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REVIEW

Copy number variation and disease resistance in plants

Aria Dolatabadian[1] · Dhwani Apurva Patel[1] · David Edwards[1] · Jacqueline Batley[1]

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Abstract Plant genome diversity varies from single nucleotide polymorphisms to large-scale deletions, insertions, duplications, or re-arrangements. These re-arrangements of sequences resulting from duplication, gains or losses of DNA segments are termed copy number variations (CNVs). During the last decade, numerous studies have emphasized the importance of CNVs as a factor affecting human phenotype; in particular, CNVs have been associated with risks for several severe diseases. In plants, the exploration of the extent and role of CNVs in resistance against pathogens and pests is just beginning. Since CNVs are likely to be associated with disease resistance in plants, an understanding of the distribution of CNVs could assist in the identification of novel plant disease-resistance genes. In this paper, we review existing information about CNVs; their importance, role and function, as well as their association with disease resistance in plants.

Introduction

With the advent of next-generation sequencing (Bayer et al. 2015) and genotyping methods such as array or bead-based genotyping (Dalton-Morgan et al. 2014; Mason et al. 2015) that generate enormous quantities of data, more genetic associations are being uncovered than ever before (Abel and Duncavage 2013; Golicz et al. 2015). However, little is known about the functional impact of copy number variations (CNVs) at the cellular and organismal level.

The identification of structural variants (SVs), especially CNVs, among the genomes of individuals has provided the rationale to redefine genomes as dynamic entities (Muñoz-Amatriaín et al. 2013). Copy number variations were first considered to reflect human diversity (Zhang et al. 2009), but studies revealed that CNVs are also common in animal (Fadista et al. 2010; Liu et al. 2010; Gazave et al. 2011; Nicholas et al. 2011; Berglund et al. 2012) and plant (Springer et al. 2009; Lee et al. 2015; Trębicki et al. 2015) genomes. Genomic data obtained from different plant species as a part of large-scale sequencing projects highlight CNV as one contributor to natural diversity on the genomic level, for example Bai et al. (2016) have validated 28 functional CNV genes including *OsMADS56*, *BPH14*, *OsDCL2b* and *OsMADS30*, implying that CNVs might be involved in control of flowering time, insect resistance, RNA interference, response to salt and dehydration stress. Most CNV genes were found to be located in non-co-linear positions by comparison to *O. glaberrima*. Several recent studies provide insights into the extent of this type of structural variation in plants; however, fewer studies have been directed towards understanding the role of CNVs in plants (Saxena et al. 2014).

Structural variation within the genome

Genomic variation can be present in many forms, including SNPs (Mason et al. 2015), variable number of tandem repeats (VNTRs; e.g. mini- and microsatellites) (Katoh et al. 2015), presence/absence of transposable elements (e.g. Alu elements; Freeman et al. 2006), and insertions, deletions, duplications, inversions, and copy number variation of DNA

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✉ Jacqueline Batley
Jacqueline.batley@uwa.edu.au

[1] School of Biological Sciences and Institute of Agriculture, University of Western Australia, Crawley, WA 6009, Australia

segments ranging in size from a few base pairs to entire chromosomes (Sebat et al. 2004; Conrad et al. 2006; Redon et al. 2006; Muñoz-Amatriaín et al. 2015). It has recently become clear that much of the natural genetic variation that exists between individuals is due to alterations in the number of copies of genes rather than small differences in the nucleotide sequence (Girirajan et al. 2011; Veltman and Brunner 2012). Understanding how structural variation affects phenotype is, therefore, a major challenge of modern genetics.

Genomic variations that involve segments of DNA larger than 1 kb in length (Feuk et al. 2006) can be classified as a structural variation of which copy number variation (CNVs) and presence–absence variation (PAVs) are the most commonly known. These can be further categorized as microscopic (detectable with optical microscopes) or sub-microscopic ranging from ~ 1 kb to 3 Mb in size (Feuk et al. 2006) depending on the method of their detection (Saxena et al. 2014). CNVs are chromosomal deletions, insertions and/or duplications that are typically defined as DNA segments that are present in a different number of copies when compared to a reference genome (Feuk, et al. 2006; Scherer et al. 2007; Fig. 1), whereas PAVs can be considered an extreme form of CNV, where the sequence is completely missing from one or more individual (Saxena et al. 2014).

There are two main mechanisms of structural variation formation. The first mechanism is known as non-homologous end joining (NHEJ) and requires very low level of sequence similarity at the breakpoints. It is the result of aberrant repair of uneven double-stranded breaks produced following DNA damage (Bignell et al. 2007; Campbell et al. 2008). A second mechanism proposed for repetitive sequences in the genome is termed non-allelic homologous recombination and this requires high sequence similarity at the breakpoints (Kolomietz et al. 2002; Kidd et al. 2008). Several other mechanisms for structural variation production have also been proposed, such as fork stalling and template switching (FoSTeS) (Stankiewicz and Lupski 2010).

CNV detection methods

Several methods have been developed to detect CNVs: quantitative and digital PCR, in situ fluorescent hybridization (Weaver et al. 2010), the paralogue ratio test (Armour et al. 2007), multiplex amplifiable probe hybridization (Armour et al. 2000) and multiplex ligation-dependent probe amplification (Marcinkowska-Swojak et al. 2013). PCR can also identify small translocations and inversions, as well as indel polymorphisms and CNVs (Wang et al. 2006). Microarray-based techniques were among the first used to detect genome-wide variation in human and plant genomes. Initial studies of CNVs in plants have used array-based approaches, for example studies in *Arabidopsis thaliana* (DeBolt 2010), maize (Swanson-Wagner et al. 2010), rice (Yu et al. 2011) and barley (Muñoz-Amatriaín et al. 2013).

Recent advances in massive parallel sequencing technology and development of novel analytical algorithms now allow for the detection of CNVs using short read sequencing data (Xi et al. 2012; Zhao et al. 2013; Wang et al. 2014). Four sequencing-based approaches are commonly used in CNV detection (Table 1): (1) the read depth (RD) approach, which relies on changes in normalized read depth to estimate gains and losses of copies; (2) the read pair (RP) approach, which is based on discordantly mapped read pairs; (3) the split read (SR) approach, which uses gapped read alignments (Alkan et al. 2011) and (4) the assembly (AS) approach

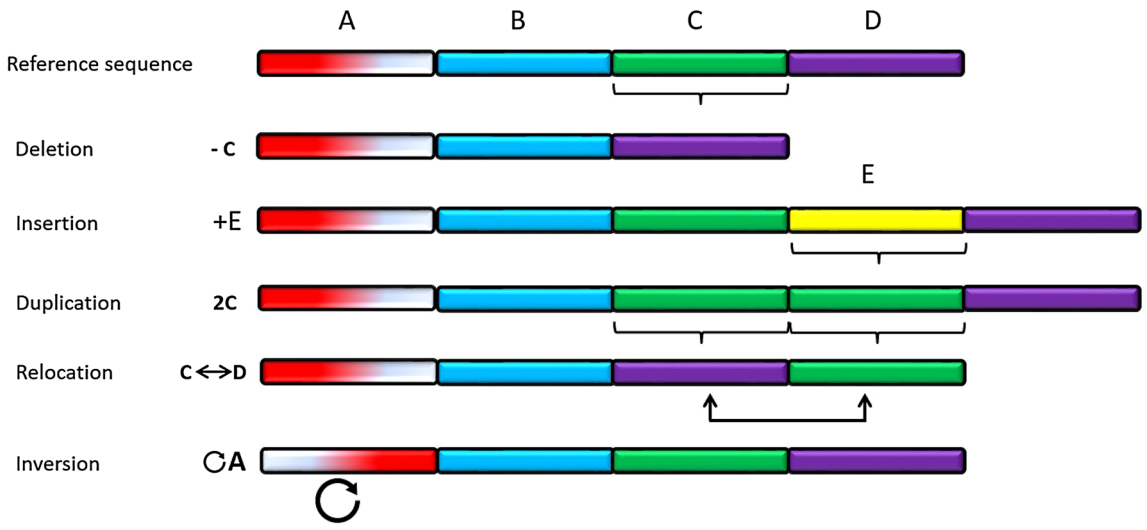

Fig. 1 Some of the types of CNVs. Deletion in segment C, insertion in segment E, duplication in segment C, relocation in segments C and D, inversion in segment A

Table 1 Copy number variation detection analysis tools for whole genome sequencing data

Name	Language	References	Availability
RP: read paired			
BreakDancer	Perl/C++	Chen et al. (2009)	http://gmt.genome.wustl.edu/packages/breakdancer/
Ulysses	Python/R	Gillet-Markowska et al. (2014)	https://github.com/gillet/ulysses
SR: split read			
PRISM	C	Jiang et al. (2012)	http://compbio.cs.toronto.edu/prism/
Gustaf	C++	Trappe et al. (2014)	http://www.seqan.de/projects/gustaf/
RD: read depth			
cm.MOPS	R	Klambauer et al. (2012)	http://www.bioinf.jku.at/software/cnmops/
CNVrd2	R	Nguyen et al. (2014)	http://www.bioconductor.org/packages/release/bioc/html/CNVrd2.html
ERDS	C	Zhu et al. (2012)	http://www.utahresearch.org/mingfuzhu/erds/
AS: assembly			
Magnolya	Python	Nijkamp et al. (2012)	http://bioinformatics.tudelft.nl/dbl/software
CA: combined approach			
Clever-sv	C++	Marschall et al. (2013)	https://code.google.com/p/clever-sv
LUMPY	C++	Layer et al. (2014)	https://github.com/arq5x/lumpy-sv

(Pirooznia et al. 2015), which generates contigs/scaffolds that are then compared with the reference genome to discover structural variation (Teo et al. 2012).

Compared with array-based approaches sequencing-based approaches, especially RP and SR, have clear advantages, including the ability to detect CNVs of relatively small sizes (< 1 kb), and to infer the breakpoints of CNVs at nucleotide level resolution (Li and Olivier 2013). This is important to assess their genomic impact and to infer their formation mechanisms (Lam et al. 2009). In plants, only a few studies have used sequencing-based approaches to date and most relied solely on the RD method (Turner et al. 2010; Cao et al. 2011; Zheng et al. 2011; Flagel et al. 2013), which may entail a size bias towards larger variants with low breakpoint resolution (Xi et al. 2012; Li and Olivier 2013).

CNVs and pangenome studies

Pangenome construction is a powerful approach which has been developed to understand the extent to which genomic variation occurs within a species. The term pangenome refers to the complete and non-redundant set of genes in the entire species; it is composed of core genes, which are present in all individuals, and variable genes, which are present only in some individuals (Golicz et al. 2016a, b; Hurgobin and Edwards 2017). Due to the presence of structural variation in the form of CNVs and PAVs, a single reference genome is not sufficient to fully represent the entire genetic diversity of a certain species. Accordingly, to obtain the complete genomic content of any given species, it is necessary to construct its pangenome.

Golicz et al. (2016a, b) found that a large number of genes with annotations related to major agronomic traits, such as disease resistance, in the *B. oleracea* pangenome were affected by PAV and CNV. Similarly, Yao et al. (2015) have reported that the variable genome of rice was enriched with genes related to defence to biotic stress, including NBS LRR genes and genes coding for protein kinases and abiotic stress tolerance. Gene copy number variation in the *B. rapa* pangenome was studied by Lin et al. (2014), who found evidence for copy number differences in a peroxidase (EC 1.11.1.7), pointing to a role for the phenylpropanoid biosynthesis pathway in the generation of morphological variation. They have reported that lower copy number of genes in turnip coding for a glucosyltransferase (EC 2.4.1.111) may cause the reduction of 4-D-glucoside, coniferin, syringin and hence increase the production of different lignins. Furthermore, 49,000–169,000 copy number variants were identified in *Medicago* genomes (Zhou et al. 2017). Li et al. (2014) established and analysed the pangenome of *Glycine soja*. They reported that intergenomic comparisons identified lineage-specific genes and genes with CNV or large-effect mutations, some of which show evidence of positive selection and may contribute to variation of agronomic traits such as biotic resistance, seed composition, flowering and maturity time, organ size and final biomass. A genome-wide analysis of structural variation in three inter-crossable poplar species: *Populus nigra*, *Populus deltoides*, and *Populus trichocarpa* was performed by Pinosio et al. (2016) to characterize the size and the composition of the poplar pan-genome. They detected a total of 7889 deletions and 10,586 insertions relative to the *P. trichocarpa* reference genome, and 3230 genes affected by CNV.

CNVs and their importance

The American geneticist Calvin Bridges first discovered CNVs in 1936, when he noticed that flies that inherit a duplicate copy of the *Bar* gene developed very small eyes. Over the past several years, many new CNVs in different species have been identified, leading researchers to believe that CNVs are as important a component of genomic diversity as SNPs.

Structural variations, including CNVs, have been identified in several plant species, including *Arabidopsis* (DeBolt 2010), barley (*Hordeum vulgare*) (Muñoz-Amatriaín et al. 2013), foxtail millet (*Setaria italica*) (Bai et al. 2013), maize (*Zea mays*) (Swanson-Wagner et al. 2010), rice (*Oryza sativa*) (Xu et al. 2012), sorghum (*Sorghum bicolor*) (Zheng et al. 2011), soybean (*Glycine max*) (McHale et al. 2012) and wheat (*Triticum aestivum*) (Nishida et al. 2013). In several cases, these structural variations were found to be associated with phenotypic variations such as leaf size in *Arabidopsis thaliana* (Horiguchi et al. 2009), fruit shape in tomato (Xiao et al. 2008), aluminium tolerance in maize (Maron et al. 2013), stress and disease resistance in barley (Muñoz-Amatriaín et al. 2013) and grain size in rice (Wang et al. 2015).

In the genome, there are regions that seem to be more prone to CNV than others, due to their specific structural features that will locally induce the mechanisms leading to CNV formation, e.g., non-allelic recombination (Zmienko et al. 2016; Samelak-Czajka et al. 2017). Differences in the DNA sequence of species' genomes contribute to their uniqueness. These variations influence many traits, including organism's fitness, susceptibility to disease and contribute to the adaptation to environmental challenges, as well as to co-evolutionary interactions between host and pathogen or a symbiont (Kondrashov 2012; Żmieńko et al. 2014).

The biological effect of CNVs is dependent on the affected sequences and their interactions with the rest of the genome. The importance of CNVs may be greater if they contain regulatory regions and/or genes and these CNVs may contribute to phenotype variation (Cong et al. 2008). Copy number variation may also have potential functional effects: they can cause changes in gene structure, gene dosage, or expression regulation, and expose recessive alleles to selection (Bickhart et al. 2012).

In the model plant species *Arabidopsis* (DeBolt 2010) and rice (Yu et al. 2011), CNVs were detected in 402 and 641 genes, respectively. Genome-wide patterns of CNVs have also been detected in sorghum by comparing two sweet and one grain inbred sorghum lines, identifying 3234 CNVs in 2600 genes (Zheng et al. 2011). Among the legumes, soybean was the first species to have its genome analysed for CNVs, and a total of 267 CNVs with an average size of 18–23 kb were detected across the genomes assayed (McHale et al. 2012). In contrast to maize (Belo et al. 2010; Swanson-Wagner et al. 2010), higher levels of CNV were identified in high-recombination regions in soybean and barley (McHale et al. 2012; Muñoz-Amatriaín et al. 2013).

Despite the prevalence of CNVs in plant genomes and their frequent overlap with protein-coding regions, only a few have been associated with particular phenotypes (Żmieńko et al. 2014). With further studies, we expect to grow our understanding of CNVs impact on plant phenotype, both in the aspect of long-term evolution as well as a mechanism of rapid adaptation to environmental challenges.

CNV: their role in plants

CNV variation has been implicated to play in role a several different processes associated with plants. The first plant species to be extensively assessed for CNVs was maize (Springer et al. 2009; Belo et al. 2010; Żmieńko et al. 2014), and many of the CNVs identified in 19 diverse inbred maize lines and 14 teosinte accessions were found to be associated with domestication (Swanson-Wagner et al. 2010; Chia et al. 2012). This identified 479 genes with higher copy number and 3410 genes with fewer copies following comparison with a reference genome (Swanson-Wagner et al. 2010).

Many CNVs have been observed in outcrossing and autogamous species (Żmieńko et al. 2014). Changes in gene copy number may provide a way to alter the effective dosage of a gene, which may directly change the phenotype. If the new variant is beneficial, the copy number in a particular region may accumulate, and the phenotypic effects may intensify. An example of rapid evolution in a plant is resistance to glyphosate in Palmer amaranth (*Amaranthus palmeri*), a major weed pest in the southern part of the United States (Żmieńko et al. 2014). It was shown that Palmer amaranth resistance to glyphosate is driven by an increase in 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) gene copy number, which is associated with increased EPSPS transcript and protein levels, as well as increased glyphosate dose–survival rate (Gaines et al. 2010, 2011; Sammons and Gaines 2014). In addition, Iwakami et al. (2017) have found differences in acetolactate synthase (ALS) gene copy numbers among thifensulfuron-methyl resistant short-awned foxtail (*Alopecurus aequalis*) accessions. They have reported that two copies, ALS1 and ALS2, were conserved in all accessions, while some carried two additional copies, ALS3 and ALS4. A single-base deletion in ALS3 and ALS4 further indicated that they represented pseudogenes. Good examples of a CNV affecting phenotype is found in the diversity of flowering times and plant heights in wheat and canola (Diaz et al. 2012; Li et al. 2012; Würschum et al. 2015; Schiessl et al. 2017). Several confirmed examples of a CNV linked to phenotype also concern plant

stress tolerance (Żmieńko et al. 2014; Sieber et al. 2016). The importance of CNV at the Fr-A2 locus was shown in durum wheat, in which the Fr-A2 locus explained approximately 90% of the genotypic variation of frost tolerance (Sieber et al. 2016). Furthermore, Würschum et al. (2017) have shown that CNV of C-repeat binding factor (CBF) genes at the Fr-A2 locus is the essential component for winter survival, with CBF-A14 CNV being the most likely causal polymorphism, accounting for 24.3% of the genotypic variance. Changes in gene copy number have been reported to be associated with tolerance to toxic soil chemicals in plants. Copy number expansion of the metal pump gene *HMA4*, for example, contributes to hyper-accumulation and hyper-tolerance to zinc and cadmium in *A. halleri* (Hanikenne et al. 2008, 2013). Similarly, boron-tolerant genotypes of barley contain four times as many copies of the boron transporter gene (*Bot1*) than intolerant genotypes (Sutton et al. 2007), and aluminium tolerance in maize is associated with higher copy number of the multidrug and toxin extrusion gene *MATE1* (Maron et al. 2013). CNVs were identified for the MATE1 gene in aluminium-tolerant lines, but these were not common in teosinte. This study suggested that multiple copies of the MATE1 gene arose recently and probably after domestication.

CNVs and disease resistance in plants

CNVs have been found to be associated with nucleotide-binding leucine-rich repeat (NB-LRR) genes and receptor-like kinase (RLK) genes, known to be involved in plant defence-related mechanisms (Saxena et al. 2014). Sequence variation within the central LRR domain and variation in LRR copy number play important roles in determining recognition specificity (Gururani et al. 2012). CNVs can also be linked to variation in gene expression (Orozco et al. 2009; Ortiz-Estevez et al. 2011). For example, Scots pine trees (*Pinus sylvestris*) were tested for CNV of a thaumatin-like protein gene involved in resistance against root rot by Šķipars et al. (2011) who identified variation in the gene copy number of the thaumatin-like protein gene.

Among the functionally annotated genes, those which are usually over-represented within CNV regions are genes encoding proteins with a nucleotide binding domain (NB) and one or more leucine-rich repeat (LRR) domains (known as NB-LRR genes), as well as genes encoding receptor-like kinases (RLK). Yu et al. (2013) identified several disease resistance genes within the CNV regions in rice (Table 2). These genes were considerably enriched for specific biological functions involved in cell death, protein phosphorylation, and defence response. Furthermore, genetic mechanisms for copy number variation of resistance genes were investigated through phylogenetic comparison of resistance genes in the Cucurbitaceae family by Lin et al. (2013). Their analysis of *R* genes showed frequent loss of *R*-gene loci in different Cucurbitaceae species (Table 2). Chalhoub et al. (2014) identified 425 nucleotide binding site leucine-rich repeat (NBS–LRR) sequences encoding resistance gene homologs in *Brassica napus* using genome sequencing. They confirmed the absence of five NBS–LRR genes from the A_n sub-genome, and three from the C_n sub-genome. This variation may reflect differential selection for resistance to diseases. Hardigan et al. (2016) examined the breadth of genome-wide structural variation in a panel of monoploid/doubled monoploid clones generated from native populations of diploid potato (*Solanum tuberosum*) and found CNVs on chromosome 11 at 42.59–43.05 Mb. This location pertained to a cluster of 16 genes encoding nucleotide binding site leucine-rich repeat (NBS–LRR) disease resistance proteins of which, 14 showed variation in copy number. Association analysis of traits involved in leaf development and disease resistance in 103 maize lines using both SNPs and CNVs revealed that CNVs contribute greatly to the variation of analysed phenotypes and provide complementary information to SNPs (Chia et al. 2012). Jamann et al. (2014) found that CNV polymorphism was significantly associated with resistance to northern leaf blight based on nested association mapping GWAS.

Gene ontology term enrichment analysis of the 672 genes located within CNV regions in soybean revealed that genes related to disease resistance response were significantly over-represented (McHale et al. 2012). In addition, it has been reported that resistance gene function is adapted to frequent re-arrangements and copy number variations (Leister et al. 1998). Copy number variation of a 31-kb repeat segment observed in different haplotypes of the *Rhg1* locus encodes multiple gene products in soybean cyst nematode (SCN)-resistant varieties (Lee et al. 2015). The cloning of *Rhg1* was the first observation that plant disease resistance loci can consist of a multigene cluster CNV of non-canonical resistance genes in tandem formation (Cook et al. 2012). In SCN-susceptible varieties, one copy of the 31-kb segment per haploid genome was present. SCN resistance was found to be associated with increased expression of CNV-related genes (Cook et al. 2012). Copy number variations related to disease resistance have also been identified in several plant species (Table 2), where disease resistance genes represent a significant fraction of genes in CNV regions and were significantly enriched for resistance gene models (Xu et al. 2012; Lu et al. 2012). For instance, Boocock et al. (2015) have identified 876 CNV regions, which spanned 3.5% of the apple genome and were enriched for genes involved in disease resistance against apple scab. Bertioli et al. (2003) showed that in peanut and legumes *R*-genes have undergone extensive copy number variation.

Table 2 CNVs identified in relation to disease resistance in different plant species

Species	CNVs number	CNVs size	Key findings	References
Apple (*Malus domestica*)	876	16.4 kb	Putative CNV regions overlapped 845 gene models and were enriched for *R*-gene models	Boocock et al. (2015)
Arabidopsis thaliana	NR	NR	53 genes of NB-LRR genes in the reference genome appeared to be deleted. Only four RLP genes appear to be deleted in at least one of the 80 accessions	Guo et al. (2011)
Peanut (*Arachis hypogaea*)	NR	NR	Most *Arachis* NBS sequences fall within legume-specific clades, some of which appear to have undergone extensive CNV expansions	Bertioli et al. (2003)
Rice (*Oryza sativa*)	1676	81.2 kb	In relation to disease resistance 1676 CNVs were identified having more copies than the reference genome	Xu et al. (2012)
	4–8.7	NR	Many rapidly evolving plant *R*-genes in maize, sorghum, *brachypodium*, and rice confer resistance to one or more strains of rice blast disease when present in a rice cultivar genome	Yang et al. (2013)
	2886	10.28 Mb	The chromosome 11 is enriched with CNV and disease resistance genes	Yu et al. (2013)
Barley (*Hordeum vulgare*)	115,003	4.4 kb	The majority of the 'cell death' genes were R-genes encoding nucleotide-binding site leucine-rich repeat (NBS–LRR) protein and affected by CNVs	Muñoz-Amatriaín et al. (2013)
Bean (*Phaseolus vulgaris*)	NR	NR	CNV data resulted in a meta-dataset of 51 strong candidate genes with convergent evidence for a role in QR	Douchkov et al. (2014)
	NR	NR	Comparisons among a few TIR–NBS–LRR paralogs within the *I* locus showed variation among them. Increases in CNV of a given sequence lead to increased sequence diversity	Vallejos et al. (2006)
	NR	NR	The copy number of *khipu* tandem repeats in relation to disease resistance varies from one *Phaseolus* species to another	David et al. (2009)
Cucurbitaceae family	NR	NR	There is low CNV of *R*-genes in Cucurbitaceae. The CNV of LRR–LRK-encoding genes is correlated with the number of NBS–LRR-encoding genes in different species. The Cucurbitaceae species have not only low copy number but also low diversity of *R*-genes	Lin et al. (2013)
Potato (*Solanum tuberosum*)	NR	NR	Late blight resistance was enhanced as copy numbers and transcript levels of *RB* transgene increased	Bradeen et al. (2009)
Solanaceae family	6013	NR	The *R*-gene copy number is inconsistent with the number of predicted genes or genome sizes among *Solanaceae* species. For example, the tetraploid tobacco has the largest genome and the largest number of predicted genes, but has low *R* gene number. CNV in the family accounted for by a Few *R* subfamilies	Wei et al. (2016)
Soybean (*Glycine max*)	1–10	NR	The sequence of the individual repeat units, as well as copy number, plays a role in the type specificity of Rhg1-mediated nematode resistance	Lee et al. (2015)

Table 2 (continued)

Species	CNVs number	CNVs size	Key findings	References
Tomato (*Lycopersicon esculentum*)	NR	NR	Soybean cyst nematode resistance mediated by the soybean quantitative trait locus *Rhg1* is conferred by copy number variation that increases the expression of a set of dissimilar genes in a repeated multigene segment	Cook et al. (2012)
	NR	NR	In striking contrast to the *Cf-9* gene family, six of seven homologs in the *Cf-2*/*Cf-5* gene family vary in LRR copy number, ranging from 25 to 38 LRRs. *Cf-5* and one adjacent homolog differ by only two LRRs	Dixon et al. (1998)
Sunflower (*Helianthus annuus*)	NR	NR	There is a correlation between high HaRGC1 paralogue copy number and functional disease resistance	Slabaugh et al. (2003)
Sorghum (*Sorghum bicolor*)	NR	NR	A key mechanism driving the rapid variation in NBS-encoding genes is the highly dynamic clustering, through lineage specific rearrangements via PAVs and CNVs	Mace et al. 2014
Rice, Sorghum, Maize, *Brachypodium distachyon*, *Populus trichocarpa*, *Carica papaya*, Soybean, *Lotus japonicas*, *Fragaria vesca*, *Theobroma cacao*	NR	NR	The particular evolution of *R*-genes via clusterization was highly dynamic through lineage-specific rearrangements leading to the observed conservation/erosion of *R*-genes collinearity between grasses, referenced as CNV and PAV	Zhang et al. (2014)

The number of CNVs detected in different species varies due to difference between genome assembly technologies

NR not reported

It is expected that high copy number of resistance genes in plants is advantageous because it will offer better resistance against pathogens (Lin et al. 2013). On the other hand, low copy number might be a result of less challenge from pathogens (Zhai et al. 2011). This supports the hypothesis that CNV and the genes encoded within these regions contribute to disease resistance in plants through natural genome variation. CNV could enable gene diversification and evolution of new resistance genes.

Conclusions and future directions

Although several projects have been completed to detect CNVs and to understand how they are implicated in different species, the field still lacks sufficient results in the area such as association of CNVs with disease resistance in plants. There are still limitations in accurate detection of CNVs, which need to be improved in future. These are not only due to the difference in the quality of different commonly used short-read NGS sequencing technologies, which can result in the detection of platform-specific variants, but also due to variations when using different, commonly used bioinformatics tools. This should be taken into account when analysing CNV data as different CNV regions were detected by Lam et al. (2012) and O'Rawe et al. (2013) when working on the same data. Nonetheless, in the future, in addition to studying the role of CNV in plant physiology, analysis and quantification of CNV in plants will likely be used in plant breeding as part of acquisition of desirable traits.

An integrated map of CNV in a plant will be helpful to understand the distribution of CNV, as well as its evolutionary mechanism. It is also useful for future mapping and cloning of *R*-genes, the most divergent gene family in plant genomes which has been shown to have considerable copy number variation, presence/absence polymorphism as well as sequence variation. Through constant improvement in genome sequencing and ever-decreasing costs of this technology, more crop genomes are being sequenced. Multiple cultivars within a species have sequences available and this is being extended to the availability of pan-genomes for many species (Golicz et al. 2015; Golicz et al. 2016a, b). These ever-increasing genomic resources will enable a higher accuracy of CNV detection and association with traits. In future, marker-assisted selection can be used as a potential tool for genetic improvement using both CNV and SNP association with disease resistance. A greater understanding of selection pressures of various diseases on CNV will further our knowledge of plant–pathogen interactions. This information will suggest a way forward where information about CNVs can be applied to trait association and breeding. Previous studies provide CNV estimates across the plant genome, enabling further research into the role of such variations in resistance genes.

The ability to use next-generation sequencing to identify CNV paves the road to make correlations between phenotypic and genotypic characteristics; therefore, detecting these variations, using new DNA sequencing technologies, is the first step towards identification of CNV-associated economic traits to integrate them into plant genomic selection programs.

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Compliance with ethical standards

Conflict of interest The authors declare no conflicts of interest.

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