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Review Article

Syntenic mapping: A powerful tool for comparative genomics in plants

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Abstract

Comparative genomics has emerged as a great tool in understanding variations/similarities among various species at molecular level. In classical genetics synteny was used to show that two or more loci are present on same chromosome. Now a day's synteny is being used to answer questions concerning homeology (the remains of completely homologous chromosomes). Chromosome/genome synteny has been observed in closely related species, having several genes with similar map orders. Synteny is helpful in comparing different genomes. It is used in the study of evolution of genomes, observe functional conservation, help in genome annotation and observe genome assembly errors. Synteny among different genomes can be detected by identification of conserved sequence elements among genomes, comparing the conserved proteins with the help of BLASTP or by the combination of both. Numerous tools are available for the detection of synteny among different genomes. Synteny analysis has been used largely to study complex genomes and helped in discoveries at genomic, chromosomal and gene levels. Syntenic mapping in plant breeding holds promising future prospects.

Keywords: Comparative genomics, Synteny, Homeology, Chromosome, Genome, Gene

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Introduction

By the advent of genome sequencing, it has become possible to compare entire genome sequences (Ghiurcuta and Moret, 2014). Comparative genomics is a field of biological research in which the genomic features of different organisms are compared (Xia, 2013). Comparative studies in biology have contributed significantly to understand the evolution of various organisms. It has worked as a great tool in this context which is being used to understand variations/similarities among various species at molecular level (amino acid/nucleic acid). Comparative genomics and its scientific effects have many practical uses (O'Brien et al., 1999). Comparative gene annotation helps to identify orthologos genes across species, especially when genes in similar locations are often orthologous (Ghedin et al., 2004). The first report of comparative genomics is referred to Thomas Morgan who used

chromosome banding techniques to compare genetic maps of different types of *Drosophila* (Morgan, 1910). Comparative genomics has been built around the idea that extensive analysis and comparison can expose components in unexplored genomes. Comparative genetic mapping emerged as an essential tool to identify similarities and differences among species. It enabled the transfer of information between different maps and assisted in reconstruction of ancestral genomes. This condition is known as synteny (Renwick, 1972). Synteny analysis allows close examination of selective and mutational forces working on chromosomal and genome structure (Ghedin et al., 2004). This review summarizes the tools and techniques used in comparative genomics and syntenic analysis.

What is Synteny?

Used in classical genetics "Synteny" (Greek; syn = together, taenia = ribbon) describes the occurrence of more than one loci on the same chromosome of two species (Renwick, 1972). The term was of great importance in the pre-genomics era when entire genome mapping techniques for detection of genes on chromosomes were not present. Concept of synteny has been expanded to answer the questions related to homeology (McCouch, 2001). Homologous genes remain on same chromosomes (synteny) and in same position (collinearity) in the course of evolution (Wang et al., 2012; Coghlan et al., 2005).

Types of Synteny

Comparative genomics depends upon the determination of homology. Homology can further be divided into two classes (i) orthology (across the genomes) and (ii) paralogy (within a genome) Qualitatively, synteny can be dived into different groups depending on the level involved. macrosynteny is the collinearity of the entire chromosomal gene order while microsynteny is the collinearity of few genes across a particular subchromosomal region and mesosynteny is the occurrence of same gene content within a chromosome without collinearity (Table 1) (Hane et al., 2011).

Degree of synteny breaks down over time by different phenomenon such as chromosomal rearrangements, gene gains/losses, and duplications of chromosomes and losses. Analysis of synteny helps scientists to answer questions which are related to the evolution of organisms and gene families. Depending upon the problem at hand the main focus of syntenic study may be upon the genes on a single chromosome on an entire genome or may be conducted between multiple organisms (Gehrmann and Reinders, 2015).

Table-1. Difference between Types of Synteny

Type of Synteny	Gene order	Gene content	Gene density
Macrosynteny	Same	Same	High
Microsynteny	Same	Same	Low
Mesosynteny	Different	Same	Extremely Low

Detection of Synteny

Synteny detection among genomes is done either by identifying long, conserved sequence elements, or by the comparison of conserved proteins with the help of BLASTP, or by the use of both methods together (Altschul et al., 1990; Mural et al., 2002).

1. BLASTP (Basic Local Alignment Search Tool for Proteins) Method: BLASTP compares a protein query sequence against a protein sequence database to find homologous sequences (Altschul et al., 1990).

Usage: It's effective for identifying similar proteins across species, providing insights into evolutionary relationships and functional conservation.

Strengths: Rapid identification of homologous proteins based on sequence similarity.

Limitations: It relies on sequence similarity, which may not capture functional similarities in cases of divergent evolution.

2. Conserved Protein Motif Analysis Method: Identifying conserved motifs involves searching for short, conserved sequence patterns or domains shared among proteins.

Tools: Programs like MEME (Multiple Em for Motif Elicitation) (Bailey et al., 2006) or Pfam database (Finn et al., 2014) can be utilized.

Usage: Helps in identifying functional domains or motifs shared among proteins, even in cases where overall sequence similarity is low.

Strengths: Captures functional conservation beyond overall sequence similarity.

Limitations: May miss distant homologs and relies on known motifs, potentially overlooking novel functional elements.

3. Combined Approach Method: Integrating BLASTP with motif analysis allows for a comprehensive assessment of sequence elements and conserved proteins.

Usage: Maximizes the chances of capturing both

overall sequence similarity and functional conservation.
Strengths: Synergizes the advantages of both methods, providing a more holistic understanding.
Limitations: Increased computational complexity and resource requirements.
4. Orthology Analysis Method: Identifying orthologs involves finding genes in different species that share a common ancestor.
Tools: OrthoFinder (Emms and Kelly, 2019), Orthologous MAtrix (OMA) (Dessimoz et al., 2005) and others help identify orthologous relationships.
Usage: Enhances the understanding of evolutionary relationships and functional conservation.
Strengths: Helps distinguish between orthologs (common ancestry) and paralogs (gene duplications within a species).
Limitations: Sensitivity to the quality of genome annotations and potential misinterpretation in cases of gene loss or complex evolutionary scenarios.
Choosing the appropriate method or combination depends on the specific research question, the nature of the data, and the available computational resources. Integrating multiple approaches often provides a more robust and comprehensive analysis of sequence elements and conserved proteins in genomics. Some important statistical parameters used for the detection of syntenic regions are:
(1) Percentage and length of identical DNA sequence among syntenic blocks
(2) Percentage of genomic sequence in the syntenic blocks
(3) Syntenic blocks distribution in the genomes
(4) Density, order, and content of genes in syntenic blocks
(5) DNA repeats content.
Results are graphically presented indicating the syntenic blocks in corresponding genomes that are used to identify genome rearrangement events (O'Brien et al., 1999).

Methods and Tools Used for Detection and Visualization of Synteny

Syntenic mapping involves comparing the arrangement of genes or other genomic features between different species. Common methodologies of syntenic mapping are discussed here in this manuscript. For the identification homologous regions and conserve gene different bioinformatics. Basic Local Alignment Search Tool (BLAST), is used for the rapid sequence comparison, by directly approximating the alignments which optimizes the measure of local similarity (Altschul et al., 1990). LAST is used for fast and sensitive comparison of large sequences with arbitrarily non-uniform composition (Frith et al., 2010). Gene groups having same gene order at DNA level can be discovered by ORTHOCLUSTER and SyMAP (Zeng et al., 2008; Soderlund et al., 2011).
Genome assembly is a large collection of short DNA sequences brought together in the form of original chromosomes from which the DNA are originated. Synteny analysis depends highly on quality of the assembly quality. High-quality genome assemblies for the species of interest, are required for ensuring accurate representation of gene order and orientation (Rhie et al., 2021). Missing sequences in an assembly may lead to missing gene annotations and subsequently missing orthologous relationships. Synteny analysis is mostly performed on fragmented assembled sequences (Liu et al., 2018).
Orthology Inference is used to Identify orthologous gene pairs to establish synteny. OrthoFinder provide highly accurate orthogroup inference about phylogenetic inference of orthologs, rooted gene trees, gene duplication events, the rooted species tree, and comparative genomics statistics (Emms and Kelly, 2019). Inparanoid (http://inparanoid.cgb.ki.se/) is online database containing collection of pairwise ortholog groups between 17 eukaryotic whole genomes. Assess the collinearity of genes in syntenic blocks, emphasizing conserved gene order and orientation. i-ADHoRe is fast and sensitive tool for genomic homology detection in extremely large data sets (Proost et al., 2012). It is used at protein level for building homologous matrix of genes which is based on the alignment of proteins and detects gene clusters by the identification of diagonal gene groups. (Vandepoele et al., 2002).
Visualizing and interpreting syntenic relationships is done by using different tools. Dot-matrix plots e.g. R2Cat and SyMAP (Husemann and Stoye, 2010; Soderlund et al., 2011) are helpful in visualizing whole genome synteny but does not work for inspecting specific regions. Modern technologies are used for visualization of synteny among different genomes at lower level. While working with large regions or organisms which are sufficiently different, they produce complicated figures (Shaw, 2008). To facilitate the display of relationships between pairs of positions 'Circos' uses a circular ideogram layout (Krzywinski et al., 2009). MCScanX identify putative

homologous chromosomal regions, and align these regions using genes as anchors (Wang et al., 2012). Visualizations for the display of multilevel synteny among multiple organisms can be done by the use of CINTENY, but it cannot visualize exons (Sinha and Meller, 2007). SYNTENY PORTAL is used for the construction, visualization and browsing of synteny blocks. VECTOR GRAPH TOOLKIT OF GENOME SYNTENY AND COLLINEARITY (VGSC) is an online service for the visualization the synteny and collinearity in the common graphical formats (Lee et al., 2016). SYNTENY TRACKER is used to identify homologous synteny blocks among genomes which can tolerate common errors in radiation-hybrid comparative maps which are used for computerized entire genome chromosome rearrangements analysis occurred during the course of evolution (Donthu et al., 2009).6. Evolutionary Analysis: Synteny analysis is helpful in answering questions related to the evolution of organisms and gene families. Examination of the evolutionary forces involved in syntenic conservation such as gene duplications, rearrangements, and selection pressures are important for the selection of specific synteny analysis to be performed (Gehrmann and Reinders, 2015).

Association of syntenic blocks with biological functions is important in understanding the impact of conserved genomic regions. EASYFIG works at multiple levels and is used for the annotation of important blocks, but this is done manually (Sullivan et al., 2011). PROTENY analyzes synteny at the exon level thus helps in revealing homologies among distant genomes (Gehrmann and Reinders, 2015).

Phylogenetic studies including multiple lineages are able to produce more accurate information about evolutionary process giving rise to the modern assemblage of a gene family (Finet et al., 2013; Li et al., 2015). Combination of syntenic mapping with phylogenetic analysis infers the evolutionary relationships and divergence times (Citerne et al., 2013). By the inclusion of genomic synteny data essential information which impacts the identification of the evolutionary history of a gene family which evolved in parallel to the ancestral genome duplication events is discovered (Gao et al., 2018).

Comparisons of multiple genomes is done in order to detect syntenic patterns across a broader evolutionary spectrum. Software including MULTIZ, MAUVE, MUGSY and SIBELIA are mostly used to analyze synteny among highly related genomes (Blanchette et al., 2004; Darling et al., 2004; Angiuoli and Salzberg, 2011; Minkin et al., 2013). Synteny in non-related genomes can be detected by making conserved splice variants by inserting and removing exons from the genes (Long et al., 2003).

Genetic maps are the order of molecular markers in a given chromosome of a particular species. It provides information about the organization of a plant genome (Duran et al., 2009). Syntenic information is integrated with genetic maps to link genomic and genetic data, aiding in marker-assisted breeding or trait mapping (Ahmad et al., 2022). Comparative mapping is an essential method to identify similarities and differences between species and is helpful in the transfer of information between different genetic maps. Comparative mapping also provides assistance for the reconstruction of ancestral genomes (Duran et al., 2009).

Due to modernization of sequencing technologies, the genomic data available in the databases has exponentially expended. However, large portion of this data is of poor quality, producing unreliable results in analyses like genome-wide synteny and gene orthology detection (Liu et al., 2018; Marks et al., 2021; Feron and Waterhouse, 2022; Wang and Wang, 2023). Likewise, the choice of parameters in comparative genomics software can significantly impact the results obtained, as default parameters are typically optimised for particular (usually gold standard) datasets (Buchfink et al., 2021; Emms and Kelly, 2019). Hence a careful validation and quality control of the data is essential for accurate and reliable results of synteny analysis (Almeida-Silva and Van de Peer, 2023).

By combining these methodologies, researchers can gain insights into the genomic conservation and evolution across species, helping understand the functional implications of syntenic relationships.

Table-2. Online Software for Synteny Detection

Software	Functions	References
SynBrowse	➢ Construct synteny blocks among multiple species genome browser database ➢ Visualize and download syntenic relationships ➢ Browse synteny blocks ➢ Download the details of synteny blocks to be used as input	Pan et al., 2005
AutoGRAPH	➢ Constructing and visualizing synteny maps between two or three species. ➢ Determination and display of macrosynteny and microsynteny relationships among species. ➢ Highlighting evolutionary breakpoints.	Derrien et al., 2007
GSV	➢ Allows users to upload files. ➢ Visualize synteny regions between two or more genomes	Revanna et al., 2011
Cinteny	➢ Finding regions syntenic across multiple genomes. ➢ Measuring the extent of genome rearrangement using reversal distance as a measure.	Sinha and Meller, 2007
Orthocluster	➢ Identification and visualization of synteny blocks	Zeng et al., 2008
Synteny Portal	➢ Construct synteny blocks among multiple species. ➢ Visualize and download syntenic relationships as high-quality images ➢ Browse synteny blocks with genetic information ➢ Download the details of synteny blocks to be used as input for downstream synteny-based analyses	Lee et al., 2016
CoGe: SynMap	➢ Generate a syntenic dotplot between two organisms. ➢ Identify syntenic regions.	Haug-Baltzell et al., 2017
Simple Synteny	➢ tool for visualization of microsynteny across multiple species	Veltri et al., 2016
Orthologous Matrix (OMA)	➢ Identify orthologs among many genomes ➢ OMA provides three different types of orthologs: pairwise orthologs, OMA Groups and Hierarchical Orthologous Groups (HOGs)	Dessimoz et al., 2005

Table-3. Standalone Software for Synteny Detection

Software	Operating System/ System Requirement	Synteny Detection	References
Mugsy	➢ x86-64-bit Linux	➢ Multiple alignments of whole genomes.	Angiuoli and Salzberg, 2011
SyMAP	➢ Linux ➢ Mac OSX. ➢ Windows (viewing and querying only) ➢ Intel systems ➢ Multiple CPUs ➢ 64-bit computer ➢ At least 5Gb RAM/CPU	➢ Computing, displaying, and analyzing syntenic alignments between medium-to-high divergent eukaryotic genomes.	Soderlund et al., 2011
Multiz		➢ Align highly rearranged or incompletely sequenced genomes	Blanchette et al., 2004

Mauve	➢ Windows ➢ Linux ➢ Mac OS X ➢ Other Unix like operating system ➢ 32/64-bit Computer ➢ Java version 1.4 or later	➢ Multiple alignment of conserved genomic sequence with rearrangements	Darling et al., 2004
Sibelia	➢ Unix-like operating systems	➢ Finds synteny blocks in multiple closely related microbial genomes.	Minkin et al., 2013
Cyntenator	➢ Linux	➢ Identifies genomic regions of conserved synteny over a large set of diverging species	Ro¨delsperger and Dieterich, 2010
DRIMM-Synteny	➢ Linux	➢ Identifying the synteny blocks in highly duplicated genomes.	Pham and Pevzner, 2010.
i-ADHoRe	➢ Linux	➢ Builds a homologous gene matrix ➢ Detects clusters of genes	Vandepoele et al., 2002; Proost et al., 2012
DAGchainer	➢ Linux	➢ Identifies chains of gene pairs sharing conserved order between genomic regions	Haas et al., 2004
ColinearScan	➢ UNIX platform. ➢ Linux X86 ➢ Linux AMD64 Solaris Sparc	➢ Sequence alignment. ➢ Collinearity between/within chromosome(s).	Wang et al., 2006
MCScan	➢ Linux Cygwin	➢ Scan multiple genomes to identify homologous chromosomal regions. ➢ Align these regions using genes as anchors. ➢ Generates synteny correspondences in Plant Genome Duplication Database.	Tang et al., 2008
r2cat	➢ Computer using Java webStart technology	➢ Visualization for synteny inspection	Husemann and Stoye, 2010
Satsuma	➢ 64-bit Linux ➢ 24 CPUs	➢ Whole-genome synteny alignments.	Grabherr et al., 2010
Easyfig	➢ Mac OS X, ➢ UnixMicrosoft Windows	➢ BLAST comparisons between multiple genomic regions. ➢ Interactively colored figures are generated and visualized.	Sullivan et al., 2011
SyDiG		➢ Uncovers synteny in Distant Genomes.	Jean and Nikolski, 2011
MapSynteny		➢ Create images to show the relationship between genetic maps and large sequences.	Fernandez et al., 2012
MCScanX	➢ Mac OS (via X11) Linux systems	➢ Identify putative homologous chromosomal regions, ➢ Align these regions using genes as anchors.	Wang et al., 2012

SynChro	➢ Linux Mac OS X	➢ Identify conserved synteny blocks. ➢ Reconstructs synteny blocks between pairwise comparisons of multiple genomes.	Drillon et al., 2014
Proteny	➢ Linux ➢ 8 cores, ➢ At least 10GB of memory.	➢ Analyze synteny at the protein level between two organisms.	Gehrmann and Reinders, 2015
OrthoFinder	➢ Linx ➢ Windows ➢ Mac OS	➢ Accurate, Fast, and comprehensive platform for comparative genomics ➢ Finds orthogroups and orthologs ➢ Infers rooted gene trees for all orthogroups ➢ Identifies all of the gene duplication events in those gene trees	Emms and Kelly, 2019
MicroSyn	➢ Windows	➢ Detection of microsynteny in a gene family	Cai et al., 2011

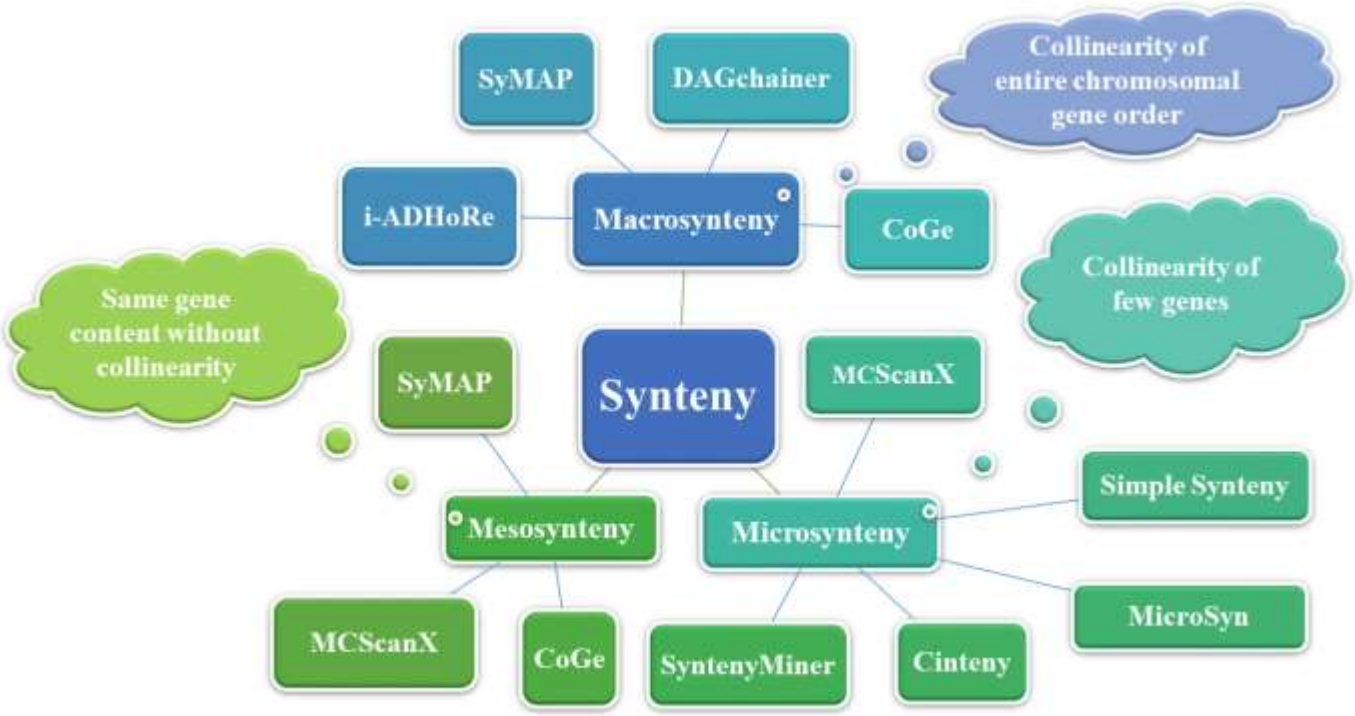

Figure-1. Types Syntenic Mapping and Important Tools for Their Detection

Use of Synteny Mapping in Discovery of New Genes/Genomes

Synteny analysis is a useful method to compare genomes. It is used to understand the evolution of organisms, functional conservation, genome rearrangements, genome annotation and genome assembly errors (Overbeek et al., 1999; Vallenet et al., 2006; Sinha and Meller, 2007; McClean et al., 2010).

A. At Genome Level

Genomics helps in the identifying presence and functions of genes in model organisms which can be

utilized to understand complex organisms using genome synteny. Research demonstrated that rice and wheat genomes had a similar structure and gene order (Wijerathna-Yapa et al., 2023). Comparative maps show that synteny and collinearity exist among eight chromosomes of rice and seven homologous chromosome groups (A, B and D) of wheat (Kurata et al., 1994). Syntenic comparison of the members of *Gramineae* family are the most developed. "Anchor probes" having low-copy cDNA have been used for the development of comparative maps among the members of grass family (Van Deynze et al., 1998).

Whole-genome comparative maps among the members of Solanaceae family have been developed. Tomato and potato genomes show collinearity of DNA markers along the 12 chromosomes (Bonierbale et al., 1998; Bukhari et al., 2022). Various events of genome duplication have indicated the evolution of Arabidopsis and tomato from a common ancestor. It has been observed by the revelation of various distributed networks of synteny (Devos and Gale, 1997; Van Deynze et al., 1998; Ku et al., 2000).

Syntenic blocks having complicated mosaic patterns have been observed between genomes of watermelon, cucumber, and melon by using cross species SSR markers (Zhu et al., 2016). Regions having synteny between sugar beet and rosid species have been detected which consists 1400-2700 genes in Arabidopsis, cacao, grapevine, and poplar (Dohm et al., 2012).

B. At chromosomal Level

A good level of collinearity has been observed among sugarcane and sorghum in four out of eight homology groups. These homology groups are syntenic to 4 sorghum chromosomes about 98- 100%. Four important chromosomal rearrangements have been identified among the remaining 4 sugarcane homology groups and sorghum out of which two are condensations of chromosomes which has reduced the basic sugarcane chromosome set from x = 10 to x = 8. This macro synteny has been observed in other members of Poaceae family like maize and helped in discovering important evolutionary relationships between sugarcane and other member species (Aitken et al., 2014).

Chestnut showed blocks of synteny with ten plant species, with the chestnut physical map alignment ranging from 10 to 39 %. At microsytenic level by the use of QTL-associated genomic sequence chestnuts showed synteny range of 5.4 to 12.9 % with other plant genomes. Both at micro and macro synteny levels in grape, poplar and peach genomes showed the most structural conservation with chestnut. These regions with synteny provide important tool for gene cataloging and defining in the QTL regions for the research advancement in chestnut blight resistance (Staton et al., 2015).

Comparison of chromosome 5 of Arabidopsis with genome of *Brassica napus* identified conserved loci among these two species. Arabidopsis chromosome 5 has 8Mb region which is having 6 highly conserved copies in the genome of *B. napus*. Genetic linkage map alignment of *B. napus* with the genomic sequence of Arabidopsis showed that for specific regions 1cM genetic distance of in *B. napus* is equivalent to 285 Kb DNA sequence of Arabidopsis. Thus, Arabidopsis can be utilized in map-based cloning of genes, identification of candidate genes and development of markers for larger genomes of *Brassica* crop species (Parkin et al., 2002).

C. At Gene Level

Studies have revealed that many cereals are syntenic. Rice and *Brachypodium* may be utilize for the identification genes/genetic markers of interest that may be utilized in breeding and research of wheat (Moore et al., 1995). Synteny played essential role in identification of the Ph1 locus in wheat which controls the fertility and stability of genome has been identified by the use of information obtained from syntenic regions in rice and brome (Griffiths et al., 2006). Conserved micro-collinearity has been observed in some regions of barley, wheat and rice. Linkage analysis DNA markers in barley has shown complete correspondence with their genetic order in rice having distance between linked sequences on rice chromosomes being <1.6 cM or <1×10° bp (1 Mb). Thus, DNA markers separated in this range are collinear in rice and barley (Dunford et al., 1995). The region of wheat chromosome 5 containing VRN1 gene is collinear with a region from rice chromosome 3 which contains the HD-6 quantitative trait locus for heading date (Kato et al., 1999). Collinearity was observed in Sh2/A1 orthologous regions of rice, sorghum, and maize and Triticeae species (Bennetzen and Ramakrishna, 2002; Li and Gill, 2002). Cloning of a gene of one plant species on the basis of position and sequence information of homoeologous region in another genus was first carried out in homologous chromosomal regions of rice (*Oryza sativa*) and barley (*Hordeum vulgare)* (Kilian et al., 1997).

Excellent examples of syntenic mapping have been obtained in legumes by the determination of genes which regulates N-fixing symbiosis relationship between rhizobia and pea by the use of *Lotus japonicus* or *Medicago truncatula* (Endre et al., 2002; Krusell et al., 2002; Limpens et al., 2003; Lévy et al., 2004; Stracke et al., 2004; Tabussam et al., 2022). Microcollinearity analysis between tomato and Arabidopsis for identification of candidate gene which controls ovate shape of tomato fruit. A 105-kb tomato genome sequence was compared against complete genome of Arabidopsis. Tomato clone indicated the conservation of gene order and content with Arabidopsis chromosomes 2-5 at four different segments. The synteny order and content of the tomato gene with these l Arabidopsis segments show that they were derived from same ancestral segment by the means of two or more rounds of large-scale genome duplication events possibly polyploidy (Ku et al., 2000).

High level microsynteny and conservation between the genomes of melon and cucumber has been observed at the DNA level. Comparison of genomic DNA of cucumber and melon flanking around the zucchini yellow mosaic virus resistance locus detected high degree of marker collinearity (Park et al., 2004; Meyer et al., 2008). Syntenic analysis of the gene family MADS-box transcription factor for complete genomes of 51 plants have showed several novel evolutionary patterns of synteny network clusters. Lineage-specific clusters have been from transposition events that controls floral development) and time of flowering in *Brassicales* and development of roots in *Poales*. Type II MADS-box gene group which consists of two large gene clusters have been identified which together control different important phenotypic functions. Conservation of synteny of many less studied classes has been identified in angiosperms (Zhao et al., 2017). Functional syntenic analysis revealed that 61 cotton ESTs involved in drought and heat tolerance had shown functional homology with 55 okra unigenes (Ahmad et al., 2022).

Future Prospects

Syntenic mapping in plant breeding holds promising future prospects. It enables the identification of conserved genomic regions across related species, aiding in the transfer of beneficial traits. This approach enhances the efficiency marker assisted selection, accelerates breeding programs and facilitates the development of with improved yield, resistance and adaptability to changing environmental conditions. As genomic tools advance, syntenic mapping is likely to play crucial role in unraveling complex genetic networks and contribute to sustainable and resilient crop production.

Conclusion

Synteny analysis has been used largely to study complex genomes and helped in discoveries at genomic, chromosomal and gene levels among the members of different plant families. In the future genome/chromosome synteny can be utilized to understand the genomic structure, DNA sequences and gene functions of the less studied crop species.

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Contribution of Authors

Ahmad I: Collected data and wrote manuscript.
Khan AI & Ali S: Contributed in literature review and editing of manuscript.
Rana RM: Conceived idea, prepared outlines and edited the manuscript.

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