association between activity of transposable elements, flowering time, and ploidy level.

While this model argues for created polyploids, it does not argue that neopolyploids cannot be formed. Many of the same expectations for created polyploids will also be true of neopolyploids. There will, however, be a few differences. Neopolyploids formed by autopolyploidy will likely have lower genetic diversity than their parents while those formed by allopolyploidy likely will have higher genetic diversity than their paternal species. It is conceivable that neo-allopolyploids may have lower genetic diversity than one or both of their parents, however, depending on the paternal species.

Further, neopolyploids will be divergent in some way from their diploid progenitors. Likely this will be in habitat preference due to gene dosage and TE activation. In *Isoetes*, the six polyploid species all are found at lower altitudes than the four diploid species (Wang et al., 2004). Different ploidy levels of primrose exhibit habitat segregation based on several climactic traits (Theodoridis et al., 2013). These and other similar changes are likely for recently formed polyploids.

Conclusions

It is admittedly difficult to test the model as outlined above given the comparative inattention that baraminology has paid to plants and the unreliability of current baraminological methods (Sanders and Cserhati, 2022). However, in time, as baraminology improves and plant baramins are delineated successfully, this model will likely be easier to test. Importantly, using polyploidy as an explanation for the diversity of plant life helps not only to explain why some postulated baramins might be so large, but also helps to account for the vast diversity of created plants without appealing to "millions of years" of mutations. As such, creation biologists should consider created polyploidy as a potential answer to this question in plants.

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