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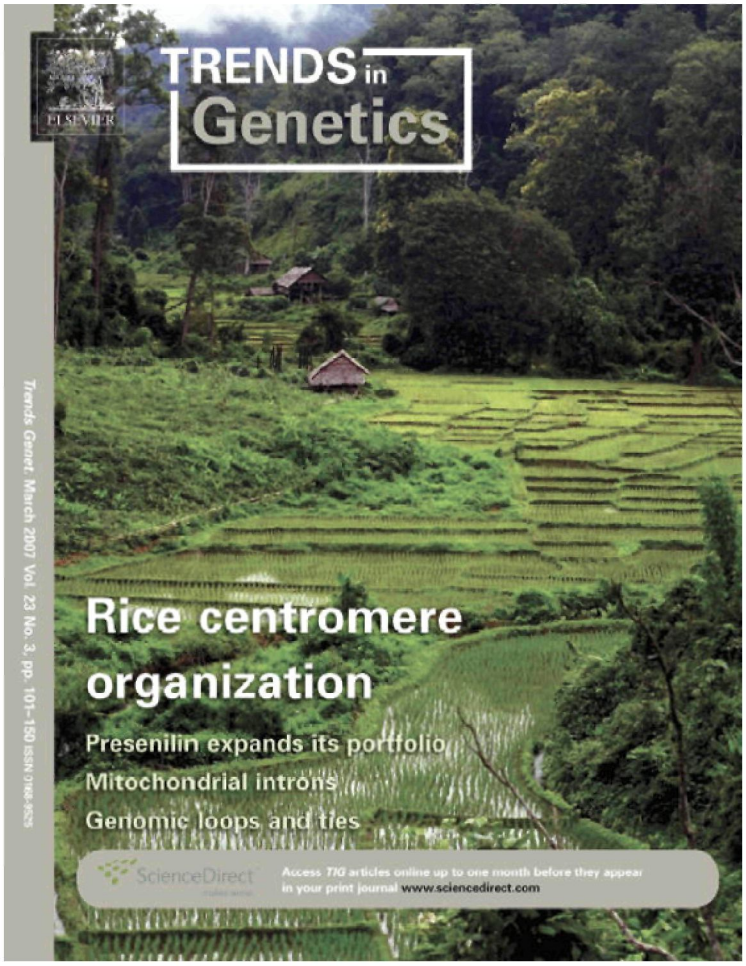

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Plant centromere organization: a dynamic structure with conserved functions

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Although the structural features of centromeres from most multicellular eukaryotes remain to be characterized, recent analyses of the complete sequences of two centromeric regions of rice, together with data from *Arabidopsis thaliana* and maize, have illuminated the considerable size variation and sequence divergence of plant centromeres. Despite the severe suppression of meiotic chromosomal exchange in centromeric and pericentromeric regions of rice, the centromere core shows high rates of unequal homologous recombination in the absence of chromosomal exchange, resulting in frequent and extensive DNA rearrangement. Not only is the sequence of centromeric tandem and non-tandem repeats highly variable but also the copy number, spacing, order and orientation, providing ample natural variation as the basis for selection of superior centromere performance. This review article focuses on the structural and evolutionary dynamics of plant centromere organization and the potential molecular mechanisms responsible for the rapid changes of centromeric components.

Introduction

The centromeres of eukaryotic chromosomes are responsible for sister chromatid cohesion (see Glossary) and for normal chromosomal segregation during mitosis and meiosis, which are essential for development and cellular proliferation in all organisms. These functions are conserved across species, but the DNA components that are involved in kinetochore formation differ greatly, even between closely related species [1–5]. Given the functional importance of centromeres and their rapidly diverging sequence, it is not surprising that many studies have focused on characterizing centromeres in terms of their structure, function and evolution. Deciphering the structural features and the sequence variation of centromeres is essential for a more complete understanding of centromere function(s). Here, we review recent studies on plant centromere organization with respect to the nature, timing, evolutionary processes and biological consequences of centromeric DNA amplification, recombination and rearrangement, thereby providing insights into the conserved functions of this dynamic structure.

Molecular components of plant centromeres

Repetitive DNA is ubiquitous and abundant in centromeric regions of higher eukaryotes. In all flowering plants investigated so far, different centromeres from an individual genome are generally composed of the same types of DNA component, mainly large arrays of centromeric satellite repeats and centromeric retrotransposons (CRs) [6–14]. However, the abundance and the arrangement of these repeats vary substantially, both within and among species [8,10,12,13,15]. In *Arabidopsis thaliana*, centromeres contain 180-base satellite repeats organized in tandem arrays that range from 0.4 to 1.4 Mb on different chromosomes. By contrast, the amount of CentO satellite DNA in rice (*Oryza sativa*) centromeres differs even more [10], ranging from 60 kb to 1.9 Mb on different chromosomes. Highly variable amounts of centromeric satellite DNA (CentC) were also detected in different maize (*Zea mays*) centromeres [6,14,15]. In general, these satellite repeats are specific to centromeric regions, with few copies and no long arrays found elsewhere in the genome [16–19], suggesting that these repeats are crucial for centromere function.

There is also substantial variation in the copy number of satellite repeats in homologous centromeric regions from different ecotypes [20], inbred lines [15] and subspecies

Glossary

Centromere drive: a model that proposes selection for the unequal transmission of competing centromeres in female meiosis.
Kinetochore formation: the formation of a protein structure that assembles on the centromere and links the chromosome to microtubule polymers, which are attached to the mitotic spindle during mitosis and meiosis in eukaryotes. The kinetochore contains two regions: an inner kinetochore, which is tightly associated with the centromeric DNA; and an outer kinetochore, which interacts with the microtubules.
Negative selection: natural selection that selectively removes rare alleles that are deleterious.
Positive selection: natural selection that favors a single allele, resulting in allele frequency continuously shifting in one direction.
Recombinational cold spots: the genomic regions where meiotic recombination is severely or completely suppressed in contrast to the genomic regions where meiotic recombination occurs normally or more frequently.
Sister chromatid cohesion: the joining of the sister chromatids of a replicated chromosome along the entire length of the chromosome, a process that occurs during mitosis. This cohesion cycle is crucial for high-fidelity transmission of chromosomes.

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[10]. For example, the centromeric region of *O. sativa* chromosome 6 contains over fourfold more copies of CentO in the *japonica* subspecies than in the *indica* subspecies [10]. A similar phenomenon was observed recently in different inbred lines of maize [15]. Given that the haplotypes compared in each of these studies diverged from each other between only a few thousand and half a million years ago [21], it is clear that rapid growth and/or shrinkage of centromeric satellite-repeat arrays can occur within short evolutionary time frames.

In addition to copy number variation among organisms, the sequence of centromeric satellite repeats differs markedly among organisms, even among closely related species [2–5]. Short conserved motifs are detected between CentO (rice) and CentC (maize) [10], suggesting that they originated from a common progenitor ~50–70 million years ago (Mya) [22]. However, a recent study using chromatin immunoprecipitation (ChIP) reported that CentO repeats were absent from the entire data set recovered from functional centromeres of *Oryza brachyantha*, a species of wild rice that last shared a common ancestor with rice only ~7–9 Mya [23,24]. A different centromeric satellite repeat, CentO-F, was found in all centromeres of *O. brachyantha*, with no detectable homologous copies in the entire *O. sativa* genome. This finding suggests that old centromeric satellite repeats have completely disappeared and that new centromeric satellite repeats have been generated in the short time since their independent descent from a common ancestor.

Centromere organization was also shown to vary greatly with respect to CRs, such as CRRs (in rice) [10] and CRMs (in maize) [25]. Similar to other long terminal repeat (LTR) retrotransposon families in centromeric, pericentromeric and euchromatic regions [26], the CRRs with two intact LTRs that were identified in centromeric regions are very young evolutionarily, most having been inserted within the past few million years [11,27]. Therefore, it is not surprising that the distribution patterns and abundance of CRs among centromeres in an individual organism or among homologous centromeres from different species are highly variable [10,15,25,28]. In all (non-centromeric) orthologous regions of grass species that have been compared, including for rice, maize, wheat (*Triticum monococcum*), barley (*Hordeum vulgare*) and sorghum (*Sorghum bicolor*), few or no specific LTR-retrotransposon insertions are detected at orthologous loci in different species [29–34], largely owing to their rapid removal by illegitimate recombination and unequal homologous recombination [35,36]. However, some highly conserved CR sequences are present in the centromeric regions of most grasses that have been investigated [37,38]. This finding suggests that CRs evolve more slowly than other retroelements because they are selected for an important centromere function, or are located in a more slowly evolving portion of the genome, or both. An exception to the general conservation of grass CRs was recently reported in *O. brachyantha*, in which CRR-related sequences were found to be absent from all functional centromeres [23].

Despite their preferential accumulation in centromeric regions, CRRs are present in pericentromeric and euchromatic regions of all 12 rice chromosomes [28]. However, retrotransposons that are not CRs are also present in centromeric regions of maize [39] and rice [12,13]. It is particularly intriguing that >50% of the retrotransposon sequences isolated by ChIP cloning in *Oryza rhizomatis*, a wild rice species that last shared a common ancestor with rice more recently than *O. brachyantha*, show clear homology to previously identified non-CRR families present in both centromeric and non-centromeric regions of rice [23]. This result supports the idea that non-CRRs could be converted to fill a functional role similar to CRRs. It is also possible that some non-CR sequences might be required for the maintenance of centromere function [25,40].

Chromatin structures of plant centromeres

Although there is tremendous divergence in centromeric DNA sequences and marked variation in centromere organization, centromeric chromatins have similar structural features in eukaryotes. In general, centromeric chromatin is distinguished from the surrounding pericentromeric heterochromatin by the presence of a specialized histone H3 called CENH3 (also known as CENP-A). CENH3 replaces the canonical histone H3 and interacts with other core histone proteins to form a specific type of nucleosome that is essential for kinetochore formation [1,41]. Species-specific CENH3 molecules have been identified in all eukaryotes investigated so far, including humans (*Homo sapiens*) [42], budding yeast (*Saccharomyces cerevisiae*) [43], *Drosophila melanogaster* [44], *Arabidopsis* [40], rice [11], maize [25], sugarcane (*Saccharum officinarum*) [45] and *Luzula nivea* [46]. Because CENH3 is present exclusively in functional domains of centromeres [1,4,47], ChIP-based analyses with a CENH3-specific antibody have been used routinely to characterize functional DNA components found to bind to CENH3, such as CentO and CRRs in rice [11] and CentC and CRMs in maize [25]. In a comprehensive ChIP-based analysis using a set of tiled DNA sequences from rice *Cen8* (the centromeric region of chromosome 8), Nagaki *et al.* identified a ~750 kb CENH3-binding domain, which defines the boundaries of functional *Cen8* [11]. The interactions between CENH3 and centromeric repeats (both CRs and centromeric satellite repeats) also have been documented recently in other plants [45,46]. Therefore, it is probable that this interaction is a universal phenomenon in the plant kingdom.

Epigenetic features of plant centromeres

Not all centromeric repeats in a centromeric region are associated with CENH3 [25,40]. For example, two ~1.4 kb CentO blocks (CentO-IV and CentO-V), which are separated from the other three main CentO blocks (CentO-I, CentO-II and CentO-III), are not found in the CENH3-binding domain of rice *Cen8* [11] (Figure 1). It is particularly intriguing that recent observations obtained from neocentromeres in primates [41] and barley [48] convincingly showed that the canonical centromeric repeats are dispensable for attaining some centromere functions. If normal centromeres are lost or inactivated, regions without centromeric repeats can recruit CENH3 and other centromere-associated proteins to assemble a

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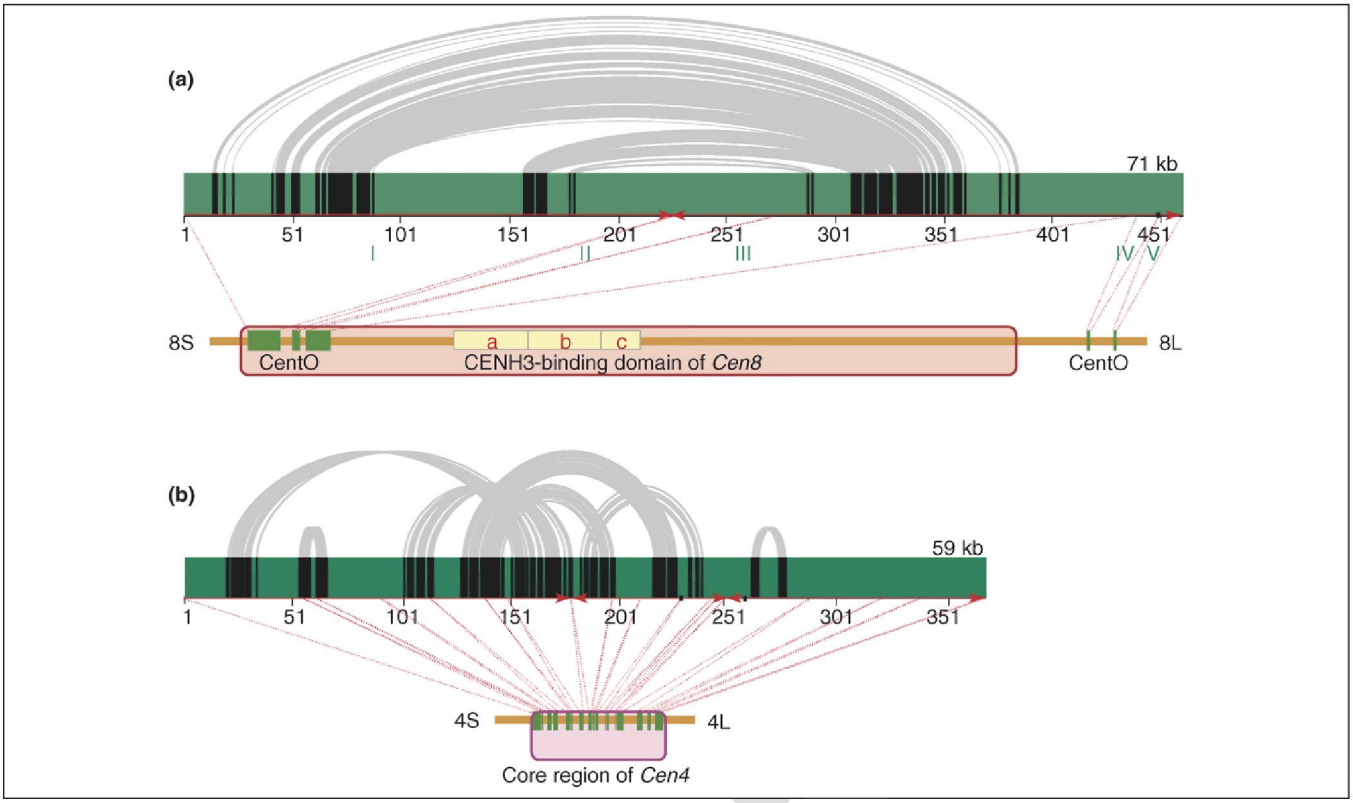

Figure 1. Segmental duplication in centromeric regions of rice. **(a)** The CENH3-binding domain of *Cen8* [11,12]. **(b)** The core region of *Cen4* [13]. Satellite arrays are shown as green blocks in the lower part of each panel, and the monomers are numbered on the basis of their positions in the respective regions. The upper part of each panel shows an enlargement of the satellite monomers (green), with the most identical monomer pairs (as revealed by phylogenetic analyses) shown as black lines [27,56] connected by curved lines. The orientations of satellite-repeat clusters or blocks are also indicated (red arrows). Boxes labeled a, b and c indicate tandemly triplicated segments.

functional kinetochore that promotes chromosome segregation [48–51]. Therefore, it is probable that epigenetic mechanisms have essential roles in mediating centromere assembly, whereas, in most higher eukaryotes, centromeric repeats seem to accumulate after a new centromere has been formed [1,2], and the repeats provide a favorable environment for establishing centromeric chromatin, probably by recruiting sequence-specific binding proteins, to ensure the stable inheritance of centromeres [47,50].

An evolutionary model involving 'centromere drive' [2,52] has been proposed recently to explain the rapid sequence divergence of the genes encoding CENH3 proteins and centromere DNA repeats. According to this model, during female meiosis in plants and animals, centromeres compete by microtubule attachments for inclusion in the single meiotic product that becomes the egg nucleus and is preferentially transmitted to the next generation. This preferential inheritance, although beneficial to the next-generation hopes of a selfish centromere, would be detrimental to the equal likelihood inheritance of parental chromosomes in mendelian genetics. Therefore, it is expected that CENH3 proteins would be selected for nonpreferential properties at the same time that centromere *cis* components (i.e. DNA and epigenetically inherited chromatin features) would be selected for preferential segregation properties. This hypothesis is supported by the findings that CENH3 and/or CENP-C, a poorly conserved centromeric protein, have undergone positive selection, thereby suppressing centromere drive by restoring meiotic parity epigenetically in plants and animals [40,53]. By contrast, both CENH3 and CENP-C show signs of negative selection in budding yeast, in which centromere drive is predicted to be absent, given the consistent equal transmission of all parental centromeres [2]. This model also is reminiscent of the meiotic drive process for maize knob repeats (which are extra-centromeric satellites), which condition preferential segregation and transmission to progeny through female meiosis [54]. The rates of transmission of these knob repeats in female meiosis correlate with the sizes of satellite-repeat arrays [55]. Assuming that centromere variants with expanded satellite-repeat arrays increase microtubule-binding ability during female meiosis in plants and animals, preferential accumulation of centromeric satellite repeats during centromere evolution would be an expected outcome of centromere drive.

Rearrangement of centromeric sequences in *Cen8* and *Cen4* of rice

Segmental duplication and inversion of centromeric DNA revealed by structural and phylogenetic analyses

Recent in-depth analyses of the rice *Cen8* and *Cen4* sequences [27,56] have provided insights into the evolutionary dynamics, processes and molecular mechanisms that have resulted in rapid amplification and variation of centromeric DNA in higher eukaryotes. One unexpected observation is the presence of large, tandemly triplicated

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segments (96 kb, 90 kb and 26 kb, respectively) in the *Cen8* region (Figure 1), accounting for 212 kb of the ~750 kb CENH3-binding domain. According to the insertion dates of shared LTR retrotransposons and the sequence identities between these three segments, it was estimated that two duplication events were involved and occurred successively at similar times within the last ~0.3 million years, and these were followed by partial deletion of one segment. In addition, on the basis of phylogenetic analysis of all satellite monomers in *Cen8*, 48 satellite monomers in CentO block I (in *Cen8*) were found to have respective best (98–99% identical) matches (i.e. monomers) arranged in opposite orientation but conserved order in CentO block III, indicating a recent segmental duplication of the CentO satellite-repeat arrays in the functional domain of *Cen8*.

A similar study was carried out on the core region of rice *Cen4* [56]. Phylogenetic analysis of all 460 satellite monomers in this core region revealed several apparent segmental duplications of CentO satellite arrays and CRRs interspersed in the satellite arrays [56]. Hence, segmental duplication is likely to be a common process driving centromeric DNA amplification, probably in all plant centromeres. An unexpected observation was that most CRRs accumulated in the core region of *Cen4* by rounds of segmental duplication rather than by integration of active elements. Given that most CRRs and the flanking CentO monomers were duplicated <0.3 Mya, it is now easier to understand why the *O. sativa* subspecies *indica* and *japonica*, which diverged from a common ancestor ~0.44 Mya [21], show high levels of haplotype variation in orthologous centromeric regions [10,27]. However, marked amplification of centromeric repeats does not result only from recent segmental duplications. More ancient duplications that have been deleted, have diverged or have been obscured by numerous more recent and overlapping DNA rearrangement events might no longer be detectable. Even in the most recently duplicated CentO satellite-repeat arrays (described earlier), insertions or deletions (indels) from a few monomers up to 130 monomers were frequent [27,56].

Because of the near-complete suppression of homologous chromosome exchange by recombination that is expected in all centromeric regions of rice [57], recombinational conversion and unequal homologous sister-chromatid recombination [58,59] are likely to be the main mechanisms underlying the duplication of CentO satellite-repeat arrays and the array-mediated duplication of CRRs [27,56]. The rates of these types of recombination might be increased by the abundance of highly homogeneous CentO satellite repeats. Although duplication of CentO satellite-repeat arrays and CRRs is frequent in the *Cen4* core region, it should be noted that unequal recombination could also lead to deletion of centromeric repeats, as is predicted to occur in the process of solo-LTR formation. Given the active expansion of CentO satellite-repeat arrays in rice centromeres [10], there are probably selective forces, such as centromere drive [2,52], counteracting the loss of centromeric satellite DNA and CRRs by unequal recombination.

Inversions of some duplicated CentO satellite-repeat arrays were revealed in *Cen8* and *Cen4* (Figure 1). Unequal recombination between homologous sequences that are present in inverted orientation and interspersed in the CentO satellite-repeat arrays would cause inversion of the sequences between the recombining sites. Because of the abundance of CRRs arranged in different transcriptional orientations in the *Cen4* core region, it is possible that recombination between CRRs has mediated the inversion of CentO arrays. This probable mechanism is supported by the presence of LTR retrotransposons (intact or fragmented) at five of the six junction sites of CentO blocks arranged in inverted orientation in *Cen8* and *Cen4* (Figure 1).

Rapid removal of centromeric DNA by unequal recombination and illegitimate recombination

Although LTR retrotransposons have preferentially accumulated in the *Cen8* region and the *Cen4* core region, processes that remove retrotransposon DNA in both regions are also active. These are reflected by the presence of solo-LTRs and various internally deleted or truncated elements [27,56]. Of the 245 LTR-retrotransposon elements or fragments identified in a 1.97 Mb region that contained *Cen8*, only 26.5% are intact elements, whereas solo-LTRs and partially deleted elements account for 24.9% and 46.2%, respectively [27]. Most solo-LTRs are the products of unequal homologous recombination between the two LTRs of a single element [35], whereas deleted or truncated elements have been generated mainly by illegitimate recombination, a mechanism that does not require extensive sequence homology [26,35]. Hence, unequal recombination and illegitimate recombination have removed most of the LTR-retrotransposon sequences from *Cen8*, and similar results were obtained for *Cen4* [56].

Deletion of LTR-retrotransposon DNA by unequal recombination and illegitimate recombination in rice has been found to be exceptionally efficient. It was estimated that at least 190 Mb of retrotransposon DNA has been removed from the rice genome by these processes in the past 4 million years [21,36]. Because the intact LTR retrotransposons in the centromeric regions of rice are as young as those in non-centromeric regions, and because the relative percentages of intact and truncated elements are similar to those observed in the entire rice genome [36], it seems that the elimination of retrotransposon DNA is similarly efficient in all parts of the rice genome. This result agrees with similar findings in *D. melanogaster* [60], for which it has been concluded that rates of DNA sequence loss are identical in euchromatic and heterochromatic regions.

Perhaps the most interesting observation regarding the structural variation of LTR retrotransposons in *Cen8* was the discovery of preferential accumulation of solo-LTRs in a subregion that includes the main CentO blocks in the CENH3-binding domain [27]. The ratio of solo-LTRs to intact elements in this subregion is approximately threefold more than in other centromeric and pericentromeric subregions and is slightly greater than in non-centromeric regions of rice [21], indicating a hot spot for unequal intra-element recombination in *Cen8*. Given the near-complete suppression of meiotic chromosomal exchange in centromeric regions that is indicated by recombinational mapping [57], and given the high ratio

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Box 1. Unanswered questions

Roles of centromeric sequences

Both CRs and centromeric satellite repeats interact with CENH3 in all plant species that have been investigated. Do these two classes of centromeric repeat have similar or distinct roles in centromere function? Non-CRs and single-copy sequences can also interact with CENH3 in some organisms [11,25,40]. Are these CENH3-binding sequences all required for centromere formation? The development of artificial plant chromosomes might provide new tools to study centromere structure and function. What are the minimal requirements for assembly of a highly efficient artificial chromosome?

Divergence of centromeric components

Centromere drive has been proposed to explain the rapid divergence of centromeric DNA and proteins (e.g. CENH3 and/or CENP-C) in most plants and animals. This model might also account for the disappearance of CentO and CRRs from functional centromeres of *Oryza brachyantha*, a wild rice species that diverged from *Oryza sativa* (rice) ~7–9 Mya. However, conserved CR sequences, centromeric satellite repeats and CENH3 were found in multiple grass species: for example, rice and maize, which diverged from each other ~50–70 Mya. Why have centromeric repeats undergone such marked changes in *O. brachyantha* but not in rice and maize? Are there genetic factors that could suppress the process of centromere drive?

Evolutionary stage of rice *Cen8*

The presence of active genes in the CENH3-binding domain of *Cen8* and of low quantities of CentO repeats in the *Cen8* region suggested that *Cen8* might represent an intermediate stage in the evolution of centromeres from genic regions, as in human neocentromeres, to fully mature centromeres that accumulate megabases of homogeneous satellite arrays [11]. However, rapid contraction or expansion, reshuffling and rearrangements of centromeric DNA are proposed to have occurred in *Cen8*. Do these changes disguise the evolutionary stage of *Cen8*?

of solo-LTRs to intact elements that has been observed in rice centromeres [27,56], it is probable that centromere recombination, whether equal or unequal, is regulated by the cells such that it is rarely associated with crossovers.

Concluding remarks

In-depth analyses of plant centromeric sequences, including the first completely sequenced rice centromeres, have deepened our understanding of the dynamic structures, variation and evolution of higher eukaryotic centromeres. High rates of unequal (and presumably equal) recombination in the centromere have been detected, suggesting that crossover suppression is the main factor underlying the traditional perception of centromeres as recombinational cold spots. Rates of DNA removal from centromeric regions also do not seem to be slower than in other parts of the genome, suggesting that selection against inserts in euchromatic regions and/or preferential insertion into heterochromatin are the main reasons for uneven LTR-retrotransposon accumulation. The results indicate that centromere function can be maintained even with high rates of local genome rearrangement, and they suggest that this rearrangement could be a considerable component of centromere drive [2,44]. Therefore, in plants and animals, this provides a basis for competition for more successful female gamete transmission of a centromere that shows superior association with the kinetochore. Although insights into the dynamic structures of plant centromeres have been gained from these exciting observations, many intriguing questions (Box 1) are also raised and need to be further investigated.

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References

1 Henikoff, S. *et al.* (2001) The centromere paradox: stable inheritance with rapidly evolving DNA. *Science* 293, 1098–1102
2 Malik, H.S. and Henikoff, S. (2002) Conflict begets complexity: the evolution of centromeres. *Curr. Opin. Genet. Dev.* 12, 711–718
3 Lamb, J.C. *et al.* (2004) What's in a centromere? *Genome Biol.*5, 239 DOI: 10.1186/gb-2004-5-9-239 (genomebiology.com)
4 Jiang, J. *et al.* (2003) A molecular view of plant centromeres. *Trends Plant Sci.* 8, 570–575
5 Henikoff, S. and Dalal, Y. (2005) Centromeric chromatin: what makes it unique? *Curr. Opin. Genet. Dev.* 15, 177–184
6 Ananiev, E.V. *et al.* (1998) Chromosome-specific molecular organization of maize (*Zea mays* L.) centromeric regions. *Proc. Natl. Acad. Sci. U. S. A.* 95, 13073–13078
7 Heslop-Harrison, J.S. *et al.* (1999) Polymorphisms and genomic organization of repetitive DNA from centromeric regions of *Arabidopsis* chromosomes. *Plant Cell* 11, 31–42
8 Copenhaver, G.P. *et al.* (1999) Genetic definition and sequence analysis of *Arabidopsis* centromeres. *Science* 286, 2468–2474
9 Kumekawa, N. *et al.* (2001) The size and sequence organization of the centromeric region of *Arabidopsis thaliana* chromosome 4. *DNA Res.* 8, 285–290
10 Cheng, Z. *et al.* (2002) Functional rice centromeres are marked by a satellite repeat and a centromere-specific retrotransposon. *Plant Cell* 14, 1691–1704
11 Nagaki, K. *et al.* (2004) Sequencing of a rice centromere uncovers active genes. *Nat. Genet.* 36, 138–145
12 Wu, J. *et al.* (2004) Composition and structure of the centromeric region of rice chromosome 8. *Plant Cell* 16, 967–976
13 Zhang, Y. *et al.* (2004) Structural features of the rice chromosome 4 centromere. *Nucleic Acids Res.* 32, 2023–2030
14 Jin, W. *et al.* (2004) Maize centromeres: organization and functional adaptation in the genetic background of oat. *Plant Cell* 16, 571–581
15 Kato, A. *et al.* (2004) Chromosome painting using repetitive DNA sequences as probes for somatic chromosome identification in maize. *Proc. Natl. Acad. Sci. U. S. A.* 101, 13554–13559
16 Lin, X. *et al.* (1999) Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*. *Nature* 402, 761–768
17 Round, E.K. *et al.* (1997) *Arabidopsis thaliana* centromere regions: genetic map positions and repetitive DNA structure. *Genome Res.* 7, 1045–1053
18 The *Arabidopsis* Genome Initiative. (2000) Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. *Nature* 408, 796–815
19 International Rice Genome Sequencing Project (2005) The map-based sequence of the rice genome. *Nature* 436, 793–800
20 Hall, S.E. *et al.* (2003) Centromere satellites from *Arabidopsis* populations: maintenance of conserved and variable domains. *Genome Res.* 13, 195–205
21 Ma, J. and Bennetzen, J.L. (2004) Rapid recent growth and divergence of rice nuclear genomes. *Proc. Natl. Acad. Sci. U. S. A.* 101, 12404–12410
22 Kellogg, E.A. (2001) Evolutionary history of the grasses. *Plant Physiol.* 125, 1198–1205
23 Lee, H.R. *et al.* (2005) Chromatin immunoprecipitation cloning reveals rapid evolutionary patterns of centromeric DNA in *Oryza* species. *Proc. Natl. Acad. Sci. U. S. A.* 102, 11793–11798
24 Dawe, R.K. (2005) Centromere renewal and replacement in the plant kingdom. *Proc. Natl. Acad. Sci. U. S. A.* 102, 11573–11574
25 Zhong, C.X. *et al.* (2002) Centromeric retroelements and satellites interact with maize kinetochore protein CENH3. *Plant Cell* 14, 2825–2836
26 Bennetzen, J.L. *et al.* (2005) Mechanisms of recent genome size variation in flowering plants. *Ann. Bot. (Lond.)* 95, 127–132

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27 Ma, J. and Bennetzen, J.L. (2006) Recombination, rearrangement, reshuffling, and divergence in a centromeric region of rice. *Proc. Natl. Acad. Sci. U. S. A.* 103, 383–388
28 Nagaki, K. *et al.* (2005) Structure, divergence, and distribution of the CRR centromeric retrotransposon family in rice. *Mol. Biol. Evol.* 22, 845–855
29 Chen, M. *et al.* (1997) Microcolinearity in *sh2*-homologous regions of the maize, rice, and sorghum genomes. *Proc. Natl. Acad. Sci. U. S. A.* 94, 3431–3435
30 Tikhonov, A.P. *et al.* (1999) Colinearity and its exceptions in orthologous *adh* regions of maize and sorghum. *Proc. Natl. Acad. Sci. U. S. A.* 96, 7409–7414
31 Dubcovsky, J. *et al.* (2001) Comparative sequence analysis of colinear barley and rice bacterial artificial chromosomes. *Plant Physiol.* 125, 1342–1353
32 Ma, J. *et al.* (2005) DNA rearrangement in orthologous *orp* regions of the maize, rice and sorghum genomes. *Genetics* 170, 1209–1220
33 Ilic, K. *et al.* (2003) A complex history of rearrangement in an orthologous region of the maize, sorghum, and rice genomes. *Proc. Natl. Acad. Sci. U. S. A.* 100, 12265–12270
34 Lai, J. *et al.* (2004) Gene loss and movement in the maize genome. *Genome Res.* 14, 1924–1931
35 Devos, K.M. *et al.* (2002) Genome size reduction through illegitimate recombination counteracts genome expansion in *Arabidopsis*. *Genome Res.* 12, 1075–1079
36 Ma, J. *et al.* (2004) Analyses of LTR-retrotransposon structures reveal recent and rapid genomic DNA loss in rice. *Genome Res.* 14, 860–869
37 Aragon-Alcaide, L. *et al.* (1996) A cereal centromeric sequence. *Chromosoma* 105, 261–268
38 Jiang, J. *et al.* (1996) A conserved repetitive DNA element located in the centromeres of cereal chromosomes. *Proc. Natl. Acad. Sci. U. S. A.* 93, 14210–14213
39 Nagaki, K. *et al.* (2003) Molecular and cytological analyses of large tracks of centromeric DNA reveal the structure and evolutionary dynamics of maize centromeres. *Genetics* 163, 759–770
40 Talbert, P.B. *et al.* (2002) Centromeric localization and adaptive evolution of an *Arabidopsis* histone H3 variant. *Plant Cell* 14, 1053–1066
41 Choo, K.H. (2001) Domain organization at the centromere and neocentromere. *Dev. Cell* 1, 165–177
42 Palmer, D.K. *et al.* (1991) Purification of the centromere-specific protein CENP-A and demonstration that it is a distinctive histone. *Proc. Natl. Acad. Sci. U. S. A.* 88, 3734–3738
43 Meluh, P.B. *et al.* (1998) Cse4p is a component of the core centromere of *Saccharomyces cerevisiae*. *Cell* 94, 607–613
44 Malik, H.S. *et al.* (2002) Recurrent evolution of DNA-binding motifs in the *Drosophila* centromeric histone. *Proc. Natl. Acad. Sci. U. S. A.* 99, 1449–1454
45 Nagaki, K. and Murata, M. (2005) Characterization of CENH3 and centromere-associated DNA sequences in sugarcane. *Chromosome Res.* 13, 195–203
46 Nagaki, K. *et al.* (2005) Visualization of diffuse centromeres with centromere-specific histone H3 in the holocentric plant *Luzula nivea*. *Plant Cell* 17, 1886–1893
47 Carroll, C.W. and Straight, A.F. (2006) Centromere formation: from epigenetics to self-assembly. *Trends Cell Biol.* 16, 70–78
48 Nasuda, S. *et al.* (2005) Stable barley chromosomes without centromeric repeats. *Proc. Natl. Acad. Sci. U. S. A.* 102, 9842–9847
49 Maggert, K.A. and Karpen, G.H. (2001) The activation of a neocentromere in *Drosophila* requires proximity to an endogenous centromere. *Genetics* 158, 1615–1628
50 Amor, D.J. and Choo, K.H. (2002) Neocentromeres: role in human disease, evolution, and centromere study. *Am. J. Hum. Genet.* 71, 695–714
51 Amor, D.J. *et al.* (2004) Human centromere repositioning 'in progress'. *Proc. Natl. Acad. Sci. U. S. A.* 101, 6542–6547
52 Malik, H.S. and Bayes, J.J. (2006) Genetic conflicts during meiosis and the evolutionary origins of centromere complexity. *Biochem. Soc. Trans.* 34, 569–573
53 Malik, H.S. and Henikoff, S. (2001) Adaptive evolution of Cid, a centromere-specific histone in *Drosophila*. *Genetics* 157, 1293–1298
54 Dawe, R.K. and Cande, W.Z. (1996) Induction of centromeric activity in maize by suppressor of meiotic drive 1. *Proc. Natl. Acad. Sci. U. S. A.* 93, 8512–8517
55 Buckler, E.S. *et al.* (1999) Meiotic drive of chromosomal knobs reshaped the maize genome. *Genetics* 153, 415–426
56 Ma, J. and Jackson, S.A. (2006) Retrotransposon accumulation and satellite amplification mediated by segmental duplication facilitate centromere expansion in rice. *Genome Res.* 16, 251–259
57 Wu, J. *et al.* (2003) Physical maps and recombination frequency of six rice chromosomes. *Plant J.* 36, 720–730
58 Smith, G.P. (1976) Evolution of repeated DNA sequences by unequal crossover. *Science* 191, 528–535
59 Dover, G.A. *et al.* (1982) Molecular drive. *Science* 218, 1069
60 Blumenstiel, J.P. *et al.* (2002) Patterns of insertion and deletion in contrasting chromatin domains. *Mol. Biol. Evol.* 19, 2211–2225

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