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''PLANT SPECIATION THROUGH CHROMOSOME INSTABILITY AND PLOIDY CHANGE: CELLULAR MECHANISMS, MOLECULAR FACTORS, AND EVOLUTIONARY RELEVANCE''

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ABSTRACT

Plant speciation and diversification strongly depend on structural changes within the nuclear genome, both at the entire ploidy and individual chromosome level. Phylogenetic, comparative mapping, and cytological studies have provided insights into the evolutionary mechanisms that shape the plant genome. These include major genome alterations, like whole-genome duplication and hybridization (auto- and allopolyploidy), but also comprise the concomitant or independent occurrence of minor chromosome changes, like aneuploidization and dysploidy (inversions and translocations). Despite the relevance of chromosomal instability as a driver for genome evolution and adaptation, little is yet known about the cellular mechanisms and processes that really underlie these modifications. Here, during this paper, we offer a comprehensive overview of somatic and meiotic defects that cause polyploidy or structural genome changes and discuss their relevance for plant genome evolution and speciation. Also, we elaborate on the existence of stress-induced changes in chromosome and ploidy integrity in plants and their putative role in boosting adaptive genome evolution in hostile environments.

Keywords

Polyploidy Speciation Unreduced gametes a neuploidy Dys ploidy Somatic polyploidization Meiotic restitution Cytological mechanisms

1. Introduction

Flowering plants (angiosperms) show a high level of biodiversity, comprising an estimated number of 352,000 species subdivided into 14,559 genera and 405 families [1]. From an evolutionary perspective, this high level of variability indicates that plants have undergone extensive diversification and radiation, progressively generating new species

adapted to a mess of environments [2], [3], [4], [5]. As sessile organisms, land plants require enhanced phenotypic adaptability and adaptability to address highly variable external parameters, like extreme climate conditions, nutrient deprivation, and ecosystem competition. On the genomic level, plant diversity correlates with a high degree of variation in overall genome size, ploidy level, and chromosome number [6], [7]. Known plant genome sizes range from 1C = 0.0648 pg in Genlisea margaretae to 1C = 152.23 pg in Paris japonica [8]. From an evolutionary standpoint, this extreme genomic variability results from a long-lasting process of genome adaptation and alter [9]. Much of this genomic variation is thanks to the action of transposable elements [10]; however, of doubtless more functional importance are the cytological mechanisms permitting interspecific hybridization, polyploidization, and genome change through meiotic and mitotic mechanisms. Numerous varieties of chromosomal adaptations and ploidy alterations result from aberrations within the ubiquitous meiotic and mitotic processes, including whole-genome duplications and chromosome rearrangements. Increasingly, these processes are found to supply underlying mechanisms for plant speciation, particularly in response to environmental change [11], [12], [13].

Recently, an excellent deal of attention has been paid to the role of individual gene doubling and whole-genome duplication (WGD) events in speciation, particularly in plants. the method of WGD has thereby been proposed to act as a significant source of evolutionary genomic variability and plasticity, hence constituting one in every of the most mechanisms driving diversification and speciation [9], [14], [15]. Indeed, several phylogenetic studies and comparative genome analyses have confirmed that almost all flowering plants have undergone one or more ancient WGDs early in their evolution which several species seem to possess experienced one or more additional rounds of newer, independent polyploidization events [16], [17], [18], [19], [20]. Also, recent comprehensive phylogenomic analyses revealed the occurrence of two WGD events in ancestral plant lineages shortly before the divergence of extant seed plants and angiosperms. a typical genome triplication event preceded the rapid radiation of core eudicot lineages, providing substantial evidence that gene and genome duplication and associ-

ated changes in chromosome stability have triggered evolutionary novelties and radiative adaptation, contributing to the increase and dominance of flowering plants [21], [22].

In plants, like in other species, polyploid genomes are typically related to major changes in genomic structure and phenotypic outcome, providing a broader basis for adaptivity and evolvability compared to their diploid counterparts. Studies using neo- and artificial polyploids have revealed that polyploidy induces distinct phenotypic and morphological changes, like differences in flowering time and flower number [23], plant part and root architecture, furthermore as alterations in plant physiology, (a)biotic stress tolerance and other developmental processes [24]. Polyploidy has also been related to increased heterozygosity, higher selfing rates, induction of asexuality, and reduced inbreeding depression [25]. within the look for the putative mechanisms behind enhanced phenotypic variability of polyploids, a mess of recent molecular and genomic studies have revealed that de novo polyploid induction causes both rapid and more prolonged changes at the genetic and epigenetic level, along with major alterations within the transcriptional landscape [26], [27]. At the onset, polyploidy is related to rapid and extensive restructuring of the genome, including profound changes in chromosome number and structure (translocations, deletions) [28], [29], [30], [31], [32] and epigenetic alterations, like transposon activation, chromatin modifications and altered methylation patterning [33], [34], [35], [36], [37], [38]. As a results of this primary ‘genomic shock’, newly formed polyploid plants often show distinct changes in their organic phenomenon profile (e.g. gene silencing), often reflected by associated changes within the phenotype [39], [40], [41], [42]. this primary period of genomic stress is commonly related to plant lethality or reproductive sterility, largely impairing the reproductive success of the newly formed polyploidy [36], [43]. Polyploids that may pass this first bottleneck of genomic instability subsequently enter a second, more prolonged phase of genome evolution, whereby duplicated genes are either progressively lost [44] or retained, often showing sub- or neo-functionalization to yield novel genetic combinations and gene complexes [45], [46], [47], [48], [49], [50], [51]. As this process reduces genomic redundancy and converts the polyploid cell into a diploid one, both on the cyto-

logical and genomic level, this evolutionary process is commonly mentioned as 'diploidization'. Hence, through the combined changes in genetic and epigenetic structure, genome duplication within the long run provides a crucial source of genetic flexibility, allowing an increased level of mutation, drift, and also the selection and therefore the associated emergence of evolutionary novelties [52]. Based on these observations, it's now generally assumed that plant evolution is characterized by repeated rounds of large-scale genome duplications (WGDs), followed by selective loss of individual genes, chromosomes, or genome fragments and associated diploidization [25], [53].

Historically, two sorts of polyploids are recognized: auto- and allopolyploids (sometimes mentioned as polysomic and disomic). Although there's ambiguity about the definition of those two categories, the first criterion for classifying a polyploid is its mode of origin. Autopolyploidy refers to polyploids originating from a polyploidization event within or between populations of one species (intraspecific), whereas allopolyploids are the results of hybridization events between different biological species (interspecific) [25], [54]. Early cytogeneticists believed chromosome pairing to be a reliable indicator of chromosome divergence and homology, using the frequency of multivalent formation as a cytological parameter to tell apart between auto- and allopolyploidy [55]. Hereby, with a high level of multivalent pairing in meiosis, I suggested strong homology between chromosome sets and hence autopolyploidy. On the contrary, the predominant kind of bivalents was thought to result from the presence of non-homologous parental chromosome sets, hence indicating allopolyploidy. Despite these classifications, the differentiation between auto- and allopolyploids isn't absolute, since multivalent formation has been observed in hybrid polyploids, and bivalent pairing has occasionally been retrieved in intraspecific polyploids [56], [57]. As a consensus and with the arrival of genetic science, auto- and allopolyploids are now considered two extreme ends of a genome duplication-constituted continuum, within which the gradient of divergence between the parental genomes (and thus also the amount of bivalent chromosome pairing) determines the amount of auto- or allopolyploidy.

Comparative genomics and phylogenetic studies suggest that both auto- and allopolyploidization have played a prominent role in plant speciation and diversification. for instance, DNA sequencing technology has detected remnants of interspecific hybridization events within the evolutionary history of the many modern polyploid species [9], [58], [59], [60], [61]. Similarly, autopolyploid origins are established for apple (Malus x Domestica) [62] and a triploid tropical lucerne cytotype (Arachis pintoi) [63]. However, despite the evolutionary relevance and occurrence, the precise mechanism(s) and cellular process(es) underlying evolutionary events of polyploid origin remain largely unknown. Currently, there seems to be a significant discrepancy between studies of speciation, which tend to require an ecological and population genetics perspective, and cytological studies of mitotic and meiotic biological process and associated alterations in chromosome behavior and genome stability. Meiotic mechanisms have occasionally been investigated about speciation [64], [65], but the experimental investigation into the role of chromosome change (aneuploidy and dysploidy) in plant speciation has traditionally lagged behind similar studies in animals [66]. However, with the arrival of genetics and genomics, next-generation sequencing, and cytogenetic techniques, the role of chromosome change in speciation events may be more thoroughly investigated [67]. Hybridization can also occur without associated genome doubling [68] and increasing evidence suggests that hybridization without polyploidy also can play a significant role in speciation events [69]. However, despite the abundant knowledge on hybridization- and polyploidization-induced genome flexibility and associated chromosome instability, the precise cytological mechanism(s) and cellular process(es) fuelling repeated boosts of diversification and speciation during plant evolution remain largely unknown.

During the last decade, a plethora of mitotic and meiotic biological process anomalies are implicated in trans-generational ploidy change and chromosome instability. To what extent these anomalies have contributed to plant speciation events remains largely elusive. However, recent studies provide preliminary evidence for the

involvement of distinct cytological processes, strongly addicted to the sort of speciation (e.g. hybridization or polyploidy) and also the presence of genetic or environmental factors. during this review, we describe the three major cytological mechanisms causing ploidy change: (1) meiotic non-reduction and 2n gamete formation, (2) somatic genome duplication, and (3) minor karyotype changes through aneuploidy and/or dysploidy, and description their role as drivers of plant speciation. We concentrate on underlying cellular defects and associated molecular regulators and description specific induction through genomic and environmental stresses, suggesting a job for stress-induced polyploidization and chromosome change in plant evolution. Recent advances in our understanding of the cytological mechanisms facilitating rapid chromosome change highlight an intimate association with environmental stress conditions and specific genomic conditions (mutations, hybridization), and suggest pathways for natural and induced species formation through changes in chromosome or ploidy constitution.

2. Meiotic non-reduction – a significant driver of poly-ploidization in flowering plants

2.1. Sexual polyploidization through unreduced gametes

The meiotic organic process could be a critical reproductive process and is tightly controlled to ensure Reductional homologous chromosome segregation and subsequent formation of haploid male and feminine gametes. In some instances, however, alterations within the meiotic program or cellular defects in meiosis I (MI) or meiosis II (MII) may switch the meiotic biological process into a mitotic-like one, generating diploid spores out of a diploid cell. This mechanism is usually termed meiotic restitution or meiotic non-reduction, and therefore the resulting gametes are spoken as unreduced or 2n gametes [70], [71], [72], [73]. Importantly, the ectopic formation of diploid gametes, rather than the conventional haploid ones, intrinsically ends up in progeny with an increased chromosome number. This mechanism of genome polyploidization is termed ‘sexual polyploidization’ and may be subdivided into two types: bi- and unilateral sexual polyploidization [54]. within the former, a fusion between two diploid gametes yields a tetraploid individual, which, counting on the selective conditions, may initiate the de no-

vo establishment of a stable tetraploid lineage. in contrast, in unilateral sexual polyploidization events, one diploid gamete fuses with a traditional haploid one to come up with a triploid embryo. Although triploid seeds are often non-viable through imbalances in parental genome dosage input within the endosperm [74], this triploid block is occasionally incomplete or absent allowing triploid planet formation [75], [76]. Meiotic organic process in these triploids is mostly extremely unbalanced yielding aneuploid gametes. However, through random segregation triploids also produce some euploid gametes, both haploid and diploid, which can contribute to the establishment of stable polyploid populations over time [77]. This process is mostly named because the triploid bridge hypothesis [54] and is recommended to play a job in evolutionary polyploidization events.

A large number of various cellular defects conferring meiotic restitution are described. From a genetic point of view, these mechanisms are classically subdivided into two main groups, namely First Division Restitution (FDR) and Second Division Restitution (SDR) (extensively reviewed in Refs. [71], [73], [76]). In brief, SDR mechanisms yield 2n gametes that are genetically love those formed by a loss of the second meiotic cellular division. SDR gametes hence contain both sister chromatids from the identical chromosome and display loss of parental heterozygosity from the centromere to the primary site of crossing-over (CO). In contrast, 2n gametes resulting from FDR-type meiotic restitution are genetically like those formed by a loss of MI. Hence, in FDR-type restitution, sister chromatids from the identical homolog are split but homologous chromosomes are retained, and resulting gametes maintain parental heterozygosity in chromosomal regions spanning the centromere to the primary CO. Interestingly, when FDR also includes an entire loss of meiotic recombination, the meiotic biological process is converted into a mitotic one, yielding 2n gametes that fully retain the parental genome constitution, including heterozygosity and epistatic interactions. this kind of meiotic restitution is usually observed in female gametogenesis of apomictic plants and parthenogenically reproducing animals as a reproductive adaptation to come up with clonal progeny.

2.2. Cellular mechanisms and genetic regulation of meiotic restitution in plants

Detailed cytological studies in several plant species have revealed that meiotic restitution can originate from a plethora of cellular defects. These are generally subdivided into three main classes: (1) alterations in meiotic spindle dynamics; (2) defects in meiotic cell plate formation and (3) omission of meiosis I or II (reviewed in Refs. [71], [72], [73]).

Alterations in meiotic spindle dynamics occur in either meiosis I or II and are caused by structural defects in spindle biogenesis, microtubule (MT) nucleation, kinetochore functioning, or spindle orientation and organization. Although these defects generally cause imbalances in chromosome dynamics and segregation, yielding aneuploid gametes, occasionally the presence of non-separated chromosomes induces a meiotic restitution event [78]. for instance in cereal hybrids, like wheat-rye F1 plants, both the ectopic formation of curved MI spindles and defects in spindle-kinetochore attachment completely block metaphase I chromosome separation and cell plate formation, yielding restituted cells which progress through MII to make dyads containing two unreduced gametes [79]. However, despite this, meiotic restitution in plants more commonly results from alterations within the three-dimensional organization of the spindle structure(s). In meiosis I, defects in bipolar spindle orientation either partially or fully omit polar-directed chromosome segregation, yielding restituted MI nuclei capable of undergoing meiosis II [80]. In meiosis II, alterations within the spatial positioning of the 2 metaphase spindles may cause a rejoining or maybe a non-disjunction of the 2 haploid chromosome sets, eventually yielding restituted nuclei [81]. Particularly in male meiocytes of dicotyledonous plants, proper perpendicular orientation of the 2 MII spindles is crucial for proper chromosome segregation and meiotic ploidy reduction [82], [83]. Indeed, the ectopic induction of tripolar (tps) and parallel (ps) or fused (fs) spindles has been found to scale back MII polarity from tetrahedral to tri- or bipolar, respectively, so MII spindles rejoin chromatids at one or both poles, generating meiotically restituted FDR-type 2n gametes [84], [85]. Interestingly, in most cases, ps, fs, and tps are jointly observed within the same flower [82], [83], [86], [87], indicating that every one three processes consti-

tute a unique outcome of 1 common cellular defect. However, up till now, the underlying mechanism has not been revealed yet.

Studies in potato and Arabidopsis thaliana have revealed a genetic background for the ps/tps/fs male meiotic defect and resulted within the identification of several proteins required for MII spindle polarity, including JASON, AtPS1 (A. thaliana PARALLEL SPINDLES 1) and AFH14 [82], [83], [88]. Mutant varieties of these proteins induce the formation of dyads and triads in male meiosis through alteration of MII spindle orientation, yielding 2n gametes capable of inducing sexual polyploidization. AFH14 is an Arabidopsis type II formin (FORMIN 14) that functions as a linking protein between microtubules (MTs) and microfilaments (MFs) [88]. AtPS1 encodes an unknown plant-specific protein with an N-terminal Forkhead Associated (FHA) domain and C-terminal PINc domain, typically involved in protein-protein interactions and RNA processing and decay (i.e. Nonsense-mediated mRNA decay), respectively [82]. JASON, on the opposite hand, is an unknown, plant-specific protein that positively regulates AtPS1 transcript levels in early-stage flower buds, suggesting that JAS controls MII spindle organization through AtPS1 [83].

Ps-induced 2n gamete formation has already been documented in several plant species and is hence considered one among the foremost routes for 2n gamete formation and sexual polyploidization in plants. Whether the meiotic ps defect and one or more underlying causative mutations have driven WGD within the evolution of sexually reproducing plants remains unknown. Interestingly, studies in potato revealed that tetraploid cultivars and related wild taxa contain a better ps allele frequency compared to the ancestral diploid population, indicating that ps and therefore the associated formation of 2n gametes are the propulsion behind the origin of cultivated tetraploid potatoes [89], [90]. Although not yet demonstrated in other naturally evolved populations, this study shows that ps and other 2n gamete-forming mutations may have laid the idea for evolutionary WGD events and associated speciation and diversification in plants.

The second style of meiotic restitution in plants involves alterations in meiotic cytokinesis. Defects in meiotic cell plate formation either originate from (1) precocious induction of cytokinesis or (2) partial or complete loss of meiotic cell plate formation, either after MI or MII [73], [84], [91], [92]. In both cases, the physical separation of nuclei following MI or MII is affected, with two or more haploid nuclei enclosed in a very common cytoplasm. Subsequent fusion of syncytial nuclei in these bi- or polynuclear cells eventually yields diploid or polyploid spores, forming a sexual basis for whole-genome doubling [93], [94], [95], [96].

Precocious induction of meiotic plasma membrane formation is simply sporadically reported, either in MI [95] or MII [85], and hence not considered a crucial mechanism for meiotic restitution. In contrast, unreduced gamete formation through the loss of cell plate formation has frequently been observed in numerous plant species [78], [91], [95], [96], [97], [98], suggesting it's a vital cellular mechanism driving sexual polyploidization. In meiocytes with a successive-type of biological process, loss of cell plate formation may either occur after MI or MII, generating FDR- or SDR-type 2n gametes, respectively [93], [99]. In simultaneous-type PMCs, which form a “double-wall” at the tip of MII, loss of meiotic plasma membrane formation may either be partial or complete, yielding diploid, triploid, or tetraploid gametes [96].

From a mechanistic point of view, loss of meiotic cell plate formation may result from several sorts of cellular anomalies, including alterations in microtubule (MT) array biogenesis or stability [100], [101], defective transport of plasma membrane material, disturbed membrane vesicle fusion [102] and reduced deposition of callose [103]. as an example, several studies employing a. thaliana mutants have revealed that structural or functional irregularities within the establishment of internuclear radial microtubule arrays (RMAs) at the top of MII causes defects in cytokinesis, hence yielding bi- or polynuclear spores [100], [101], [104], [105]. additionally to those ‘basal’ cytokinetic defects, alterations in meiotic cytokinesis may additionally occur as a secondary effect resulting from irregularities in spindle elongation or orientation. Indeed, studies on the maize MATH-BTB domain protein MAB1 revealed that the shorter spindles in mab1 RNAi meiocytes

cause an insufficient separation of telophase II nuclei, impairing subsequent internuclear cell membrane formation and hence generating bi- or polynuclear spores [106]. Moreover, an intensive analysis of MT structures in potato and Populus meiocytes demonstrated that alterations in tetrahedral MII nuclei positioning through irregularities in spindle orientation cause defects in interzonal RMA formation, indicating that meiotic non-reduction by ps, fs, and tps actually results from 'secondary' defects in MII cell plate formation [85], [92].

Thirdly, meiotic restitution may originate from an entire omission of 1 of the meiotic cell divisions. within the case of loss of MI, both the processes of meiotic recombination and reductional cellular division are omitted, and MII separates sister chromatids into two diploid FDR-type daughter cells, genetically similar to the parental line [107], [108], [109], [110]. This process of clonal gamete formation is said as diplosporous apomeiosis [111], [112] and is usually observed in apomictically reproducing species, both in plants yet as in other eukaryotic clades [113], [114], [115]. Contrary to loss of MI, failure of MII still enables homologous recombination and MI chromosome segregation, however, separation of sister chromatids doesn't occur. Instead, centromeric cohesion is lost at the tip of MII, yielding dyads that contain SDR-type 2n gametes [109], [116].

In sexually reproducing species, loss of meiotic cellular division has also repeatedly been observed [107], [117], [118], [119], [120], and hence is also considered an alternate mechanism driving natural polyploidization. Moreover, apomeiosis and clonal 2n gamete formation is that the rule apomictically reproducing species, indicating that the developmental switch from meiosis to apomeiosis forms a natural pathway for plant reproductive evolution [121], [122]. In support of this, phylogenetic studies revealed that in many species apomixis evolved repeatedly from sexual pathways, and this in several independent origins [123], [124]. More importantly, in most species apomixis has been found strongly correlated with genomic instability and polyploidy [25], [125], [126], suggesting that the method of apomeiosis not only confers agamogenesis but also induces transgenerational ploidy increase, and hence drives evolutionary polyploidization [127],

[128]. Although still under debate, it's postulated that polyploidy hereby functions as a genomic stabilizing factor, reducing the impact of deleterious mutations within the short term and hence providing a selective advantage over diploid apomicts [129], [130], [131].

Progression of the meiotic cell cycle and consolidation of reductional division in sexually reproducing species is tightly controlled by a fancy network of (epi-)genetic factors [132], [133]. Interestingly, genetic defects in a number of these regulators are found to induce meiotic restitution and 2n gamete formation (extensively reviewed in Refs. [72], [73]), indicating that (epi-)genetic defects in meiotic cell cycle regulation may constitute a basis for sexual WGD. as an example, genetic studies in Arabidopsis have identified two proteins, e.g. TAM (TARDY ASYNCHRONOUS MEIOSIS) and GIG1/OSD1 (GI-GAS CELL1/OMISSION OF MEIOTIC DIVISION1) that are required for progression of meiotic biological process, and more specifically the MI-to-MII transition. As a result, functional loss of 1 of those proteins causes a whole omission of MII, generating dyads that contain SDR-type 2n gametes [109], [116]. GIG1/OSD1 is an inhibitor of the Ana-phase Promoting Complex/Cyclosome (APC/C) and functions within the maintenance of elevated CDK (CYCLIN-DEPENDENT KINASE) levels after MI [134], [135]. TAM, on the opposite hand, encodes an A-type cyclin, e.g. CYCA1;2, that forms a functional complex with CDKA;1, to control meiotic cell cycle progression [116], [136]. Besides regulators of MI-to-MII cell cycle transition, several other proteins implicated within the initiation of meiotic biological process, e.g. the mitosis-to-meiosis switch, are identified. These include the Arabidopsis meiotic prophase I protein DY-AD/SWITCH1 [108], [137], [138], the APOLLO (APOmixis-Linked Locus) histidine nu-clease recently identified in Boechera [139], the maize DMT102 and DMT103 DNA-methyltransferases [140], the maize AGO104 (ARGONAUTE 104) protein [110] and its Arabidopsis ortholog AGO9 [141] and other proteins acting within the 24 nucleotides siRNA-mediated silencing pathways, like RNA-dependent RNA polymerase 2 and 6 (RDR2 and RDR6), SUPPRESSOR of GENE SILENCING 3 (SGS3), DICER-LIKE 3 (DCL3) and POLYMERASE IV and V (NRPD1a and b). Functional loss of function of

every of those proteins induces a whole omission of MI, yielding meiocytes that skip re-combination and reductional organic process and directly undergo equational biological process to provide clonal 2n megaspores. Genetic analyses revealed that every one these proteins are either involved within the regulation of MI chromosome dynamics [142], [143] and histone patterning [144], small RNA-mediated signaling and gene si-lencing or DNA methylation [140], indicating that meiotic induction and also the meiosis-apomeiosis decision is under a powerful epigenetic control (extensively reviewed in [73]). Altogether, these findings demonstrate that alterations within the (epi-)genetic machinery controlling reproductive pathways, like initiation of meiosis and regulation of meiotic cell cycle progression, may cause meiotic non-reduction (e.g. loss of MI or MII), hence forming a molecular trigger for the formation of 2n gametes capable of conferring sexual polyploidization. However, whether such aberrations have actually contributed to evolutionary relevant polyploidization and speciation events apart from induction of ap-omictic reproduction remains unknown.

2.3. Meiotic restitution upon hybridization drives allopolyploid induction and spe-ciation

Many polyploid speciation events involve the intercrossing of two closely or more dis-tantly related species to get a stable allopolyploid lineage. At the genomic level, these ‘polyploid hybrids’ benefit both from fixed heterozygosity likewise as from chromosome redundancy, providing them increased genomic flexibility upon which selection can act. Studies in wheat and Brassica have also revealed that neo-allopolyploids display rapid and pervasive alterations at the DNA sequence and epigenetic profile level [145], [146], [147], including alterations in DNA methylation patterning [148], [149], reciprocal trans-locations [30], insertions/deletions, elimination of low-copy non-coding DNA sequences [150], aneuploidy [151], [152] and loss of 5S DNA unit classes [153]. This (epi-)genetic variability and resulting transgressive segregation is believed to supply allopolyploids a powerful evolutionary advantage, which can explain their widespread occurrence, in natural still as agronomic populations. a considerable amount of research has been per-formed in search of the cellular mechanism(s) underlying allopolyploid origin. The very

early maxim of “hybridization followed by genome doubling” proposes by Ö. Winge (1917) was repudiated by (1975) [154], who made the primary strong case for the involvement of meiotic mechanisms and specifically unreduced gametes, in allopolyploid formation events. Subsequently, increasing evidence has supported the role of meiotic non-reduction and sexual polyploidization in F1 hybrids as a serious route for allopolyploid formation (comprehensively reviewed by Ramsey and Schemske [54]).

F1 plants resulting from wide hybridization events generally produce non-viable gametes thanks to instabilities in meiotic chromosome segregation and gametophytic aneuploidy. These F1 meiotic defects typically originate from irregularities in MI homologous chromosome pairing; a process that strongly depends on the sequence similarity of the 2 parental genotypes [155], [156], [157]. If homologous chromosome pairs aren't present, as is that the case in wide hybridization events (e.g. genome composition AB), the pairing of homoeologous chromosomes is strongly disrupted and chiasmata univalents rather than recombining bivalents are formed at metaphase I. thanks to the absence of bivalent-based bipolarity, univalents segregate randomly at anaphase I, yielding unbalanced MI products that become aneuploid gametes [158], similar as in a-and desynaptic mutants and haploid lines [159], [160], [161]. Although the induction of gametophytic aneuploidy may occasionally result in variations in chromosomal structure and duplicate number [162], resulting gametes are generally non-viable [158]. Strikingly, despite this meiosis-based gametophytic sterility, F1 hybrids generally still produce alittle or sometimes sizable amount of seeds, which in most cases have a duplicated chromosome number [163], [164], [165], [166]. Cytological and genotypic analysis of de novo F1 Amphi- or polyploids revealed that this can be caused by the induction of meiotic restitution and also the associated formation of unreduced gametes [163], [167], [168], [169], [170], [171]. Importantly, studies in several plant species have revealed that the precise mechanism of meiotic restitution differs by hybrid type, largely looking on the extent of homologous chromosome pairing and hence on the relatedness of the first parent lines.

2.3.1. Cellular mechanism of meiotic restitution in F1 hybrids depends on parental genome divergence

In the case of hybridization between two remote genotypes, like wheat-rye and other cereal wide crosses, resulting F1 hybrids shows an entire lack of pairing and crossing-over, yielding univalents rather than bivalents at metaphase I (Fig. 1). The cytological analysis revealed that these univalents either show unidirectional segregation to at least one pole, yielding an asymmetrical dyad composed of 1 anucleate cell and one cell with a restituted nucleus or display chromosome lagging and thus remain positioned at the cell equator [80], [164], [172]. Alternatively, in some cases, MI shows a retrograde migration of telophase I chromosomes from the poles back to the middle of the cell [79]. all told these cases, MI yields a non-reduced diploid cell that progresses through the second meiotic cellular division to create a dyad containing two unreduced 2n gametes [173]. Interestingly, studies in Lilium interspecific hybrids and haploid Arabidopsis have revealed that univalents have the potential to divide equationally during MI, indicating that the whole loss of bivalent formation may convert the double meiotic biological process into one mitotic one [174], [175]. This process is often noted as a ‘single-division meiosis’ (SDM) [173], [176], or a ‘mitotic-like division’ [169], [170]. However, during a strict sense, SDM represents an extreme variety of univalent-induced delay of MI chromosome segregation, completely impairing distinction between the 2 meiotic cellular divisions and hence mimicking a mitotic cell division. In support of this, SDM and FDR have often been found to co-exist in F1 amphidiploid [165], [173]. Interestingly, an analogous kind of meiotic restitution also occurs in synaptic accessions and (poly-)haploid lines that show an entire loss of homolog interaction and bivalent formation [102], [164], [177], [178], indicating that meiotic restitution is directly because of structural alterations in MI chromosome segregation and isn't intrinsically caused by genetic defects that alter meiotic biological process. Since altogether these cases meiotic restitution involves an entire loss of MI, including both reductional cellular division and recombination (FDR-type sensu strict), resulting gametes are genetically the image of the parent and hence generate an autopolyploid version of the first hybrid. Despite their hybrid origin, these so-called strict allopolyploids act as homozygous diploids

with strict bivalent chromosome pairing and disomic inheritance, for instance, demonstrated in newly formed Arabidopsis suecica (2x = 26) allopolyploids [179].

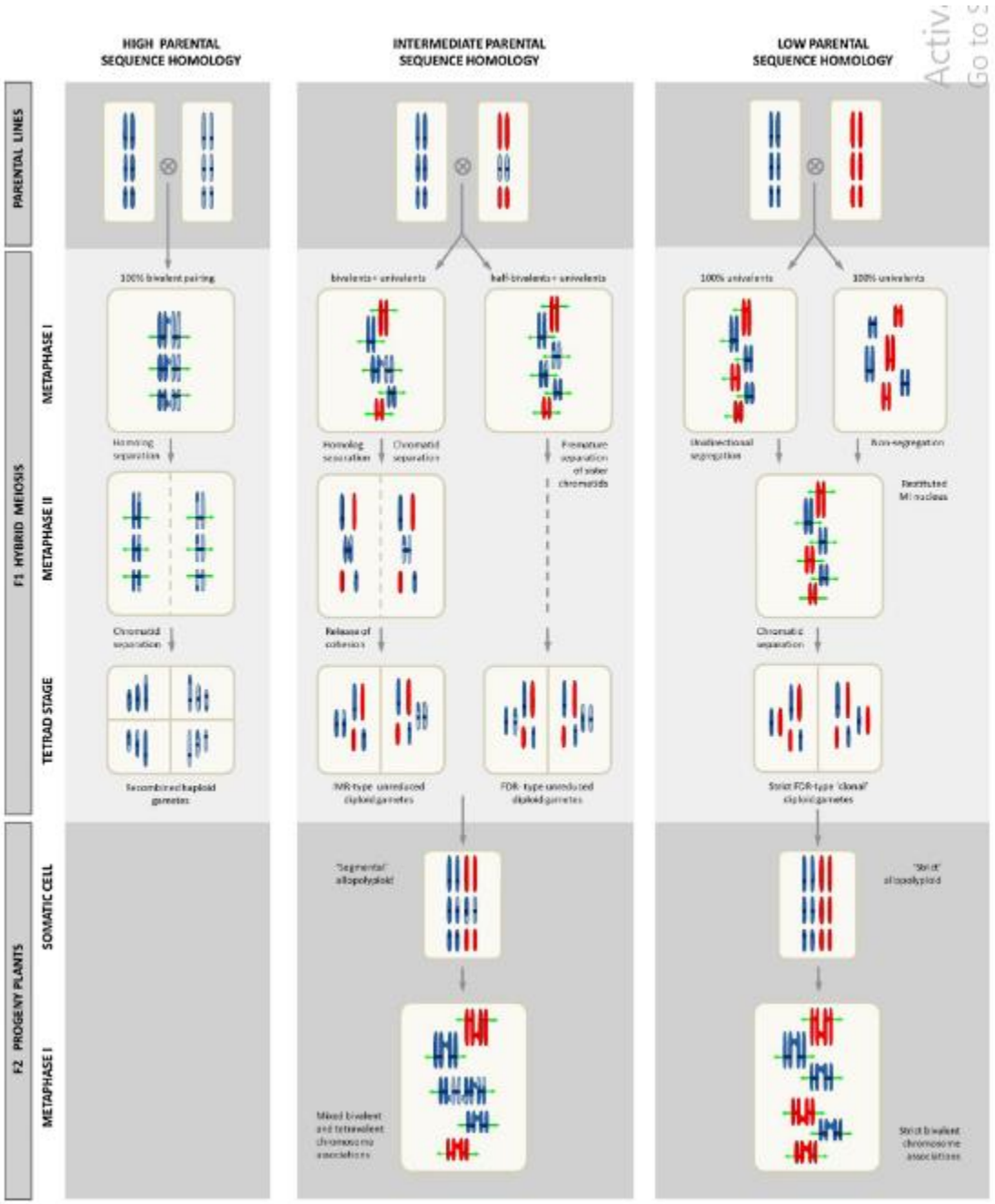

Fig. 1. The impact of sequence homology between parent progenitor genomes on meiotic restitution in their F1 progeny.

In the case of intercrossing two more closely related species that share a particular level of genomic sequence similarity (e.g. homology), resulting F1 hybrids may additionally exhibit events of meiotic restitution and 2n gamete formation, albeit at a significantly lower rate compared to hybrids with more divergent genomes [180], [181]. From a cytological perspective, the mechanism of meiotic non-reduction is extremely like the one observed in (Amphi-)haploid meiosis, with lagging chromosomes remaining at the MI equatorial cell plate that eventually restitutes the primary meiotic biological process. However, in hybrids with homeologous subgenomes, the genotypic constitution of resulting 2n gametes differs significantly from those produced by a strict FDR-type mechanism, as pairing and recombination may occur between (some) homeologous chromosomes. This behavior is exemplified by the presence of bivalents and/or multivalents, physically exchanging genetic material, amongst the opposite non-recombining univalents [63], [182], [183]. counting on the precise model of chromosome segregation and more specifically on the timing of bivalent dissociation, two putative mechanisms of meiotic restitution are possible, each producing 2n gametes that slightly differ in their genetic make-up. just in case of a premature loss of bivalent association, for instance in prolonged metaphase I state, both univalents and half-bivalents exhibit an equational cellular division, yielding FDR 2n gametes that largely maintain parental heterozygosity, apart from the regions that have undergone reciprocal recombination (non-strict FDR). Alternatively, when bivalents maintain chiasmata links up till anaphase I and properly attach to the bipolar spindle, meiotic non-reduction typically involves a reductional division of bivalents along with equational segregation of univalents, giving rise to unreduced gametes that don't comply to an FDR-type, but instead are cherish a so-called indeterminate (IMR)-a variety of meiotic restitution [73], [174]. Importantly, besides parental genome exchange through homologous recombination, genetic variability in IMR 2n gametes is additionally increased by the dissimilar transmission of parental chromosomes [174]. thanks to the partial homology of the parental taxa, resulting allo-

polyploids of both varieties of meiotic restitution (i.e. non-strict FDR and IMR) show a mixture of bivalent and quadrivalent MI chromosome pairing, hence conferring a mix of di- and tetrasomic inheritance. These polyploids, often observed as segmental allopolyploids [184], form a vital a part of this natural and agronomic polyploid population, e.g. as shown by several cytological, molecular, and genome sequencing studies [152], [185], [186], [187], [188] providing substantial evidence for the occurrence of both FDR- and IMR-type restitution, including partial homeologous recombination, in allopolyploid plant speciation [29].

Altogether these findings support the hypothesis that meiotic restitution upon hybridization forms a very important driver for allopolyploid origin, and additionally indicate that the frequency and sort of meiotic restitution (FDR sensu strictu, FDR- and IMR-type) strongly depends on the parental genome constitution, and more specifically on DNA sequence divergence and structural dissimilarities. As a general rule, the increasing divergence of the parental genomes progressively hinders homeologous pairing and recombination, inducing FDR- and IMR-type meiotic restitution in meiocytes containing partially divergent genomes and FDR sensu strictu when genomes are highly divergent. Although the presented model for allopolyploidization presumably presents an oversimplified view, excluding the role of gene dosage and transcriptional and genetic alterations, the essential principle of hybridization-induced meiotic restitution may constitute a general system explaining allopolyploid origin (strict and segmental) during plant evolution. In support of this, Hunter et al. [189] demonstrated that progenitors of polyploid hybrids show significantly higher genetic divergence than those underlying homoploid hybridization, confirming the notion that parental genome divergence in an exceedingly hybridization context drives whole-genome duplication and hence allopolyploid speciation.

2.3.2. Molecular basis for meiotic non-reduction and 2n gamete formation in F1 hybrids

From a mechanistic point of view, it's suggested that the induction of meiotic restitu-

tion and therefore the frequency of its occurrence in F1 hybrids largely depends on the presence of univalents and hence on the dearth of pairing caused by sequence non-homology, instead of on specific genetic defects [164]. In support of this, Wang et al. [190] found that F1 hybrids resulting from allotetraploid T. turgidum x tetraploid Ae. tausschii crosses (yielding ABDD genotypes) don't undergo meiotic non-reduction, whereas their triploid polyploid variants (ABD genotype) do, indicating that homologous pairing interferes with the induction of meiotic restitution. In agreement with this, induction of pairing and bivalent formation in wheat/rye F1 hybrids, by using wheat parents with single rye chromosome substitutions, caused a better preference for the reductional, meiotic-like pathway, whereas a whole failure of bivalent pairing induces meiotic restitution and 2n gamete formation [191]. Similarly, studies in Triticum turgidum revealed that the univalent-associated induction of meiotic restitution normally occurring in synthetic haploids [164] is impaired in 5D-5B chromosome substitution haploids, because of the induction of homologous chromosome pairing and bivalent formation (by the absence of the Ph1 locus) [192]. In contrast to the current hypothesis, Pignone [193] found that amphidiploid T. turgidum x Ae. longissima hybrids (ABS1, 2n = 21) and also the corresponding backcrosses to T. turgidum (AABBS1, 2n = 35), which demonstrate a high level of bivalent formation, both exhibit an equational division of univalents, indicating that in some cases genetic factors or other parameters is also involved within the induction of meiotic non-reduction.

As an underlying molecular basis, it's been suggested that increasing deviations in DNA sequence similarity between parental chromosome sets may impair the only strand-based DNA homology search in prophase I, reducing the amount of D-loop structures that form a transient interhomolog linkage which are required for homologous pairing, synapsis and recombination [194], [195]. Alternatively, divergence in sequence homology may alter chromatin remodeling capacities during early meiotic stages, hence affecting the method of pairing and recombination [196], [197]. In support of this, studies in wheat-rye hybrids revealed that perturbations in hom(e)logout chromosome pairing are closely related to asynchronies in prophase I chromatin condensation and failure in het-

erochromatin change [198], [199] and eventually induce meiotic restitution and 2n gamete formation [172]. Additionally, chemical induction of chromosome condensation has been found to induce homeologous pairing in wheat interspecific hybrids, indicating that a synchronized change in chromatin remodeling is crucial for MI reductional biological process [200]. associated with this, Rezaei et al. [201] suggested that meiotic instabilities in triticale are caused by structural differences in parental chromatin configuration, with rye displaying large telomeric blocks of heterochromatin and wheat showing a smaller and intercalary band of heterochromatin. Since the alignment of meiotic homologs generally initiates from the (sub-)telomeric regions [202], differences in chromatin state may hence impair hom(e)log recognition and pairing [197], thereby yielding chiasmata chromosomes capable of inducing meiotic restitution. Alternatively, loss of reductional organic process in F1 hybrids may additionally result from defects in kinetochore functioning and associated delay in meiotic cell cycle progression or by inactivation of MTs or kinetochores because of structural and/or functional incompatibilities within the amphidiploid MI chromosome set [172]. In support of this, Cai et al. [175] revealed that tetraploid wheat cv. 'Langdon' (LND) displays a syntelic orientation of sister kinetochores at MI, whereas its polyploid variant and interspecific hybrids with Ae. tauschii display an amphibolic orientation, conferring bipolar segregation of sister chromatids rather than hom(e)blogs. the stress created by this amphibolic orientation of sister kinetochores, along with the persistence of centromeric cohesion up till anaphase II, is thereby suggested to create a mechanistic basis for the onset of 'SDM' meiotic restitution. Moreover, since the amphibolic association was only observed in synapsed chromosomes, Cai et al. [175] suggested that synapsis acts because
the predominant think about the determination of MI kinetochore orientation,
and intrinsically forms a vital structural consider the choice whether to divide equationally or equatorially. this is often in agreement with the observation that a high level of chromosome pairing and synapsis prevent meiotic non-reduction and 2n gamete formation [190]. In support of this, Ressurreição et al. [203] found that the induction of asynapsis within the N5DT5B variant of Chinese Spring wheat (5D nullisomic and 5B tetrasomic, absence of the Lpt gene) [204] by low temperatures induces meiotic non-

reduction, even when the 2 homologs are present. These findings provide strong evidence that the absence of synapsis instead of the haploid condition is that the key feature switching syntelic to amphibolic kinetochore attachment and eventually inducing meiotic restitution in wheat. Moreover, since N5DT5B shows a reduced level of crossing-over [205], haploidy-dependent induction of meiotic restitution, for instance, observed in newly formed F1 hybrids and another amphidiploid, is also directly due to defects in synapsis and recombination, typically occurring as secondary effects of alterations in meiotic homo(eo)logos recognition and pairing.

2.3.3. Genetic factors promoting F1 hybrid-associated meiotic restitution: lessons from Triticeae

Besides spontaneously occurring meiotic non-reduction, several studies have demonstrated the existence of genetic factors that induce/enhance the amount of meiotic restitution upon hybridization. Particularly within the Triticeae tribe, the genetic influence of the oldsters on the genome doubling capacity of resulting F1 hybrids has repeatedly been documented. A recent study of quite 100 kinds of T. turgidum x Ae. tausschii combinations revealed high variability in selfed seed set, reflecting genetic differences within the T. turgidum germplasm to induce meiotic restitution [180]. this is often in agreement with earlier reports, which demonstrate a high variability in chromosome doubling capacity of specific tetraploid wheat varieties upon hybridization with Ae. tausschii [206], [207]. Genetic studies hereby found that the wheat cultivar Langdon (LDN) carries a gene for meiotic restitution, causing high-frequency FDR and partial fertility in hybrid combinations with rye and Ae. squares [208]. supported observations using LDN durum D-genome disomic substitution lines, Xu and Joppa [209] found that the underlying FDR-inducing gene is presumably located on chromosome 4A, however, the precise gene and underlying molecular mechanism has not yet been identified. Similarly, Zhang et al. [169] found that emmer wheat also induces high-level FDR-type meiotic restitution in F1 hybrids with Ae. tauschii which this can be controlled by one or more nuclear genes. Although little is thought about the function of those Triticum 'meiotic restitution' genes, the finding that 2n gamete formation is merely promoted in an (Am-

phi)haploid background and not within the usual diploid state Zhang et al. [169] suggests that these genes may only function within the partial or complete absence of chromosome pairing.

Interestingly, besides emmer and wheat, Ae. tauschii also harbors some level of natural variability in its genome doubling capacity upon hybridization with T. turgidum [210], [211]. Using two representatives Ae. tausschi accessions, an intensive QTL mapping approach hereby identified six QTLs that positively regulate F1 genome doubling and fertility recovery [212]. Although these QTLs may harbor genes implicated in numerous reproductive activities, Matsuoka et al. [212] argued that the majority if not all QTLs are involved within the regulation of meiotic non-reduction, with two QTLs containing putative 'meiotic restitution' genes; namely, Taf1 which is involved in female sterility [213] and Ph2, which could be a suppressor of homeologous pairing. Ph2 is a component of the pairing homoeologous (Ph) gene system in wheat, which negatively regulates interactions between non-homologous chromosomes (A, B, D, etc.), thereby ensuring diploid-like meiosis and disomic inheritance in polyploid genomes. The Ph system consists of a significant pairing locus, e.g. Ph1, on chromosome 5B [214], [215], an intermediate one, e.g. Ph2, on 3D [216], [217] and several other additional minor loci [218], [219]. Interestingly, loss of Ph1 in amphidiploid genome combinations and associated induction of homoeologous pairing has been found to scale back the capacity of WGD in corresponding hybrids, whereas its presence significantly enhances meiotic restitution [168], [220], indicating that Ph1 and related genes is also important drivers for F1 amphidiploid meiotic non-reduction and allopolyploid induction. Recently, genetic studies identified Ph1 as a serious regulator of meiotic CDK activity [221], [222], [223], with major implications in early MI stage chromatin remodeling and induction of synapsis [196], [222], [224], [225], [226], whereas the intermediate pairing locus Ph2 positively controls the progression of synapsis [227], providing a molecular basis for the regulatory function of Ph-related genes within the induction of meiotic restitution and 2n gamete formation.

Recently, studies using haploid variants of wheat-rye substitution lines revealed interesting behaviors associated with meiotic restitution. Zelkova et al. [228] thereby found that a 6R(6A) substitution induces equational-type division of univalents resulting in meiotically restituted dyads, whereas other lines (2R(2D)1 and 2R(2D)3) exhibit a reductional-type of meiotic chromosome segregation. These findings indicate the existence of 1 or more 'promotive or suppressive meiotic restitution genes' on chromosomes 6R and 2R, respectively. In line with this, rye chromosome 2R has already been found to act as a suppressor of meiotic non-reduction in wheat-rye polyhaploids [229]. Although a putative role for the underlying genes within the structural and functional organization of centromeres and associated kinetochore orientation has been postulated, corresponding genes and associated molecular mechanism(s) haven't been identified yet. it's possible, however, that both the 6R and 2R genes have a sway on homoeologous pairing and recombination, and hence act as indirect molecular regulators of haploid-induced meiotic restitution, just like Ph in wheat.

Altogether, these data suggest that loci involved within the suppression of homoeologous pairing, e.g. through chromatin remodeling and initiation of synapsis, is also involved within the induction and/or promotion of meiotic restitution and sexual polyploidization in F1 hybrids. However, whether these loci actually operated as genetic drivers of hybrid polyploidization, fuelling allopolyploid speciation, remains unknown. Classically, Ph1 and related loci are thought to result from mutations occurring after allopolyploid origin, i.e. following hybridization and polyploidization, as a mechanism to stabilize newly formed allopolyploid genotypes by cytological diploidization of meiotic organic process [221]. However, supported the above-mentioned observations, one could assume that Ph1 or other loci suppressing homeologous interaction, were already present within the parental lines and hence significantly promoted sexual polyploidization in newly formed hybrids through the inherent induction of meiotic restitution (e.g. thanks to an absence of pairing). Moreover, since this process directly produces neo-allopolyploids with an inherent suppression of homologous chromosome pairing, this theory not only implicates an enhanced success rate of allopolyploid origin but also

provides a mechanism for reducing adverse meiotic irregularities and genomic instabilities in early-stage allopolyploid speciation [25], [30], [230], [231], substantially promoting its fitness and establishment. In support of this, several authors have suggested the existence of Ph-like genes in diploid wheat species [182], [232], [233], thereby postulating that they only became effective in Amphi(ha)ploid situations as a results of hybridization or polyploidization [234]. Similarly, standing variation for the flexibility to suppress homologous recombination in newly formed hybrids has also been reported in Lilium diploids [235]. Interestingly, an analogous theory has recently been postulated for the origin and evolution of autopolyploids. supported an in depth genome sequence analysis Hollister et al. [230] found that the AaASY1 allele, i.e. one amongst the alleles reducing pairing frequency in Arabidopsis arenosa tetraploids [236], occurs at very low frequencies within the corresponding diploid cytotype, indicating that it should have formed a genetic basis for promoting ancient polyploidization events, thereby inherently providing a molecular basis for the diploidization and hence stabilization of autopolyploid meiosis.

2.4. Stress-induced meiotic restitution drives WGD under adverse conditions

2.4.1. Stress-induced meiotic restitution in plants: cellular mechanism and molecular regulation

In flowering plants, the reproductive pathway and particularly the method of male gametogenesis is very sensitive to abiotic stresses. Indeed, several studies on differing kinds of plants have revealed that adverse environmental conditions, like heat, cold, drought, and salt stress have a detrimental effect on male spore formation and pollen maturation, significantly affecting male fertility and seed set [237]. In most cases, stress-induced male sterility is caused by a precocious or delayed programmed degeneration of the tapetal cell layer, i.e. the encircling cell layer that nurtures the developing microspores, and associated changes in microspore and pollen homeostasis [238]. Alternatively, under certain stress conditions, male sterility is directly caused by alterations in sugar metabolism, impairing proper energy supply to the developing microspores, and other functional irregularities that cause a failure of gamete formation and/or fertilization

(reviewed in [237]).

Interestingly, despite the negative impact of abiotic stress on sporogenesis and reproduction, under certain instances (a)biotic stress alters the method of gametogenesis in such how that it promotes genetic flexibility and evolutionary adaptiveness of the resulting progeny. More specifically, there's accumulating evidence that temperature stress, and putatively other stresses, induces or enhances meiotic non-reduction and also the associated formation of 2n gametes [239], hence forming a basis for stress-induced sexual polyploidization events. In rose (genus Rosa), for instance, short periods of warmth stress (e.g. 48 h at 36 °C) ectopically induce the formation of parallel and tripolar MII spindles, rather than the traditional perpendicular ones, producing dyads and triads that contain FDR-type 2n gametes [240]. These heat-induced changes in MII spindle orientation will be caused by alterations within the structural set-up of MII cell polarity, e.g. through defects in γ-tubulin-based MT organizing centers, or may alternatively depend on changes within the molecular regulation of MII meiocyte polarity, e.g. for instance through a decreased AtPS1 or JASON functionality [237]. The occurrence of fused, parallel, and/or tripolar spindles in male MII has already been described in several plant species, including Solanum [241], Populus [87], [92], lucerne, Impatiens [242], Agave [99], Lotus tenuis [243] and sweet potato [86], potentially reflecting a gentle sort of heat-induced meiotic non-reduction. Moreover, almost like in rose, high temperatures have also been reported to reinforce male 2n gamete formation in other species, including Lotus tenuis [243], diploid chili (Capsicum annuum L. 'Xianjiao'; 35.5 °C, 4 h) [244], and wheat species [201], suggesting that prime temperatures or heat shocks have a general potential to induce sexual polyploidization and WGD, presumably via ps-mediated male meiotic restitution. Interestingly, recent studies in poplar (Populus L.) have revealed that heat stress might also affect the reductional character of female meiotic organic process, yielding unreduced megaspores capable of inducing sexual polyploidization [245], [246]. Moreover, looking on the timing of the warmth treatment (during MI or MII), female sporogenesis either produces FDR or SDR 2n gametes [245]. altogether flowering plants, female meiosis exhibits a successive-type of cytoki-

nesis and hence doesn't depend upon specific spindle orientations during MII. Thus, during this case, heat-induced meiotic restitution isn't supported MII spindle irregularities, but rather on alterations in cell cycle regulation or semipermeable membrane formation. Alternatively, heat-induced 2n gamete formation may result from defects in synapsis and CO and associated failures in bivalent formation, inducing meiotic non-reduction in a very similar way as in amphidiploid and synaptic meiocytes. In support of this, both Wang et al. [245] and Lu et al. [246] found that the MI pachytene to diplotene stages comprise the foremost optimal period for heat-induced restitution of MI in poplar. Additionally, studies in Allium ursinum have revealed that prime temperatures affect the biogenesis and stability of the synaptonemal complex in early-stage prophase I [247], precluding recombination and CO and reducing the amount of interhomologous recombination events [248]. the same reduction in chiasma frequency has been reported in heat-stressed grasshoppers, however, during this case, univalents and therefore the associated induction of meiotic restitution have not been observed [249]. Likewise, mild heat stresses (from 22 to 30 °C) in barley were found to induce spatiotemporal alterations in meiotic axis formation and recombinational protein loading, eventually causing alittle but significant reduction in mean chiasma frequency, although without induction of meiotic restitution [250]. These observations all at once suggest that heat-induced meiotic non-reduction through asynapsis only occurs under specific conditions, namely in an exceedingly temperature range that causes an entire loss of chiasmata without impairing meiocyte viability.

Similar to heat stress, short periods of cold also increase the gametophytic ploidy level, however, the underlying mechanism appears completely different. A recent study during a. thaliana revealed that short periods of cold (1–40 h at 4–5 °C) disrupt the ultimate step of meiotic organic process, i.e. post-meiotic cytokinesis and cytomembrane formation, eventually yielding dyads, triads, and monads that contain syncytial microspores [96]. Moreover, since syncytial nuclei fuse before pollen mitosis I then show a standard progression through microsporogenesis, this process generates diploid or polyploid pollen, capable of conferring sexual polyploidization. Cytologi-

cal examination of Arabidopsis PMCs revealed that cold stress doesn't affect meiotic chromosome behavior, as has repeatedly been observed in animal meiosis [251], but instead specifically disrupts the biogenesis of the internuclear radial microtubule arrays (RMAs) at telophase II, which normally function as phragmoplast-like structures that mediate post-meiotic cell membrane formation [252]. Accordingly, subcellular localization of organelles and subsequent deposition of callose at developing MII cell plates is impaired, leading to a partial or complete loss of meiotic cell plate formation. Formation of diploid and polyploid pollen upon exposure to cold has also been observed in several other plant species, including Japanese persimmon (Diospyros kaki Thunb.) [253], Brassica [254] and Dasypyrum [255]. However, for these species, the precise cellular mode of polyploid gamete formation has not yet been resolved. Molecular insights into the mechanism by which cold affects meiotic cell plate establishment may come from observations during a wheat thermosensitive genic male sterile (TMGS) line that shows alterations in MI cell plate assembly upon exposure to low-temperature stress (10 °C) [256], [257]. Large-scale transcriptomics hereby revealed that cold alters the expression of several key actin regulators and other genes implicated within the dynamic organization of the cytoskeleton, like actin-depolymerization factor, profilin, formin, violin, and LIM domain protein, suggesting that cold-induced defects in meiotic cytokinesis may have a transcriptional basis [257]. Moreover, since formins play a task in meiotic RMA formation [88], these proteins are thought to be one amongst the first factors underlying the cold sensitivity of meiotic cell plate formation [237]. Generally, in both mitotic and meiotic cells, low-temperature stress features a direct negative impact on the soundness of microtubules and associated cytoskeletal figures [258], [259]. In budding yeast meiosis, this can be among an arrest of cellular division and an associated down-regulation of genes required for cell cycle progression, meiotic differentiation, and development [260]. supported this, it's thought that meiotic RMA and phragmoplast structures in plants are structurally more sensitive to cold which their disintegration causes alterations in meiotic cell cycle progression, including defects in cell plate formation and polynuclear spore formation. Despite the absence of clear underlying regulatory mechanisms, the impact of adverse temperatures on male sporogenesis and also

the associated induction of sexual polyploidization through 2n gametes constitutes a chic mechanism to extend genomic flexibility (e.g. polyploidy) as an adaptive mechanism to address adverse conditions [96], [240]. Whether this process is actively regulated or forms an indirect consequence of structural defects in meiotic biological process remains elusive and forms a crucial subject of future studies

3. Somatic polyploidization

3.1. Natural pathways for somatic polyploidy in plants

Whole-genome doubling in plants doesn't only depend upon alterations of the meiotic cell cycle but might also be conferred by somatic ploidy instability [54], [181]. Indeed, the ectopic induction of polyploidy in mitotically dividing somatic or reproductive tissues forms an alternate mechanism for inducing WGD in plants. However, whether such ectopic events of ploidy increase actually result in a stable transgenerational induction of whole-genome duplication largely depends on the mode of reproduction and therefore the affected tissue type. In plants with a vegetative mode of reproduction, ectopic genome duplication in tissues required for asexual propagation (stolons, bulbs, rhizomes) may result in the establishment of stable polyploid lineages. In contrast, in plants that reproduce sexually, only somatic polyploidization events within the L2 layer [280], that provides rise to the reproductive tissues, and in (pre-)meiotic or gametophytic cells, like micro-and megaspores [281], cause a transgenerational fixation of polyploidy. Ectopic polyploidization events in other tissue types do provide a short lived increase in ploidy, but don't seem to be maintained within the next generation, and intrinsically cannot form a basis for evolutionary WGD events.

In theory, somatic polyploidization in plants can originate from two different mechanisms; endoreduplication and endomitosis. Although both mechanisms confer duplication of genomic DNA content, endoreplication basically involves a terminal switch from the mitotic G1-S-G2-M cell cycle to repeated cycles of S- and G-phases, generating chromosomes with multiple sister chromatids (e.g. polytonal), whereas endomitosis is caused by a selected loss of the M phase, yielding cells with a duplicated number of

chromosomes [247], [282]. Endoreduplication is quite rare in animals but common in plants, and is believed to supply a cellular mechanism for the rapid increase of metabolic activity and cell size in specific organ types [283], [284], [285]. However, despite its biological relevance, endoreduplication has only during a few cases been reported in reproductive tissues [286]. Moreover, since this only occurred in artificially generated lines (e.g. AP3::FZR OE) and eventually led to an arrest of subsequent embryo development [287], ectopic induction of endoreduplication is possibly not a typical mechanism for transgenerational induction of WGD. Also, ectopic genome doubling through endoreduplication has often been related to terminal differentiation [284] and organic process arrest and, in additional extreme cases, with tumorigenesis and defects in ploidy stability [282], possibly indicating that it constitutes an evolutionary dead end. In contrast, somatic polyploidy through endomitosis doesn't represent a typical plant process [288], aside from those events occurring in anther tapetum development [289], [290], but instead mostly occurs as an ectopic aberrant cellular division under special conditions [291], eventually yielding cells with a doubled set of chromosomes. Since these cells behave as real tetraploid or polyploid cells, showing normal mitotic organic process and balanced chromosome segregation [292], endomitosis doesn't cause developmental aberrations, hence forming a putative basis for whole-genome duplication. In support of this, several studies have reported the occurrence of ectopic endomitosis (e.g. by antimitotic drugs) as a basis for polyploid tissue induction [293], [294] and, occasionally, for polyploid progeny formation [295]. within the latter cases, the ectopic occurrence of endomitosis specifically occurred in pre-meiotic, meiotic, or gametophytic cells, hence yielding diploid and/or polyploid gametes that were capable of performing sexual polyploidization. supported their mode of formation, diploid gametes resulting from somatic polyploidization events are termed 2x gametes, contrasting with the 2n (unreduced) gametes formed by meiotic restitution [71].

3.2. Cellular mechanisms causing (pre-)meiotic endomitosis and gametophytic ploidy increase

Generally, ectopic induction of endomitosis occurs through alterations within the final

steps of mitotic cellular division, e.g. in chromosome segregation or post-mitotic plasma membrane formation. Indeed, all cellular alterations that impair bipolar chromosome separation after metaphase I or that affect the biogenesis of the internuclear semipermeable membrane at the tip of mitosis may cause ‘mitotic restitution’, eventually resulting in a duplication of the cell's chromosome number (Fig. 2). Bipolar chromosome segregation during anaphase I largely depend upon three factors: (1) intercellular organization of the spindle origins to opposite sides of the cytoplasm; (2) amphitelic attachment of the spindle microtubules to the centromeres through kinetochore functioning [296] and (3) progressive movement of sister chromatids to the spindle poles. Cytological studies in several species have demonstrated that irregularities in one in all these processes, like defects in spindle body duplication in yeast and loss of essential kinetochore components [297], [298], causes an entire failure of mitotic kart division, yielding polyploid endomitotic cells [299]. In plants, similar defects are found to induce chromosomal instabilities, including endomitotic polyploidization. However, reported cases have only been observed under artificial conditions (genetic knock-outs and overexpression) and barely cause polyploid progeny [134], [300].

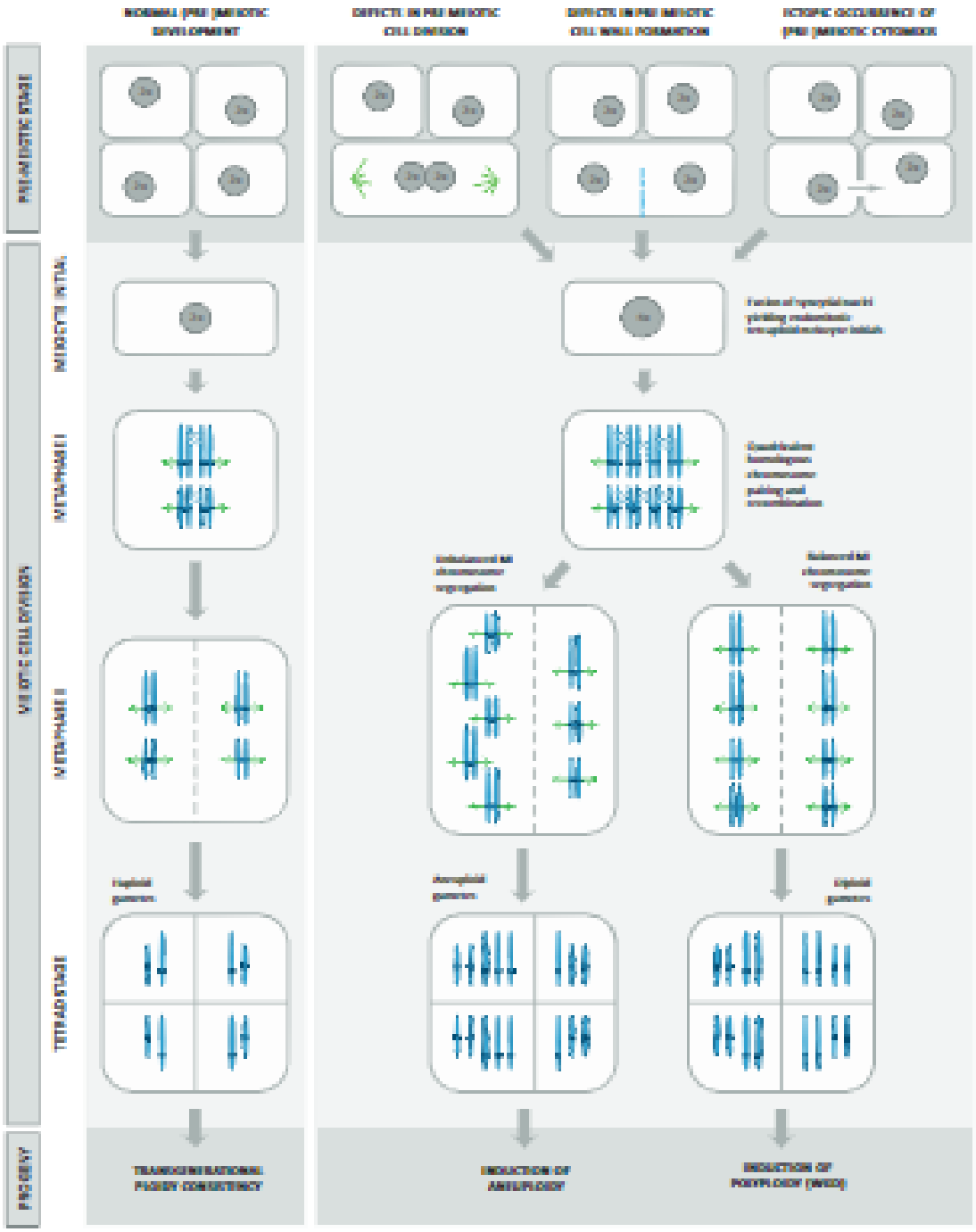

Fig. 2. Mechanisms and outcomes of pre-meiotic endomitosis.

After mitotic chromosome segregation, cytokinesis consolidates the ploidy stability of

the cell lineage by generating an internuclear cytomembrane. In plants, the building of the semipermeable membrane involves many tightly regulated subprocesses, including phragmoplast formation, a fusion of Golgi-derived vesicles, callose deposition, etc. [301], [302], and alterations in each of those processes are found to come up with syncytial nuclei, that eventually fuse to create polyploid endomitotic cells [303], [304], [305], [306]. Studies using Arabidopsis mutants have revealed that strong and prolonged defects in vegetative cell plate formation typically result in lethality (apoptosis), possibly caused by developmental irregularities and progressive genomic instabilities related to uncontrolled polyploidization. In contrast, when defects in vegetative cell wall formation are rather mild and only occur occasionally, associated polyploidization events is tolerated, eventually yielding chimeric mixoploid plants [304], [306]. Moreover, if such mild defects in plasma membrane formation occur in reproductive tissues, like archesporal pre-meiotic or early-stage meiotic cells, associated polyploidization events form a basis for 2x gamete formation and sexual polyploidization. Indeed, cytological studies in a very. thaliana and tomato revealed that cytokinetic defects in meiocyte archesporal cells end in tetraploid and sometimes polyploid meiocyte initials that, upon progression through meiosis I and II, yield functional diploid and polyploid gametes, capable of generating polyploid progeny [306], [307]. However, in line with the autopolyploid nature of resulting meiocytes, MI often shows multivalent pairing and unbalanced chromosome segregation, typically leading to a mixture of polyploid and aneuploid gametes. As such, ectopic induction of pre-meiotic endomitosis through defects in cytokinesis may form a basis for euploid WGD events, but also other, rather minor, or additional changes in chromosome stability, like aneuploidy, nullisomy, and polysomy [304]. As cytokinesis may be a highly regulated process, requiring an intricate interplay between several cellular processes, including cytoskeletal dynamics, cell cycle regulation, vesicle trafficking, lipid metabolism, and signaling pathways, a mess of genetic disorders are described that affect vegetative cell wall formation and associated ploidy stability [308]. However, most of those genetic defects (e.g. knoll, keule, Hinkel, Runkel, Pilz, etc.) cause early-stage lethality [309], whereas only some end in polyploid meiocytes and sexual polyploidization. as an example, Arabidopsis loss-of-function mutants

for SMT2, a sterol-methyl transferase implicated in structural sterol synthesis, exhibit non-lethal defects in vegetative cell wall formation and thereby ectopically from tetraploid meiocytes and diploid gametes in both male and feminine sporogenesis [306]. an identical phenotype has been observed within the specific et2 allele of GSL8, i.e. a callose synthase required for cell wall establishment, whereas other gsl8 alleles cause seedling lethality. These findings taken together indicate that specific defects in several processes implicated in-wall establishment may form a cellular basis for pre-meiotic endomitosis and associated induction of sexual polyploidization.

Ectopic induction of (pre-)meiotic endomitosis and associated formation of 4x meiocytes and 2x gametes might not only result from defects in mitotic biological process but also can originate from cellular defects resulting in migration of chromosomes from one cell to the neighboring one [310]. This process is usually termed cytotoxic and refers to the intercellular transfer of chromatin, single chromosomes, or whole chromosome sets (nuclear migration) through cytoplasmic connections or via direct cell fusion. When occurring in meiotic or pre-meiotic cells, cytotoxic often ends up in erratic meiosis, characterized by defects in chromosome organization and segregation [311], [312], [313], [314], [315]. However, occasionally, cytomixis might also end in the formation of stable poly- or aneuploid meiocytes capable of generating functional gametes with an increased chromosome number, hence forming a putative basis for WGD and karyotype change [310], [316], [317]. In Chrysanthemum zawadskii and C. indicum, for instance, Kim et al. [318] demonstrated that fusion of two adjacent PMCs occasionally occurs early in meiosis I, generating tetraploid meiocytes that proceed through meiosis which consequently yield diploid pollen. Cytomixis has been described in many species [310], [312], [316], [317], [319], [320], [321] and is taken into account a widespread present phenomenon, characteristic of both vegetative and generative tissues. Interestingly, cytomixis is most often detected in meiotic cells, especially in microsporocytes and never in megasporocytes, and thereby predominantly occurs in meiotic prophase I [313], [317], [319], [320], indicating that the first PMC stage structurally or functionally facilitates intercellular chromatin movement. Preliminary studies in several

plants, including Medicago, Chlorophytum and Himalayan poppy suggest that the method of cytomixis is under genetic control which within the case of meiotic cells this presumably involves meiosis-specific genes and associated signal transduction pathways [312], [314]. However, the precise underlying molecular mechanisms and genetic control systems of cytomixis haven't yet been elucidated [322].

3.3. Endomitosis and evolutionary speciation

From the attitude of evolutionary significance, several lines of evidence suggest that (pre-)meiotic endomitosis, either through mitotic or cytokinetic defects or cytomixis, may have contributed to evolutionary speciation, either by inducing WGD events or by conferring other changes in chromosomal stability. Firstly, the ectopic formation of tetraploid meiocytes and also the associated production of 2n gametes through (pre-)meiotic genome doubling has been observed to occur spontaneously in several crops and natural plant species, including Aegilops, Himalayan poppy, Dactylis, grass, Medicago, Festuca, Avena, and rye [310], [312], [323], [324], [325], [326], [327], [328], indicating that it's a present phenomenon, capable of conferring sexual polyploidization. Secondly, in some plant species, (pre-)meiotic endomitosis and polyploid meiocyte formation appear strongly correlated with adverse climate [304], [329], [330], indicating that somatic ploidy change may act as a stress-induced mechanism, conferring adaptive chromosomal change or polyploidization to deal with (a)biotic stress environments. as an example, in interspecific sorghum hybrids, syncytial microsporocytes were only observed under conditions of heat and moisture stress and not under more optimal growing conditions [331]. Similarly, in Lindelofia longiflora (Royle ex Benth.) (Family: Boraginaceae), sporadic events of PMC fusion and early PMC syncytia formation were only observed upon exposure to low temperatures [332]. Also, in Salvia miltiorrhiza PMCs, cytometric chromosome migration is more frequent under high-temperature conditions compared to in restraint conditions [320]. Interestingly, studies in Arabidopsis revealed that the ectopic induction of endomitotic polyploidy through defects in cytokinesis predominantly occurs in flower organs, and only rarely in vegetative tissues, suggesting that the ploidy stability of reproductive tissues is extremely sensitive to defects in cell plate

and semipermeable membrane formation [306]. Abiotic stress-induced alterations in plant cytokinesis and semipermeable membrane establishment may therefore constitute a cellular pathway for the ectopic induction of WGD in reproductive tissues, thereby representing an alternate mechanism of stress-induced 2n gamete formation and sexual polyploidization. Thirdly, (pre-)meiotic endomitosis and particularly cytomixis are found to occur more frequently in polyploid lineages and genetically unbalanced plants, like haploids, aneuploids, and hybrids [321], indicating that these phenomena may have driven WGD and other changes in ploidy and chromosome configuration during plant evolution. Conversely, Sidorchuk et al. [319] found that a duplication of the chromosome number increases the frequency of meiotic cytomixis, suggesting that polyploidy enhances cytomixis and not contrariwise. However, despite this discrepancy, there's ample evidence suggesting that cellular mechanisms inducing somatic endomitosis may have contributed to evolutionary WGD events or other changes in genomic speciation.

4. Karyotype change: aneuploidy, dysploidy, and chromosome rearrangements

4.1. Definitions and overview

Aneuploidy refers to the loss or gain of whole chromosomes, or in a very broader sense parts of chromosomes, relative to a longtime karyotype [333]. Dysploidy on the opposite hand involves structural changes within the genome that don't end in the loss or gain of genetic information, but that alter the gross chromosome number via chromosome rearrangements [334]. Other chromosome rearrangements like translocations, inversions, chromosome fusions, and breakages might not lead to changes in chromosome number and hence dysploidy, but may nevertheless play a task in speciation events. Chromosome rearrangements are often tolerated where aneuploidy is not: monosomies and nullisomics are often lethal in non-polyploid lineages. Somatic aneuploidy is never detected in established plant species, although this might ensue to the decreased viability of aneuploid chromosome complements instead of the absence of aneuploid gametes [335], [336]. However, aneuploid progeny does commonly result from de novo allopolyploids [333] or triploids [77], [337]. Major karyotypic chang-

es like dys- and aneuploidy may result from alterations in vegetative cell division, but normally result from irregularities in meiotic biological process. Meiotic mechanisms inducing both aneuploidy and dysploidy in plants include non-homologous recombination, asynapsis, loss of recombination, and chromosome segregation defects [71], [162], [338], just like as described in human aneuploidy [339]. Interestingly, the identical mechanisms that create to unreduced gametes, e.g. through incorrect spindle fiber alignment, asynapsis, or defects in recombination, may also end in the exclusion of 1 or more chromosomes from the resulting nuclei, yielding aneuploid gametes. “Micronuclei” observable post-meiosis are owing to such excluded chromosomes, either comprising univalents, acentric fragments resulting from non-homologous recombination events or inversion heterozygotes, or “laggard” chromosomes.

4.2. Karyotype change primarily results from non-homologous recombination events

Generally, changes in karyotype configuration primarily result from non-homologous recombination events: interpretations of chromosome fusions, fissions, translocations, and inversions are all readily explicable through this single, experimentally validated mechanism [334]. During meiosis, recognition of homologous chromosomes occurs supported DNA sequence similarity, although with the elimination of repetitive sequences [156]. Although this can be not a replacement concept, exactly how DNA sequence similarity dictates homolog recognition and also the exact cellular mechanisms underlying this recognition process are still unknown [340]. In hybrid genotypes or allopolyploidy genomes, the method of homolog recognition often suffers from the presence of homeologous sequences, e.g. resulting from previous whole-genome duplication events and/or sequence diversification. Stretches of ancestrally-related chromosomes (homeologs) or chromosome fragments are often similar enough to initiate pairing and recombination, physically exchanging dissimilar parental sequences or chromosome parts by establishing physical sites of crossing-over (e.g. chiasmata) [341]. reckoning on the pre-existing degree of fractionation between ancestral subgenomes (how rearranged homeologous chromosomes are relative to every other) crossover events may thereby form the idea for major or minor chromosome rearrangements.

Different genetic and genomic factors influence the chances of non-homologous recombination and hence putative chromosome rearrangement events occurring. Autopolyploids and allopolyploids, newly formed between closely related species, usually have the best degree of sequence similarity between hom(e)logs and hence display a comparatively low degree of genome differentiation thanks to chromosome rearrangements. Indeed, individuals or species with high homology between chromosomes or subgenomes are predicted to point out a greater degree of non-homologous chromosome association than individuals or species with more distantly related subgenomes or chromosomes (see Section 2.3.1). This has been experimentally verified in Brassica haploids and hybrids [342], [343], confirming the notion that both genome structure [344], [345] and therefore the presence of additional unpaired chromosomes [346] also affect non-homologous recombination and genome rearrangement.

Genetic control of non-homologous chromosome pairing is additionally a serious factor affecting the chances and rates of chromosomal rearrangements. In allopolyploid bread wheat, the Ph1 locus effectively prevents non-homologous pairing interactions between closely related chromosomes from the A, B, and D genomes [221]. Recent studies have found that Ph1 comprises a cluster of cyclin-dependent kinase (Cdk-like) genes [221], [222], and presumably regulates meiotic chromosome dynamics, e.g. homoeolog recognition and pairing, by suppressing Cdk2-type activity through the assembly of defective Cdk2-like gene products [223], [226]. More specifically, Ph1 is believed to manage homolog pairing and synapsis by coordinating chromatin remodeling on both homologs chromosomes [196], [200]. In support of this, in allopolyploids, lack of synchronization between homoeologous chromosomes for chromatin conformational changes is believed to scale back the prospect of pairing between homologs [341].

Other genetic loci affecting the frequency of non-homologous chromosome pairing have also been identified in Brassica [347], [348], [349], and recently in Arabidopsis polyploids [231]. However, these genetic loci have a quantitative instead of qualitative effect

on non-homologous pairing and appear to control differently to Ph1. for instance, the pairing locus PrBn in B. napus was found to affect frequency but not a distribution of crossover events at meiosis [349], which suggests a unique regulation of non-homologous pairing to Ph1.

In genera and families with stronger genetic control of non-homologous chromosome pairing, chromosomal rearrangement events is also rarer than in families that are more permissive of non-homologous chromosome associations at meiosis. However, genetic control of non-homologous chromosome pairing continues to be not well understood. In plants, the sole allopolyploid species that this has been characterized at a molecular level is bread wheat (Triticum aestivum) [341], although elucidation of those mechanisms in B. napus is ongoing [350]. within the future and with the appearance of whole-genome sequencing approaches to phylogenetics and ancestral karyotype reconstruction, the link between permissiveness of non-homologous recombination and phylogenetic relationships within genera could also be elucidated.

4.3. Molecular and cytological mechanisms for aneuploidy

Laggard chromosomes are common in hybrids and new allopolyploids and should result from differences in progression through the meiotic or mitotic cell cycle between chromosomes belonging to every of the parental subgenomes [351]. In some wide hybrids, like wheat (Triticum aestivum) × cereal (Pennisetum glaucum) [352], wheat x maize crosses [353] or common barley × H. Bulbosum [354], chromosome elimination by laggard exclusion occurs rapidly during meiosis or early mitotic divisions, eventually eliminating one complete parental chromosome set. This was hypothesized to occur thanks to unequal interaction of centromeres from each parent with the mitotic spindle, and therefore the molecular basis of this effect has since been attributed to the action of centromeric histone H3 (CenH3) [161], [355]. Loss of CenH3 proteins has since been found to cause centromere inactivation and subsequent chromosome loss, and uni parental genome elimination in newly formed hybrids attributed to cross-species differences in centromeric CenH3 incorporation [356]. In intervspecific Hordeum bulbosum

x H. Vulgare hybrid zygotes, CenH3 is gradually lost and not replenished in H. bulbosum chromosomes over successive mitoses after zygote formation [356], a bearing hypothesized to be associated with poor synchronization of H. bulbusom chromosome replication with the cell cycle [351]. Interestingly,the timing of chromatin condensation during chromosome replication is additionally thought to be the first mechanism preventing non-homologous chromosome pairing in allopolyploids [226], [341], as mentioned previously. Hence, the timing of chromosome replication in each subgenome may constitute the first means by which chromosome segregation and interactions are regulated in allopolyploids to confirm meiotic stability. CenH3-mediated chromosome loss is additionally temperature-dependent [351], supporting a typical theme of meiotic and mitotic instability in response to worry, potentially providing a source of novel variation for stress escape.

4.4. Somatic aneuploidy

Somatic aneuploidy has rarely been assessed in plants, but may occur naturally in many established species and sometimes particularly tissue types, particularly in polyploid plants. Somatic aneuploidy has been detected in Arabidopsis suecica [357], a natural allotetraploid, in potato-tomato hybrids [358] and also in several other crop plant species [359]. Aneuploidy is additionally commonly induced by tissue culture (reviewed by Damato [360]), and by several known chemical and environmental mutagens (reviewed by Sharma [359]). In plants, somatic aneuploidy may occur in undifferentiated tissues that then form generative organs, subsequently leading to meiotic production of aneuploid progeny. Somatic aneuploidy can also be tolerated at high levels in plants which will reproduce clonally, and chimeric aneuploid sectors may contribute to the formation of recent plants through vegetative propagation (e.g. tillers or rhizomes).

4.5. the link between chromosome rearrangements and speciation

From an evolutionary or phylogenic perspective, most speciation events appear to involve dysploidy, as these styles of genome change differentiate extant species. Comparative karyotypes between mammals demonstrate this idea readily: overall genome

conservation is high across species, but with chromosome fusions, fissions, and rearrangements differentiating species karyotypes [361]. Modern molecular, genomic, and cytogenetic tools are allowing greater elucidation of historical karyotype rearrangements than ever before. In Arabidopsis [362], Cucumis [363], Brassica [364], Sinapis [365], maize, rice, sorghum, and Brachypodium [366], among others, ancestral karyotypes are elucidated and divergence between extant species revealed to be the results of chromosomal rearrangements.

However, differences between species as a results of karyotype variation offer purely a retrospective viewpoint: what evidence is there for speciation events occurring as a right away results of chromosomal reshuffling, instead of as a function of species divergence over time? Two different models are proposed for the role of chromosome rearrangements in speciation events: e.g. the “hybrid sterility” and “suppressed recombination” model [367]. within the “hybrid sterility” model, chromosome rearrangements aid within the reproductive isolation of overlapping populations through reduced fertility in individuals heterozygous for these chromosome rearrangements [367], [368]. within the “suppressed recombination” model, suppression of recombination over inversion regions may favor the buildup of locally-adapted alleles within this region, aiding in genetic differentiation of geographically-overlapping populations [368], [369]. Chromosome rearrangements distinguishing the karyotypes of two closely related taxa that subsequently hybridize (homoploid hybridization) may additionally lead on to genetic isolation of the hybrids from their parent species if backcrosses are subsequently sterile [370]. The role of chromosome inversions in speciation via reproductive isolation has been studied in fruit flies, mosquitoes, and butterflies [371] and in models for speciation [372], but isn't recommend as a primary drive for speciation in most genera [361]. Meiotic mechanisms like reduction of recombination between diverged homologous chromosomes have occasionally been investigated about speciation [373], but overall far less experimental investigation has taken place into the role of chromosome changes in speciation in plants compared to in animals [66], [374]. Recent research in Helianthus has provided some support for speciation via chromosomal rearrangements and re-

combination suppression, with genomic regions related to particular chromosome rearrangements between species also related to restricted gene flow between these species [375], thereby somewhat contradicting previous research [376]. However, chromosome rearrangements have also been more directly linked to speciation via reproductive isolation during this genus [377]. Dysploidy has also recently been proposed because the most evidence of speciation within the monocot genus [378] although the evidence against this citing lack of allelic differentiation between karyotypically diverse Carex lines has also been obtained [379]. As such, further research is required to work out the precise role of karyotype change, and specifically the genetic effects of chromosome rearrangements in facilitating speciation events [67].

In the angiosperms, which are now known to own several basal polyploidy events [21], genome redundancy provided by historic polyploidization events can give much greater karyotypic variation within species without subsequent loss of fertility [9], as observed in (for example) translocation heterozygotes in allopolyploid rape [380]. If the fertility of a translocation heterozygote, i.e. the F1 between two genotypes differing by chromosomal translocation, isn't significantly reduced, these changes may rarely end in reproductive isolation, a minimum of in polyploid plants. Chromosome rearrangements are the smallest amount disruptive to the genome and absolute gene dosage of all ploidy-related mechanisms for speciation and differentiate the karyotypes of most extant species. Hence, chromosome change may play a cryptic or accessory role within the majority of speciation events.

4.6. Aneuploidy and speciation

Aneuploidy has often been dismissed as a possible consider speciation and karyotype evolution [381], because of the destabilizing effect on organic phenomenon caused by duplication or deletion of some chromosomal regions of the genome but not others. this might lead to altered dosages for genes involved within the same pathways or networks, to potentially detrimental effect [382]. However, aneuploidy may additionally confer beneficial effects: improved growth and proliferation is usually a consequence of aneuploidy

in tumors [383] and yeast [384], whether or not examples in additional complex taxa are sparse. Aneuploidy is additionally frequently observed in nature, generally in plants with polyploid genomes or lineages. Examples include Tragopogon [188], Rutidosis grasses [385], Malus [386] and within the complex Hieracium and Pilosella lineages [387]. Recently, evidence for complex hybridization and accompanying aneuploidy resulting in a brand new, established species was also obtained within the Cardamine genus (Asteraceae) [388]. Aneuploidy can even be an intermediate stage within the establishment of novel euploid karyotypes: Arabidopsis triploids bring about to aneuploid progeny that stabilize at either the diploid or tetraploid level after some generations [77]. Moreover, research in Malus also suggests that in some cases aneuploid gametes or cytotypes may have a plus over euploid gametes or cytotypes, contributing to increased heterozygosity and genetic variation [386]. the upper genome redundancy offered by polyploid genomes may allow greater tolerance of chromosome loss compared to diploid genomes. The prevalence of aneuploidy in interspecific hybrids and polyploids also suggests that this phenomenon may occasionally contribute to the establishment of latest karyotypes, as suggested by the few samples of speciation via aneuploidy to date obtained in plants.

4.7. Cryptic aneuploidy in allopolyploids:

homoeologous chromosome substitutions

A style of cryptic aneuploidy in new allopolyploids has recently been discovered. this way of aneuploidy, which has been observed in young allopolyploid Tragopogon micelles [188], [389] and in resynthesized Brassica napus [152] involves loss and gain of closely related homologs, but with retention of overall homeolog dosage balance. As an example of this dosage compensation effect, for closely related whole-chromosome homeologs A1 and B1, a given plant may retain the expected A1-A1 and B1-B1 homologous chromosomes, or instead have a chromosome complement of A1-A1-A1-A1 (nullisomy–tetrasomy) or A1-B1-B1-B1 (monosomy–trisomy); overall chromosome number and “dosage” of homeologs is retained despite cryptic aneuploidy. The mechanistic basis for this effect is maybe associated with poor genetic regulation of homeolog recogni-

tion, i.e. incorrect separation of homologs and homologs by the cell machinery during meiosis [390], let alone selection for gametes maintaining the right copy number of homologous and homeologous chromosomes [152]. The formation of tetravalent during meiosis I and subsequent tetrasomic inheritance (distributed inheritance of 0–4 chromosomes from the tetravalent) has been documented in several autopolyploid species, including blueberry [391], bird's foot clover [392], Heuchera grossulariifolia [393], Paspalum simplex [394] and potato [395]. Partial or intermediate tetrasomic inheritance also can occur (occasional formation of tetravalent), particularly in hybrid species [396]. This dosage compensation mechanism, which rearranges chromosome karyotype without the loss of gene information accompanying other sorts of aneuploidy, has been postulated to steer to speciation after karyotype stabilization [32].

4.8. Dispensable, “B” and sex chromosomes

In some species, specific individuals can contain one or more chromosomes that are additional to the species karyotype; that's, not every member of the species will contain these additional chromosomes. These additional chromosomes comprise several broad categories. “B” chromosomes are generally defined as chromosomes that aren't present in every individual of a species, don't constitute a reproduction of an existing chromosome within the standard species karyotype (“A” chromosome set), don't recombine with other chromosomes at meiosis and are inherited during a non-Mendelian or irregular fashion (reviewed by Jones and Houben [397]). Although B chromosomes do derive from A chromosomes, the common consensus is that B chromosomes don't generally facilitate evolution or drive speciation events; and after all, are generally detrimental “parasites” on the host genome [398]. Heteromorphic sex chromosomes, generally defined as chromosomes that contain sex-determination loci that don't recombine at meiosis [399], also provide an example of a awfully specific style of karyotypic variation within species. Interestingly, the evolution of sex chromosomes may comprise a special case of evolution via chromosome rearrangements, whereby sex chromosomes evolve via suppression of recombination (reviewed by Charlesworth et al. [399]). other forms of “dispensable” chromosomes that don't fit into the above categories are common in fungi

(reviewed by Covert [400]) but have yet to be identified in plants. Further investigation of those phenomena about speciation and with the help of genome resequencing technologies may lend further weight to the role of dispensable chromosomes in plant speciation.

4.9. Environmental stress can trigger ploidy change

The environment may play a significant role in dictating whether and the way chromosome rearrangement and even aneuploidy events can result in speciation. Firstly, positive or negative selection for particular karyotype changes may occur as a results of environmental factors. These karyotype changes is also either novel or pre-existing within populations: minor chromosome rearrangements within species are now known to be common as resequencing becomes increasingly accessible, with insertion/deletion (indel) and translocation variation observed between accessions or cultivars in maize [401], rice [402] and Brassica [380] and with other species predicted to point out similar trends. Environmental selective pressure may care for karyotypic variation within a species within the same way as on more conventional allelic variation, with an identical potential endpoint of speciation and reproductive isolation with sufficient divergence. Secondly, karyotype change may additionally be induced by environmental effects, particularly by affecting non-homologous recombination frequencies [334]. In plants, homologous recombination is understood to be plagued by both biotic and abiotic factors [403], including ionizing and UV radiation [404], temperature, and day/night duration [405]. Specific environmental effects on non-homologous recombination rates are largely unknown. However, the hypothetical conservation of mechanisms leading to both homologous and non-homologous recombination [350] suggests that non-homologous recombination should be similarly littered with environmental conditions, particularly stress. Possibly, karyotype change could also be faster under stressful environmental conditions, which might facilitate the generation of novel genetic diversity and maybe even speciation as an dodging. Future studies may lend weight to the present speculation.

5. Conclusions

Understanding the cytological mechanisms underlying plant speciation events is critical in building correct models for karyotype and genome evolution and informing phylogenetic analysis. Cytological mechanisms underlie and tie together the complex relationship between individual plant genomes, populations, and species. As well, knowledge of the effect of environmental variables on underlying molecular mechanisms contributing to chromosome and ploidy change over generations will help us understand and predict how speciation occurs in response to environmental change. Despite increasingly widespread awareness and recognition of the role of whole-genome duplication events and hybridization as critical processes shaping the flow of plant genome evolution [406], there's still a good deal of uncertainty on the mechanistic processes underlying these phenomena.

In this review, we offer an in depth overview of what we now realize sexual and somatic polyploidization in plants, in addition as recent developments in understanding the role of dysploidy and aneuploidy in speciation. We cover the three main cytological mechanisms accountable for meiotic restitution: alterations in spindle fiber dynamics, defects in meiotic cell plate formation, and omission of the primary or second meiotic division; then persist to debate meiotic restitution in interspecific F1 hybrids as an evolutionary mechanism for allopolyploid speciation, and the way this can be stricken by the degree of relationship between the parental genomes. We discuss genetic control of meiotic restitution events and speculate on how stress-induced meiotic restitution can drive sexual polyploidization under adverse conditions. Up up to now information on molecular and cytological mechanisms and stress responses within the promotion of somatic polyploidization, aneuploidy, dysploidy, and chromosome rearrangements are discussed, and that we show how these lesser-known processes may contribute to speciation.

Not only are mechanistic constraints on karyotype and genome evolution often disregarded, as advance by Schubert and Lysak [334], but terminology like “whole-genome

duplication events" is commonly accustomed gloss over our lack of information of the doubtless long and complicated processes involved in speciation via chromosome change, polyploidy, and interspecific hybridization. Greater awareness of the categories and underlying mechanisms that are accountable for these speciation "events" may aid researchers at the innovative of genomics and phylogenetics to entertain more complex hypotheses and identify genomic clues referring to the evolutionary history of extant species. for instance, chromosomal rearrangements and fragment loss commonly attach to meiotic restitution mechanisms in hybridization events between closely-related species. Hence, cryptic allopolyploidy is also the reason behind any "bursts" of chromosome rearrangements observed in genomes over evolutionary timescales. Divergence times and subsequent allopolyploidization events between species may additionally be assessed in light of data associated with the prospect of genomic rearrangements vs. easy meiotic control in allopolyploids with greater divergence between subgenomes [407]. Greater attention may additionally be paid to the potential role of hybridization without accompanying genome doubling and of chromosome rearrangements in providing functionally adaptive variation and facilitating speciation via specialization to different ecological niches within a population [69], [368].

Meiotic restitution, aneuploidy, chromosome rearrangements, and somatic doubling all constitute cellular mechanisms which will originate ploidy change, particularly in stress response. These mechanisms may all be co-opted as a method for adaptive speciation in response to changing environments, either by providing novel combinations of parent genetic variation as a resource for further environmental selection or by producing transgressive phenotypes through the generation of novel genetic, genomic, and epigenetic variation. Interestingly, a good deal of accumulated evidence is now suggesting that the meiotic and mitotic cell cycles are indeed highly liable to environmental factors, as we discussed previously. Hence, these mechanisms may facilitate diversification and even allow "emergency speciation" in response to environmental stresses. Further research linking molecular mechanisms to cytological behavior to genome evolution and speciation at the population and environmental level are going to be needed to com-

pletely elucidate the complex interactions resulting in these proposed effects.

With the arrival of high-throughput genetic science and up to date advances in DNA sequencing technologies, the time is ripe for experimental investigations into the cellular and molecular origin of plant speciation events [408]. Genomic signatures of cryptic hybridization or genomic introgression events [409], complex evolutionary histories of extant species [388], and also the underlying bases for meiotic stabilization in novel polyploid species [31], [410] may all become amenable to interrogation. as well as recent advances in our understanding of the molecular and cytological mechanisms underlying ploidy change, and therefore the effects of the environment on these important speciation processes, the long run holds promise for a deep understanding of how speciation processes shaped the globe around us.

References

[1] .B. Bremer, K. Bremer, M.W. Chase, M.F. Fay, J.L. Reveal, D.E. Soltis, P.S. Soltis, P.F. Stevens, A.A. Anderberg, M.J. Moore, R.G. Olmstead, P.J. Rudall, K.J. Sytsma, D.C. Tank, K. Wurdack, J.Q.Y. Xiang, S. Zmarzty, A.P. Grp
An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG III Bot. J. Linn. Soc., 161 (2009), pp. 105-121
Google Scholar

[2] R.M. Bateman, P.R. Crane, W.A. DiMichele, P.R. Kenrick, N.P. Rowe, T. Speck, W.E. Stein Early evolution of land plants: phylogeny, physiology, and ecology of the first terrestrial radiation Annu. Rev. Ecol. Syst., 29 (1998), pp. 263-292 Google Scholar

[3].L.E. Graham, M.E. Cook, J.S. Busse
The origin of plants: Body plan changes contributing to a significant evolutionary radiation Proc. Natl. Acad. Sci. U. S. A., 97 (2000), pp. 4535-4540
Google Scholar

[4] P.S. Soltis, D.E. Soltis
The origin and diversification of angiosperms
Am. J. Bot., 91 (2004), pp. 1614-1626
Google Scholar

[5] A.A. Agrawal, M. Fishbein, R. Halitschke, A.P. Hastings, D.L. Rabosky, S. Assmann
Evidence for radiation from a phylogenetic study of plant defenses
Proc. Natl. Acad. Sci. U. S. A., 106 (2009), pp. 18067-18072
Google Scholar

[6] M.D. Bennett, I.J. Leitch
Angiosperm DNA C-values database, release 4.0
(2003)http://www.rbgkew.org.uk/cval/homepage.html
Google Scholar

[7] E.A. Kellogg, J.L. Bennetzen
The evolution of nuclear genome structure in seed plants
Am. J. Bot., 91 (2004), pp. 1709-1725
Google Scholar

[8]M.D. Bennett, I.J. Leitch
Nuclear DNA amounts in angiosperms: targets, trends and tomorrow
Ann. Bot., 107 (2011), pp. 467-590
Google Scholar

[9] A.R. Leitch, I.J. Leitch
Genomic plasticity and therefore the diversity of polyploid plants
Science, 320 (2008), pp. 481-483

Google Scholar

[10] .T.P. Michael
Plant genome size variation: bloating and purging DNA
Brief. Funct. Genomics (2014), 10.1093/BGP/elu1005
(in press) Google Scholar

[11].J.A. Fawcett, S. Maere, Y. Van de Peer
Plants with double genomes may need had a much better chance to survive the Cretaceous-Tertiary extinction event
Proc. Natl. Acad. Sci. U. S. A., 106 (2009), pp. 5737-5742
Google Scholar

[12].M. Ha, E.D. Kim, Z.J. Chen
Duplicate genes increase expression diversity in closely related species and allopolyploids Proc. Natl. Acad. Sci. U. S. A., 106 (2009), pp. 2295-2300
Google Scholar

[13] .K. Vanneste, G. Baele, S. Maere, Y. Van de Peer
Analysis of 41 plant genomes supports a wave of successful genome duplications in association with the Cretaceous–Paleogene boundary Genome Res., 24 (2014), pp. 1334-1347
Google Scholar

[14] M.E. Schranz, S. Mohammad, P.P. Edger
Ancient whole genome duplications, novelty, and diversification: the WGD Radiation Lag-Time Model Curr. Opin. Plant Biol., 15 (2012), pp. 147-153
Google Scholar

[15] S. Magadum, U. Banerjee, P. Murugan, D. Gangapur, R. Ravikesavan

Gene duplication as a serious force in evolution
J. Genet., 92 (2013), pp. 155-161
Google Scholar

[16] .A.H. Paterson, J.E. Bowers, B.A. Chapman
Ancient polyploidization predating divergence of the cereals, and its consequences for comparative genomics Proc. Natl. Acad. Sci. U. S. A., 101 (2004), pp. 9903-9908
Google Scholar

[17].L.Y. Cui, P.K. Wall, J.H. Leebens-Mack, B.G. Lindsay, D.E. Soltis, J.J. Doyle, P.S. Soltis, J.E. Carlson, K. Arumuganathan, A. Barakat, V.A. Albert, H. Ma, C.W. dePamphilis Widespread genome duplications throughout the history of flowering plants
Genome Res., 16 (2006), pp. 738-749
Google Scholar

[18] .O. Jaillon, J.M. Aury, B. Noel, A. Policriti, C. Clepet, A. Casagrande, N. Choisne, S. Aubourg, N. Vitullo, C. Jubin, A. Vezzi, F. Legeai, P. Hugueney, C. Dasilva, D. Horner, E. Mica, D. Jublot, J. Poulain, C. Bruyere, A. Billault, B. Segurens, M. Gouyvenoux, E. Ugarte, F. Cattonaro, V. Anthouard, V. Vico, C. Del Fabbro, M. Alaux, G. Di Gaspero, V. Dumas, N. Felice, S. Paillard, I. Juman, M. Moroldo, S. Scalabrin, A. Canaguier, I. Le Clainche, G. Malacrida, E. Durand, G. Pesole, V. Laucou, P. Chatelet, D. Merdinoglu, M. Delledonne, M. Pezzotti, A. Lecharny, C. Scarpelli, F. Artiguenave, M.E. Pe, G. Valle, M. Morgante, M. Caboche, A.F. Adam-Blandon, J. Weissenbach, F. Quetier, P. Wincker, F.-I. Public The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla
Nature, 449 (2007), pp. 463-467
Google Scholar

[19] .H.B. Tang, X.Y. Wang, J.E. Bowers, R. Ming, M. Alam, A.H. Paterson
Unraveling ancient hexaploidy through multiply-aligned angiosperm gene maps

Genome Res., 18 (2008), pp. 1944-1954
Google Scholar

[20]. Y. Van de Peer, J.A. Fawcett, S. Proost, L. Sterck, K. Vandepoele
The flowering world: a tale of duplications
Trends Plant Sci., 14 (2009), pp. 680-688
Article

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