Synteny: recent advances and future prospects

Renate Schmidt

Their small sizes have meant that the *Arabidopsis* and rice genomes are the best-studied of all plant genomes. Although even closely related plant species can show large variations in genome size, extensive genome colinearity has been established at the genetic level and recently also at the gene level. This allows the transfer of information and resources assembled for rice and *Arabidopsis* to be used in the genome analysis of many other plants.

Addresses
Max-Delbrück-Laboratorium in der Max-Planck-Gesellschaft, Carl-von-Linné-Weg 10, D-50829 Köln, Germany;
e-mail: rschmidt@mpiz-koeln.mpg.de

Current Opinion in Plant Biology 2000, **3**:97–102

1369-5266/00/$ – see front matter

Abbreviations
cM centi Morgan
RFLP restriction fragment length polymorphism

Introduction

Molecular markers are widely used to study the organisation of plant genomes, and genetic linkage maps based on molecular markers have been assembled for many different plant species. Restriction fragment length polymorphism (RFLP) markers are cDNA, gene or random DNA sequences, which can reveal restriction-site polymorphisms in the DNA of different individuals in a genomic DNA blot hybridisation [1]. The high conservation of gene sequences during evolution allows the use of RFLP markers derived from one species in genetic mapping experiments in closely related species. The use of the same set of RFLP markers for genetic mapping in related species can lead to the construction of comparative genetic maps of these species. Such experiments reveal the degree of conservation of gene repertoire and order of markers between different species (Figure 1).

A limited number of markers are usually used for comparative genetic experiments; this confines the information gained from comparative genetic mapping experiments to the gross chromosomal organisation. Information about areas of the chromosomes that lie between the markers can be obtained only by cloning and characterising these regions in detail. Comparative physical mapping and sequencing experiments can highlight the extent to which local gene order, orientation and spacing are conserved between species (Figure 2).

Given a high degree of genome colinearity at a broader genetic level as well as at the gene level, comparative genome mapping experiments can serve as an efficient tool for transferring information and resources from well-studied genomes, such as those of *Arabidopsis* and rice, to related plants. With this prospect in mind, comparative genome analysis studies have been focussed on the Brassicaceae and the Poaceae families.

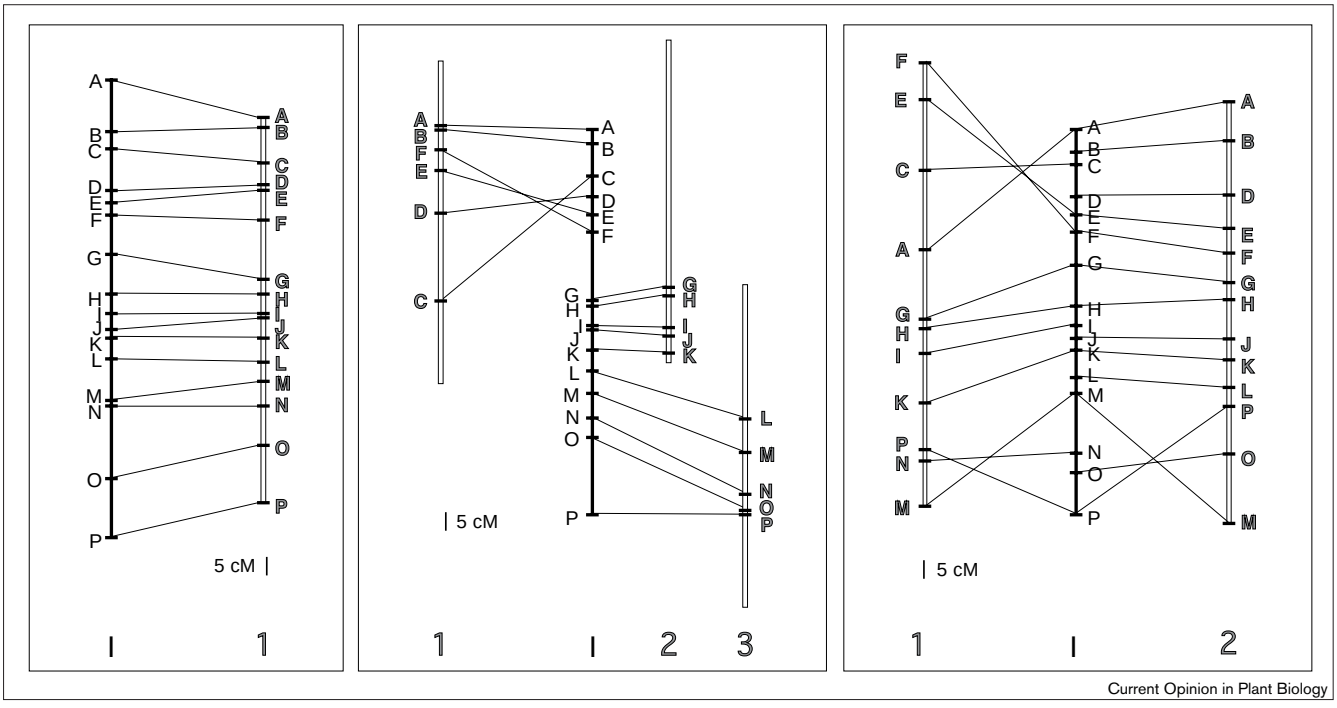
Comparative genetic mapping experiments

The first comparative genetic mapping experiments in plants were performed on members of the Solanaceae family. Tomato, potato and pepper share the same chromosome number, although their genome sizes show a two-fold to four-fold variation. These experiments established that most markers are well conserved between potato and tomato; moreover, an extensive conservation of marker order was found [2,3]. Differences in marker organisation on the 12 tomato and potato chromosomes were explained by five chromosomal inversions [4]. A high conservation of gene repertoire was also found in a comparison of the tomato and pepper genomes [5,6]. A minimum of 22 chromosome breaks had, however, to be assumed to account for the differences in marker arrangement on the tomato and pepper chromosomes. Both inversion and translocation events have been implicated in the genome rearrangements [6].

A remarkable degree of genome conservation has been established in comparative genetic mapping experiments for the Poaceae family, although genome sizes vary as much as 40-fold between some of the species, and despite the fact that they diverged as long as 60 million years ago [7••]. Genetic mapping experiments in allohexaploid wheat revealed that most gene sequences are triplicated on the A, B and D genomes. Furthermore, the three sets of the seven homeologous chromosomes show overall colinearity. Evidence of a few translocation events was, however, also found [8]. Within the Triticeae tribe, extensive colinearity was established, for example, for the homeologous chromosomes of wheat, *Triticum monococcum*, *Triticum tauschii* and barley, and consensus maps were developed [9,10]. Multiple rearrangements distinguish the rye and *Aegilops umbellulata* genomes from the wheat genome [8,11].

Species belonging to the tribe Andropogonae (e.g. maize, sorghum and sugarcane) have also been studied intensively. Maize probes cross-hybridize strongly with sorghum and sugarcane DNA; the first conserved linkage arrangements between sorghum and maize were detected as early as 1990 [12]. The three species display a high degree of genome colinearity, with the sorghum and sugarcane genomes showing the more similar chromosome organisation [13–15]. Most of the sorghum–sugarcane synteny groups show homology to two different regions in the maize genome. These closely match areas of the maize genome, which have previously been shown to be

Figure 1



Patterns of genome colinearity. The use of the same set of molecular markers (A–P) for genetic mapping experiments in different species allows the alignment of the resulting chromosome maps. In the left part of the figure, two chromosome maps (I and 1) are shown, which are completely colinear. The central part of the figure outlines the case in which a chromosome from a particular species (I) shares colinear segments with several chromosomes of another species (1–3) indicating translocation events. Inversions of entire chromosome arms or smaller chromosomal segments are also frequently observed in comparative genetic mapping experiments. If a diploid and a tetraploid species are compared, markers will generally reveal two loci in the tetraploid species. In the right part of the figure, chromosomes 1 and 2 of a tetraploid species are aligned with chromosome I of the diploid species. Depending on the degree of polymorphism between the two species analysed, not all of the markers will reveal two different loci in the tetraploid species, as indicated for example for markers B and N.

duplicated [16]; this is consistent with the view that maize is of tetraploid origin.

Comparative genetic mapping experiments with rice, wheat and maize indicated that genome colinearity is observed even in species belonging to different subfamilies of the Poaceae [17]. A close examination of data for the rice, maize and wheat genomes revealed conservation of gene order for 19 distinct rice linkage segments, which make up the 12 rice chromosomes [18]. These linkage segments can describe the marker arrangement on the 7 wheat and 10 maize chromosomes. The tetraploid nature of the maize genome is also highlighted in this representation, because each of the rice linkage segments corresponds to two different maize chromosomes [18]. The concept of describing colinearity on the basis of rice linkage segments has been very fruitful and has made it possible to make multiple alignments of chromosome maps for the foxtail millet, oats, pearl millet, maize, rice, sugarcane, sorghum and Triticeae genomes [7••]. The inclusion of more markers and particularly sets of markers, which show good correspondence to many different genomes in the colinearity studies [19•], will refine and clarify colinearity relationships [20].

Most importantly, the recognition of putative orthology of monogenic or quantitative traits across different species is facilitated by comparative mapping experiments [21]. This has been elegantly documented by the mapping and cloning of homologues of the *Arabidopsis GAI* gene that encode a gibberellin-response modulator from maize, rice and wheat. Both the wheat and maize genes correspond to dwarf loci [22••]. Similar studies were performed with pathogen resistance gene homologues; in these cases, however, resistance-gene-like sequences were frequently found in non-syntenic map positions [23]. This finding can be explained by rapid reorganisation of regions encoding resistance genes [23].

The aligned maps can be exploited to identify many different markers from a variety of species for a given genomic region. This is especially useful for fine-scale mapping or map-based cloning experiments. Such experiments also detect minor rearrangements, which can disturb the overall colinearity [24,25,26•].

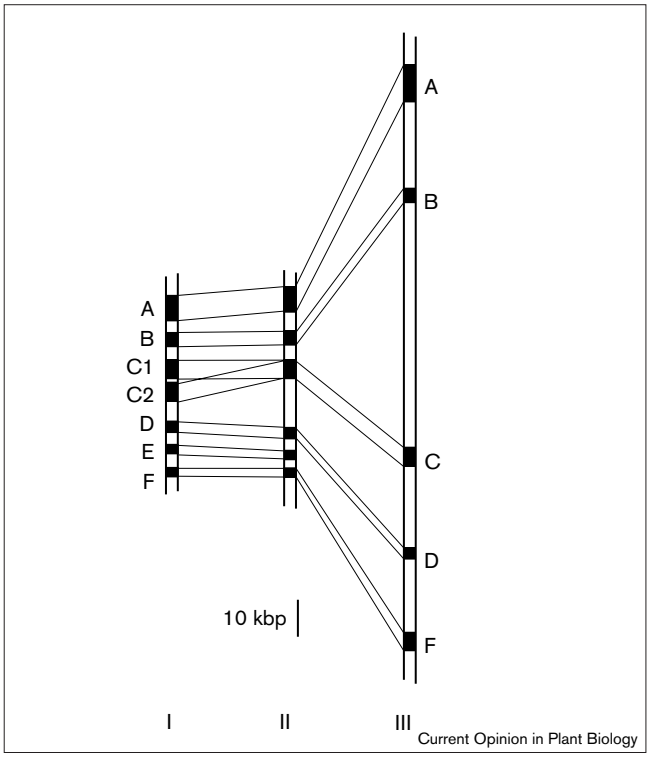
In the Brassicaceae family, the *Brassica* species have been thoroughly studied using comparative genetic mapping experiments. An almost complete conservation of gene

repertoire was found. In spite of similar genome sizes, *Brassica oleracea*, *Brassica rapa* and *Brassica nigra* display different chromosome numbers, and their genomes are distinguished by multiple rearrangements. The mapping experiments also revealed extensive duplications, with many of the chromosomal segments being present in three copies [27]. The view that genomes of species belonging to the Brassicaceae are distinguished by a large number of translocations and inversions has been further corroborated by genome-wide comparative genetic mapping experiments of *Arabidopsis thaliana* and *B. oleracea*. Colinear segments spanning 3.7–49.6 centi Morgans (cM) were found [28]. A detailed comparison of the *A. thaliana* and *B. nigra* genomes suggests that ~90 rearrangements have taken place since the divergence of these two species; the average length of the colinear segments was estimated at 8 cM. Estimates of divergence time for these species vary widely from 10 to 35 million years; nevertheless, the observed rate of chromosomal rearrangements distinguishing the *A. thaliana* and *B. nigra* genomes is far higher than the values that have been observed in the Poaceae family [29••]. Comparing the *A. thaliana* with the *Brassica* genomes further substantiated the view that the modern diploid *Brassica* species have descended from a hexaploid ancestor [28,29••,30•,31,32].

Microcolinearity

The extensive genome colinearity established in comparative genetic mapping experiments has raised the question of whether such a high degree of colinearity is also found at the level of genes. This has been addressed by characterising and comparing small genomic regions in rice, maize and sorghum [33]. This work revealed that the *sh2* and *a1* genes are physically closely linked in all three species but the distances between the genes vary widely. In maize, *sh2* and *a1* are separated by ~140 thousand base pairs (kbp), whereas in sorghum and rice, they are only 19 kbp apart. Two tandemly repeated copies of the *A1* gene were discovered in sorghum. In contrast, in maize and rice only a single copy of this gene was found in the analysed regions [33]. Comparative sequence analysis of these rice and sorghum regions demonstrated that high degrees of sequence homology between the genomes are limited to exon sequences [34]. It has been noted that this feature can be exploited to identify gene sequences in complex genomes efficiently because only such sequences will cross-hybridise with DNA from related species, whereas repetitive DNA sequences are largely species-specific [35]. A high degree of microsynteny was also found in a comparison of the *adh* region of maize and sorghum [36••]. Nine candidate genes were discovered in a 225 kbp maize sequence. The homologues in sorghum were found in the same order as in maize but in a region spanning <80 kbp. Despite the smaller size of the sorghum *adh* region, evidence of five additional genes was detected. The presence of many retrotransposons causes the maize *adh* region to be larger than that of sorghum [36••]. A similarly detailed study comparing the 22 kDa α-zein cluster in sorghum and maize lead to the same conclusions [37]. Hence, repetitive elements located amid genes contribute considerably to the four-fold difference in the genome sizes of sorghum and maize.

Figure 2



Patterns of microsynteny. A comparative analysis of orthologous genomic regions derived from different species (I–III) at the sequence level reveals a high conservation of gene sequences, which are indicated as black boxes (A–F). In contrast, intergenic sequences do not show significant homologies. Evidence for deletions and duplications of gene sequences have been observed in microsynteny studies; these cases are illustrated in the figure. Gene E is deleted in species III, whereas species I harbours two copies of gene C. Comparison of the arrangement of genes in species differing in genome size (species II and III) shows that some of the differences in genome size can be attributed to size differences in the intergenic regions.

Microcolinearity was also revealed when receptor-like kinase genes were studied in wheat, barley and rice. These genes were tightly clustered: even in the large wheat and barley genomes the gene density in these regions is as high as that generally found in the *Arabidopsis* genome [38•].

So far, microsynteny studies in the Brassicaceae have been performed mainly with comparative physical mapping studies. Genetic and physical mapping of a set of five genes (which are located on a 15 kbp segment of *A. thaliana* chromosome 3) in *B. rapa*, *B. oleracea* and *B. nigra* showed that the five gene sequences were physically closely linked in a single linkage-group in all three *Brassica* species. Additionally, one or two incomplete clusters were found in all three species [39]. The same strategy

has been used to compare the organisation of a 30 kbp segment of *A. thaliana* chromosome 4, which carries six genes with the corresponding regions in *B. nigra* [40]. One region carrying all six genes was documented; however, this genome segment was considerably larger in *B. nigra* than in *A. thaliana*. Additional partial clusters were found in the *B. nigra* genome [40].

A detailed comparison of the *S* locus region from *Brassica campestris* with the homeologous region in *A. thaliana* revealed extensive colinearity at scales smaller than a million base pairs, as well as evidence for small deletions [41•]. Three of the 21 *A. thaliana* genes that map to this 275 kilobase-pair region did not, however, hybridise with *B. campestris* DNA, and no evidence for the presence of the *B. campestris SLG* and *SRK* genes was found in *A. thaliana*. Additional copies of this genomic region were not detected in the *B. campestris* genome [41•].

The characterisation of loci corresponding to an *A. thaliana* segment that carries the *RPM1* pathogen resistance gene flanked by two putative genes, *GTP* and *M4*, in *B. napus*, revealed the presence of six loci, only two of which contained a copy of *RPM1*. All *B. napus* loci displayed similar sizes to that of the *A. thaliana* locus. The data suggest that *RPM1* has been lost by deletion from two of the triplicated loci in the diploid *Brassica* progenitor [30•].

So far, large duplicated segments have not been studied in great detail in *Brassica* species, so an overall assessment of the colinearity of duplicated segments cannot be given. The data obtained so far do, however, suggest the frequent occurrence of inversions and deletions [30•,31,32,39,40].

In some genomic regions, the *Brassica* and *Arabidopsis* homeologous segments are very similar in size, whereas in other areas the size of the *Brassica* homeologue is drastically increased in comparison with its *Arabidopsis* counterpart [30•,39,40,41•]. Nevertheless, genome colinearity is extensive enough to permit the transfer of a lot of information and resources, which have been assembled in the framework of the *Arabidopsis* genome project, to *Brassica* relatives. For example, loci controlling flowering time in *Brassica* are being characterised by exploiting information on the *Arabidopsis* genes that are involved in this mechanism [31,42,43].

Conclusions

In the past few years, many comparative genetic mapping experiments have revealed extensive genome colinearity between plant species belonging to the same family. More recently, microsynteny studies have confirmed that colinearity is also generally observed at the level of genes. Thus, the exploitation of genome colinearity can aid fine-mapping and map-based cloning experiments in many plant species, especially in crop plants that have large genomes. The genetic mapping of agronomically interesting loci is performed in the species with the large genome, and cloning is then performed using information from closely related model organisms for which ample genomic resources have been established. More information on different genomic areas is, however, needed because, for example, the study of pathogen resistance-like genes suggests that the rapid reorganisation of genomic regions can result in non-syntenic map positions for interesting loci.

The microsynteny studies are providing invaluable information on genome organisation. The few case studies undertaken so far indicate that different areas of the genome might show distinct organisational patterns with regard to gene density. The revelation of more information about the structure of large as well as duplicated plant genomes is particularly important because this might provide new avenues for the study of complex genomes.

In the vast majority of cases, comparative mapping experiments have studied species belonging to the same family. Although initial observations indicate that synteny might be extrapolated to more distantly related species [44], these experiments are hampered by the low degree of sequence homology between distantly related species. Although highly conserved gene sequences can be used for the cross-hybridisation experiments, they limit the source of suitable markers for such experiments and consequently a lot of putative conserved linkages might escape detection. Attempts to establish colinearity between the rice and *Arabidopsis* genomes suggest that colinearity has been eroded to the point that it cannot be detected in comparative genetic mapping studies [45••]. However, as the *Arabidopsis* genomic sequencing project nears completion and with the rice genome project underway, future comparisons will rely on sequence homologies and will be performed on computers.

Acknowledgements

I thank M Rossberg and B Schulz for helpful comments on this manuscript.

References and recommended reading

Papers of particular interest, published within the annual period of review, have been highlighted as:

- • of special interest
- •• of outstanding interest

1. Chang C, Meyerowitz EM: **Plant genome studies: restriction fragment length polymorphism and chromosome mapping information.** *Curr Opin Genet Dev* 1991, **1**:112-118.

2. Bonierbale MW, Plaisted RL, Tanksley SD: **RFLP maps based on a common set of clones reveal modes of chromosomal evolution in potato and tomato.** *Genetics* 1988, **120**:1095-1103.

3. Gebhardt C, Ritter E, Barone A, Debener T, Walkemeier B, Schachtschnabel U, Kaufmann H, Thompson RD, Bonierbale MW, Ganal MW *et al.*: **RFLP maps of potato and their alignment with the homoeologous tomato genome.** *Theor Appl Genet* 1991, **83**:49-57.

4. Tanksley SD, Ganal MW, Prince JP, de Vicente MC, Bonierbale MW, Broun P, Fulton TM, Giovannoni JJ, Grandillo S, Martin GB *et al.*: **High density molecular linkage maps of the tomato and potato genomes.** *Genetics* 1992, **132**:1141-1160.

5. Tanksley SD, Bernatzky R, Lapitan NL, Prince JP: **Conservation of gene repertoire but not gene order in pepper and tomato.** *Proc Natl Acad Sci USA* 1988, **85**:6419-6423.

6. Livingstone KD, Lackney VK, Blauth JR, van Wijk R, Jahn MK: **Genome mapping in *Capsicum* and the evolution of genome structure in the Solanaceae.** *Genetics* 1999, **152**:1183-1202.

7. •• Gale M, Devos KM: **Plant comparative genetics after 10 years.** *Science* 1998, **282**:656-659.
The review summarises the achievements of comparative mapping experiments in the past decade.

8. Devos KM, Gale MD: **The genetic maps of wheat and their potential in plant breeding.** *Outl Agric* 1993, **22**:93-99.

9. Van Deynze AE, Nelson JC, Yglesias ES, Harrington SE, Braga DP, McCouch SR, Sorrells ME: **Comparative mapping in grasses. Wheat relationships.** *Mol Gen Genet* 1995, **248**:744-754.

10. Dubcovsky J, Luo M-C, Zhong G-Y, Bransteitter R, Desai A, Kilian A, Kleinhofs A, Dvořák J: **Genetic map of diploid wheat, *Triticum monococcum* L., and its comparison with maps of *Hordeum vulgare* L.** *Genetics* 1996, **143**:983-999.

11. Zhang H, Jia J, Gale MD, Devos KM**: Relationships between the chromosomes of *Aegilops umbellulata* and wheat.** *Theor Appl Genet* 1998, **96**:69-75.

12. Hulbert SH, Richter TE, Axtell JD, Bennetzen JL: **Genetic mapping and characterization of sorghum and related crops by means of maize DNA probes.** *Proc Natl Acad Sci USA* 1990, **87**:4251-4255.

13. Dufour P, Deu M, Grivet L, D'Hont A, Paulet F, Bouet A, Lanaud C, Glaszmann JC, Hamon P: **Construction of a composite sorghum genome map and comparison with sugarcane, a related complex polyploid.** *Theor Appl Genet* 1997, **94**:409-418.

14. Guimarães CT, Sills GR, Sobral BW: **Comparative mapping of Andropogoneae: *Saccharum* L. (sugarcane) and its relation to sorghum and maize.** *Proc Natl Acad Sci USA* 1997, **94**:14261-14266.

15. Ming R, Liu S-C, Lin Y-R, da Silva J, Wilson W, Braga D, van Deynze A, Wenslaff TF, Wu KK, Moore PH, Burnquist W *et al.*: **Detailed alignment of *Saccharum* and *Sorghum* chromosomes: comparative organization of closely related diploid and polyploid genomes.** *Genetics* 1998, **150**:1663-1682.

16. Helentjaris T, Weber D, Wright S: **Identification of the genomic locations of duplicate nucleotide sequences in maize by analysis of restriction fragment length polymorphisms.** *Genetics* 1988, **118**:353-363.

17. Ahn S, Anderson JA, Sorrells ME, Tanksley SD: **Homoeologous relationships of rice, wheat and maize chromosomes.** *Mol Gen Genet* 1993, **241**:483-490.

18. Moore G, Foote T, Helentjaris T, Devos K, Kurata N, Gale M: **Was there a single ancestral cereal chromosome?** *Trends Genet* 1995, **11**:81-82.

19. • Van Deynze AE, Sorrells ME, Park WD, Ayres NM, Fu H, Cartinhour SW, Paul E, McCouch SR: **Anchor probes for comparative mapping of grass genera.** *Theor Appl Genet* 1998, **97**:356-369.
A set of well-characterised probes has been assembled for comparative mapping experiments in grasses. Its use will facilitate the integration of mapping data.

20. Wilson WA, Harrington SE, Woodman WL, Lee M, Sorrells ME, McCouch SR: **Inferences on the genome structure of progenitor maize through comparative analysis of rice, maize and the domesticated Panicoids.** *Genetics* 1999, **153**:453-473.

21. Paterson AH, Lin Y-R, Li Z, Schertz KF, Doebley JF, Pinson SRM, Liu S-C, Stansel JW, Irvine JE: **Convergent domestication of cereal crops by independent mutations at corresponding genetic loci.** *Science* 1995, **269**:1714-1718.

22. •• Peng J, Richards DE, Hartley NM, Murphy GP, Devos KM, Flintham JE, Beales J, Fish LJ, Worland AJ, Pelica F *et al.*: **'Green revolution' genes encode mutant gibberellin response modulators.** *Nature* 1999, **400**:256-261.
The authors illustrate how comparative genetic-mapping studies can be exploited to identify and isolate genes. The cloning of dwarf genes encoding gibberellin-response modulators in wheat and maize is reported.

23. Leister D, Kurth J, Laurie DA, Yano M, Sasaki T, Devos K, Graner A, Schulze-Lefert P: **Rapid reorganization of resistance gene homologues in cereal genomes.** *Proc Natl Acad Sci USA* 1998, **95**:370-375.

24. Foote T, Roberts M, Kurata N, Sasaki T, Moore G: **Detailed comparative mapping of cereal chromosome regions corresponding to the *Ph1* locus in wheat.** *Genetics* 1997, **147**:801-807.

25. Kilian A, Chen J, Han F, Steffenson B, Kleinhofs A: **Towards map-based cloning of the barley stem rust resistance genes *Rpg1* and *rpg4* using rice as an intergenomic cloning vehicle.** *Plant Mol Biol* 1997, **35**:187-195.

26. • Zwick MS, Islam-Faridi MN, Czeschin DG Jr, Wing RA, Hart GE, Stelly DM, Price HJ: **Physical mapping of the *liguleless* linkage group in *Sorghum bicolor* using rice RFLP-selected sorghum BACs.** *Genetics* 1998, **148**:1983-1992.
The paper points out the use of fluorescent *in situ* hybridisation experiments using bacterial artificial chromosome clones as probes for comparative physical mapping experiments.

27. Lagercrantz U, Lydiate D: **Comparative genome mapping in *Brassica*.** *Genetics* 1996, **144**:1903-1910.

28. Kowalski SP, Lan T-H, Feldmann KA, Paterson AH: **Comparative mapping of *Arabidopsis thaliana* and *Brassica oleracea* chromosomes reveals islands of conserved organization.** *Genetics* 1994, **138**:499-510.

29. •• Lagercrantz U: **Comparative mapping between *Arabidopsis thaliana* and *Brassica nigra* indicates that *Brassica* genomes have evolved through extensive genome replication accompanied by chromosome fusions and frequent rearrangements.** *Genetics* 1998, **150**:1217-1228.
A very detailed comparison of genome colinearity in the Brassicaceae revealing an exceptionally high rate of chromosomal rearrangements.

30. • Grant MR, McDowell JM, Sharpe AG, de Torres Zabala M, Lydiate DJ, Dangl JL: **Independent deletions of a pathogen-resistance gene in *Brassica* and *Arabidopsis*.** *Proc Natl Acad Sci USA* 1998, **95**:15843-15848.
This paper describes how duplicated chromosomal regions have been subjected to microsynteny studies. Differences in the organisation of duplicated regions are explained by deletions of changed gene sequences.

31. Lagercrantz U, Putterill J, Coupland G, Lydiate D: **Comparative mapping in *Arabidopsis* and *Brassica*, fine scale genome collinearity and congruence of genes controlling flowering time.** *Plant J* 1996, **9**:13-20.

32. Cavell AC, Lydiate DJ, Parkin IAP, Dean C, Trick M: **Collinearity between a 30-centimorgan segment of *Arabidopsis thaliana* chromosome 4 and duplicated regions within the *Brassica napus* genome.** *Genome* 1998, **41**:62-69.

33. Chen M, SanMiguel P, de Oliveira AC, Woo S-S, Zhang H, Wing RA, Bennetzen JL: **Microcolinearity in *sh2*-homologous regions of the maize, rice, and sorghum genomes.** *Proc Natl Acad Sci USA* 1997, **94**:3431-3435.

34. Chen M, SanMiguel P, Bennetzen JL: **Sequence organization and conservation in *sh2/a1*-homologous regions of sorghum and rice.** *Genetics* 1998, **148**:435-443.

35. Avramova Z, Tikhonov A, SanMiguel P, Jin Y-K, Liu C, Woo S-S, Wing RA, Bennetzen JL: **Gene identification in a complex chromosomal continuum by local genomic cross-referencing.** *Plant J* 1996, **10**:1163-1168.

36. •• Tikhonov AP, SanMiguel PJ, Nakajima Y, Gorenstein NM, Bennetzen JL, Avramova Z: **Colinearity and its exceptions in orthologous *adh* regions of maize and sorghum.** *Proc Natl Acad Sci USA* 1999, **96**:7409-7414.
The most detailed microsynteny study so far, clearly providing evidence for a high degree of colinearity at the gene level between maize and sorghum.

37. Messing J, Llaca V: **Importance of anchor genomes for any plant genome project.** *Proc Natl Acad Sci* 1998, **95**:2017-2020.

38. • Feuillet C, Keller B: **High gene density is conserved at syntenic loci of small and large grass genomes.** *Proc Natl Acad Sci USA* 1999, **96**:8265-8270.
This paper provides evidence of clusters of high gene density in large grass genomes. Repetitive elements are largely absent from these clusters. The resulting high gene density in the clusters is similar to that found in the small *Arabidopsis thaliana* genome.

39. Sadowski J, Gaubier P, Delseny M, Quiros CF: **Genetic and physical mapping in *Brassica* diploid species of a gene cluster defined in *Arabidopsis thaliana*.** *Mol Gen Genet* 1996, **251**:298-306.

40. Sadowski J, Quiros CF: **Organization of an *Arabidopsis thaliana* gene cluster on chromosome 4 including the *RPS2* gene in the *Brassica nigra* genome.** *Theor Appl Genet* 1998, **96**:468-474.

41. Conner JA, Conner P, Nasrallah ME, Nasrallah JB: **Comparative**
• **mapping of the *Brassica S* locus region and its homeolog in *Arabidopsis*: implications for the evolution of mating systems in the Brassicaceae.** *Plant Cell* 1998, **10**:801-812.

A detailed microsynteny study providing evidence of overall genome colinearity. Deletion/insertion of gene sequences does, however, result in disrupted microsynteny.

42. Osborn TC, Kole C, Parkin IAP, Sharpe AG, Kuiper M, Lydiate DJ, Trick M: **Comparison of flowering time genes in *Brassica rapa*, *B. napus* and *Arabidopsis thaliana*.** *Genetics* 1997, **146**:1123-1129.

43. Bohuon EJR, Ramsay LD, Craft JA, Arthur AE, Marshall DF, Lydiate DJ, Kearsey MJ: **The association of flowering time quantitative trait loci with duplicated regions and candidate loci in *Brassica oleracea*.** *Genetics* 1998, **150**:393-401.

44. Paterson AH, Lan T-H, Reischmann KP, Chang C, Lin Y-R, Liu S-C, Burow MD, Kowalski SP, Katsar CS, DelMonte TA *et al.*: **Toward a unified genetic map of higher plants, transcending the monocot–dicot divergence.** *Nat Genet* 1996, **14**:380-382.

45. Devos KM, Beales J, Nagamura Y, Sasaki T: ***Arabidopsis*–rice: will**
•• **colinearity allow gene prediction across the eudicot–monocot divide?** *Genome Res* 1999, **9**:825-829.

A comparison of *Arabidopsis* chromosome 1 sequences and rice expressed sequence tags was performed to identify orthologous genes. The rice sequences were then genetically mapped to assay for colinear segments in the *Arabidopsis* and rice genomes. This paper highlights the difficulties of performing comparative genetic-mapping experiments between distantly related species.