ORIGINAL ARTICLE

Comparative RNA-Seq profiling of a resistant and susceptible peanut (*Arachis hypogaea*) genotypes in response to leaf rust infection caused by *Puccinia arachidis*

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Abstract

The goal of this study was to identify differentially expressed genes (DEGs) responsible for peanut plant (*Arachis hypogaea*) defence against *Puccinia arachidis* (causative agent of rust disease). Genes were identified using a high-throughput RNA-sequencing strategy. In total, 86,380,930 reads were generated from RNA-Seq data of two peanut genotypes, JL-24 (susceptible), and GPBD-4 (resistant). Gene Ontology (GO) and KEGG analysis of DEGs revealed essential genes and their pathways responsible for defence response to *P. arachidis*. DEGs uniquely upregulated in resistant genotype included pathogenesis-related (PR) proteins, MLO such as protein, ethylene-responsive factor, thaumatin, and F-box, whereas, other genes down-regulated in susceptible genotype were Caffeate *O*-methyltransferase, beta-glucosidase, and transcription factors (WRKY, bZIP, MYB). Moreover, various genes, such as Chitinase, Cytochrome P450, Glutathione S-transferase, and R genes such as NBS-LRR were highly up-regulated in the resistant genotype, indicating their involvement in the plant defence mechanism. RNA-Seq analysis data were validated by RT-qPCR using 15 primer sets derived from DEGs producing high correlation value ($R^2 = 0.82$). A total of 4511 EST-SSRs were identified from the unigenes, which can be useful in evaluating genetic diversity among genotypes, QTL mapping, and plant variety improvement through marker-assisted breeding. These findings will help to understand the molecular defence mechanisms of the peanut plant in response to *P. arachidis* infection.

Keywords RNA-seq · Plant-fungus interaction · Transcriptome · RT-qPCR · Rust disease

Abbreviations

GO	Gene Ontology
DEG	Differentially Expressed Gene
NGS	Next Generation Sequencing
PR	Pathogenesis related
GST	Glutathione S-Transferase
JA	Jasmonic Acid
ERF	Ethylene responsive factor
RT-qPCR	Reverse Transcription quantitative PCR

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Introduction

Arachis hypogaea L., commonly known as peanut, is a self-pollinated, allotetraploid ($2n = 4x = 40$) with a genome size of 2891 Mbp (Chen et al. 2016). It is believed that *A. hypogaea* were developed through a natural cross among two species; *A. ipaensis* and *A. duranensis* followed by chromosome doubling (Mondal and Badigannavar 2018). Peanut is an important crop as its seeds are a key source of edible oil (Wan et al. 2018). Additionally, peanut also contains vital nutrients, such as vitamins, proteins, fatty acids, salts, and minerals, which contribute to the routine nutritional requirements in the human body (Chen et al. 2019). Semi-arid tropical and semi-tropical regions are suitable for

the cultivation of peanuts. Approximately, 27 million ha of land in the world is under peanut cultivation, yielding up to 43 million tons of pods/annum (Liu et al. 2017). India is the second-highest producer of peanuts worldwide, contributing 6.8 million tons by cultivation from 5.8 million ha of its agricultural land during 2017 (faostat.fao.org).

The production of this crop is affected by three main types of foliar fungal disease, known as rust, early, and late leaf spot, which are caused by *Puccinia arachidis*, *Cercospora arachidicola*, and *Phaeoisariopsis personata*, respectively. The most commonly observed diseases leading to biotic stress in peanut plants are rust and early leaf spot, resulting in more than 50% yield losses (Subrahmanyam et al. 1984). Peanut rust infection causes not only a loss of crop productivity but also affects the quality of oil extracted from the seed, its haulm, and the yield of fodder. Various chemical agents and fungicides are available to regulate this disease, but the use of a fungicide is not a viable option economically and it is unsafe for human health and the environment. The development and characterization of naturally-resistant host-plant species is the most effective approach for implementing disease management without the use of hazardous chemical agents (Sujay et al. 2012). Traditionally, resistance to pathogen was established via the conventional breeding process in peanut, although conventional methods are laborious and consume more time and effort. In recent years, advancements in biotechnology and molecular biology have made it easier to identify the molecular markers responsible for host-plant resistance and facilitate the data availability of crop genomes (Varshney et al. 2014).

Various molecular methods, such as RFLP, AFLP, Microarray, and RNA sequencing, were utilized to analyse the gene expression levels in plants. RNA-Seq can be utilized for gene discovery, identification of SNPs, other functional markers, and comparative studies of transcriptomes under various physiological conditions that lead to altered metabolic processes. It has better practical reproducibility and greater accuracy in the estimation of entire gene expression levels in a genome (Liu et al. 2015). Molecular interactions between peanut plant and fungal pathogen *P. arachidis* have received very little attention, and no studies have been conducted in this regard so far, to the best of our knowledge. RNA-Seq analysis in *A. hypogaea* has been conducted during seed development (Zhang et al. 2012), to identify resistance to *R. solanacearum* infection (Chen et al. 2014), but no such study has been reported for *P. arachidis* pathogenesis. A similar study reported an interaction between *Oryza sativa* and *Magnaporthe oryzae*, a filamentous fungus as a causative agent of rice blast disease (Kawahara et al. 2012). A genome analysis study of *Puccinia striiformis*, a pathogen that causes wheat yellow rust, revealed the presence of two important proteins (polymorphic and haustorial expressed secreted proteins) responsible for pathogenicity

(Cantu et al. 2013). In soybean, genome-wide annotation revealed that the WRKY family was an effective agent during soybean rust infection, caused by *Phakopsora pachyrhizi* (Bencke-Malato et al. 2014), as well as identified the genes involved in phenylpropanoid pathway during the defence mechanism (Hossain et al. 2018). The RNA-Seq database has important information about a huge number of active crops. At present, discovering such genic putative markers is fast and less expensive, and can be further applied in the resistant trait development program.

Materials and methods

Plant materials and experimental design

Peanut leaves samples of both genotypes were grown at the Department of Biotechnology and Biochemistry, Junagadh Agricultural University, Junagadh, Gujarat, India (21º30′23.2″N, 70º26′57.2″E). The selection of genotypes was based on the level of resistance against rust disease (Mondal et al. 2008). Inoculation was done on 40-day old plants of resistant as well as susceptible genotypes of *A. hypogaea* by spraying spore suspension (50,000 spores per ml water) mixed with Tween 80 (Sigma-Aldrich, MO, USA). The plots were irrigated and optimum growth conditions for *A. hypogaea* were maintained viz. high humidity and temperature at ~ 25 ℃, by covering the plots with a thin plastic sheet (Subrahmanyam et al. 1995). Infection was successful when spraying was done in the evening time. The control treatments received sterile water without any culture inoculation and were maintained under the same environmental conditions.

Leaves of both the genotypes were collected in triplicates at two different stages, i.e. control stage (before inoculation) and infected stage (24 h post-inoculation). All biological replicates were pooled, and samples were preserved in liquid nitrogen. These frozen samples were stored at − 80 ℃ for carrying out further experiments. Simultaneously, a microscopic study was carried out to study pathogen morphology and to investigate the release of uredospore which is necessary for confirmation of pathogenic activity (Fig. 1). Plants were kept under observation for 15 days post-inoculation to study disease development. During sporulation, orange colour pustules of rust could be observed on the abaxial leaf surface of peanut. Two types of samples were generated from both the genotypes and were designated as resistant infected (RI) and resistant control (RC) for resistance genotype, while susceptible infected (SI) and susceptible control (SC) for susceptible genotype, indicating infection stage and control stage respectively. As stated earlier, in the present study two variables were taken, one was based on variety (RI/SI) and another was based on biotic stress condition (RI/
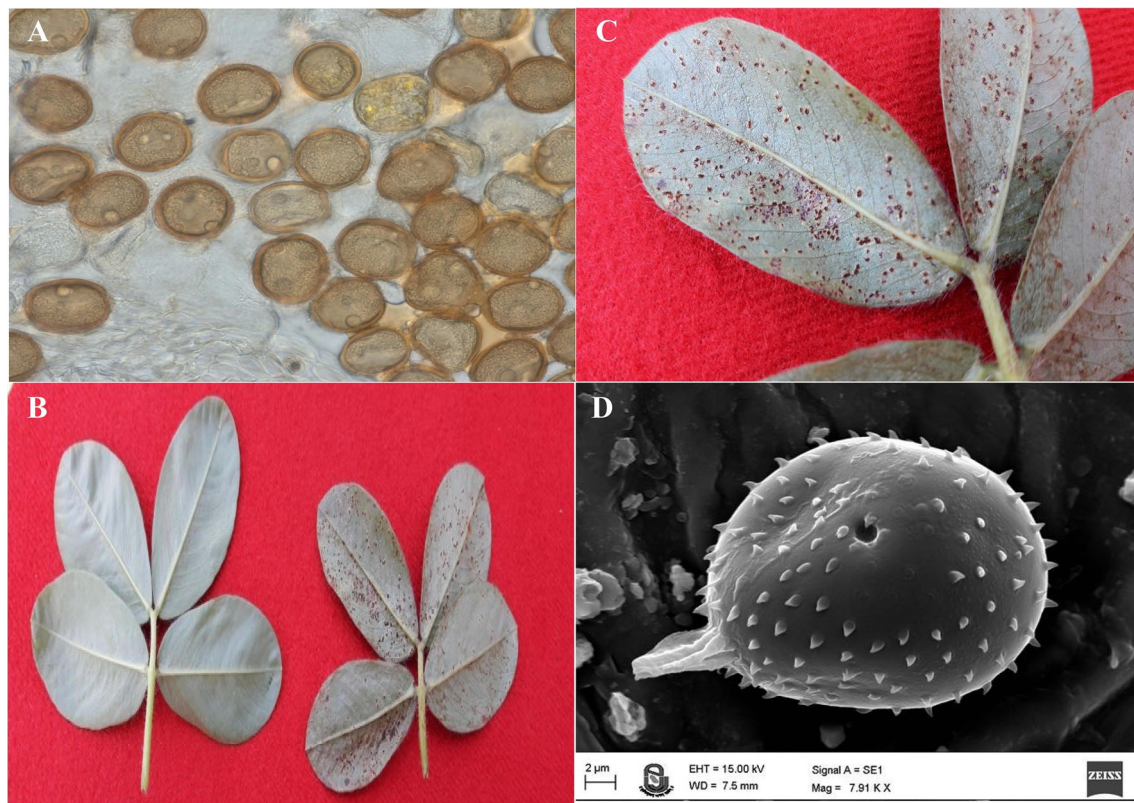
Fig. 1 Disease symptoms and fungal spore morphological study by microscopy **a** Uredospore of *Puccinia arachidis*, **b** JL-24 (susceptible) (control) v/s (infected), **c** sporulation on peanut leaves, **d** electron microscopy of *P. arachidis* spore

RC and SI/SC). The summary workflow of the experiment is shown in Fig. 2.

## Isolation of purified mRNA and cDNA library preparation

Total RNA was extracted from the leaf samples using the RNeasy Plant Mini Kit (Qiagen, CA, USA) as per the instructions provided by the manufacturer. Contamination by genomic DNA was taken care of by treating the extracted total RNA using DNase I (Fermentas, MA, USA) at 37 °C for 1 h. Contamination and degradation of RNA were monitored by electrophoresis on 1.2% denaturing formaldehyde agarose gel. The required concentration of RNA for sequencing was quantified using a Qubit RNA Assay Kit (Invitrogen, CA, USA). Further, the integrity of isolated RNA was assessed using RNA Nano 6000 Assay Kit, Bioanalyzer 2100 (Agilent Technologies, CA, USA). Isolation of mRNA from total RNA was performed by Dynabeads mRNA DIRECT Purification Kit (Invitrogen, CA, USA), and was further assessed by RNA 6000 Pico LabChip kit (Bioanalyzer 2100) (Agilent Technologies, CA, USA). To generate RNA-Seq data, cDNA libraries of samples were prepared using Ion Total RNA-Seq Kit v2 (Thermo Fisher Scientific, MA, USA). Purification of double-stranded cDNA and size selection was done using AMPure XP beads (Invitrogen, CA, USA). Enrichment of desired size fragments was performed by amplification of the library with barcoded primers. The cDNA libraries of 100 pM were assigned to create several copies of fragments by performing emulsion PCR process in the Ion torrent OT2 machine. Finally, the Ion Torrent S5 sequencer system (Thermo Fisher Scientific, MA, USA) with a 540 chips format was used to sequence the fragments created.

Alignments of generated read and Gene Ontology analysis of DEGs

Quality of RNA-Seq library was assessed by the Ion Torrent S5 pipeline and FastQC software (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/) (Brown et al. 2017). To control sequence quality, low-quality data containing < 50 bp reads, homopolymers, adaptor dimers, and ambiguous bases ('N') were filtered using the PRINSEQ tool. Further, a downstream analysis was also performed to remove sequencing reads having quality scores lower than 25 (Schmieder and Edwards 2011). The genome-A (*Arachis duranensis*) and genome-B (*Arachis ipaensis*) from the two wild peanut diploid ancestors were used as the reference

Fig. 2 A detailed workflow performed for the identification of DEGs and designing EST-SSRs in resistant and susceptible genotypes of *Arachis hypogaea*
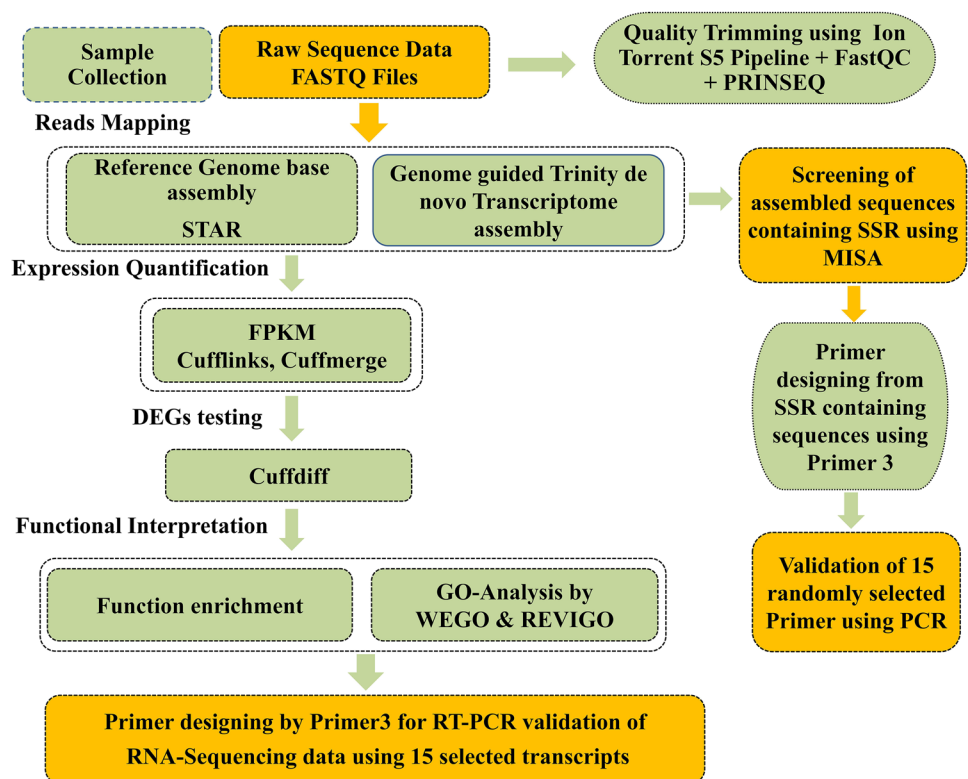
genome for alignment. GFF files for both genomes were retrieved from the PeanutBase website (https://peanutbase.org) and used for alignment (Peng et al. 2017). The filtered reads were mapped onto the reference genome of peanut using STAR 2.5.1a software (https://github.com/alexdobin/STAR/releases/) (Dobin and Gingeras 2015). DEGs among infected and control (non-infected) leaf samples of both the genotypes of peanut were identified by the Cuffdiff tool in the Cufflinks package (https://sihua.us/Cufflinks.htm) (Trapnell et al. 2010; Ghosh and Chan 2016). Moreover, the abundance of normalized transcripts was also estimated using the same tool and represented as fragments per kilobase per million mapped reads (fpkm) (Trapnell et al. 2009). For downstream statistical analysis of DEGs, a false discovery rate (FDR) of < 0.05 and p-value < 0.01 with at least a Log2

fold-change ≥ 1 were considered to produce high-quality data (Li et al. 2015). For the depiction and comparison of several expressed sequences shared by different samples in the form of Venn diagrams, VENNY software was used (Oliveros 2007). Cleaned reads per library are displayed in Table 1. Raw sequences for all rust infected leaf samples were deposited at https://www.ncbi.nlm.nih.gov/bioproject/PRJNA489546/ and those of control samples were deposited at https://www.ncbi.nlm.nih.gov/bioproject/PRJNA490412/.

Enriched GO analysis of DEGs was carried out by REVIGO software (Supek et al. 2011). Comparative GO analysis of RI/RC and SI/SC pairs was performed by WEGO software (Ye et al. 2006). In gene ontology, transcripts were classified into three different categories viz. cellular component, biological process, and molecular functions along with

Table 1 Summary of reference based assembled transcripts from RNA-Seq of the susceptible and resistant genotypes of *Arachis hypogea* at control and infected stages

	SI	RI	SC	RC
Number of transcripts	14,916,661	17,502,719	17,336,240	36,625,310
RNA-Seq length (bp)	2,388,143,923	2,761,143,610	2,928,728,266	5,127,297,546
Average transcript length (bp)	160	158	169	140
Total read counts after quality filtration	12,669,594 (84.94%)	14,779,667 (84.44%)	15,038,010 (86.74%)	31,262,640 (85.36%)
Number of uniquely mapped reads	4,999,181 (39.46%)	10,218,232 (69.14%)	10,728,674 (71.34%)	19,233,708 (61.52%)
Number of reads mapped to multiple loci	2,099,015 (16.57%)	3,747,309 (25.35%)	3,757,635 (24.99%)	9,796,877 (31.34%)
Average contig length after mapping (bp)	137	147	152	125

their fraction ratio based on the number of genes (Supek et al. 2011). For identification of important regulatory pathways and networks, KAAS (KEGG Automatic Annotation Server: https://www.genome.jp/kegg/kaas/) was used against the *Arabidopsis thaliana* and *Glycine max* gene datasets using the bi-directional best hit (BBH) method (Liu et al. 2013b).

Validation of RNA-Seq data by RT-qPCR

RT-qPCR technique was used to confirm the differently expressed genes identified by RNA-Seq analysis. Fifteen primer sets were designed for the 15 genes that were randomly selected from the pool of DEGs for RT-qPCR (Koringa et al. 2013; Rajkumar et al. 2015). RT-qPCR experiment was carried out in the ABI 7500 Fast Real-Time PCR Detection System (Thermo Fisher Scientific, MA, USA). Online primer designing tool, Primer3 was used for designing specific primers (Untergasser et al. 2007). A QuantiTech Reverse Transcription kit (Qiagen, CA, USA) was used to synthesize cDNA. The same RNA samples were used for both cDNA synthesis as well as RNA-Seq analysis. For RT-qPCR, designed primers (Table 2) and QuantiFast SYBR Green PCR Kit (Qiagen, CA, USA) were used. The program details of RT-qPCR set to obtain desired amplicons are as follows: initial denaturation with 95 ℃ for 5 min followed by 35 cycles of melting and annealing-extension at 95 ℃ for 10 s and 60 ℃ for 30 s, respectively. The reaction mixture was prepared by mixing 1 µl of template cDNA, 1 µl of specially designed forward and reverse primer (concentration of each primer: 10 pM), 10 µL SYBR Green Master Mix (2×) and the final reaction volume was made up to 20 µl by addition of nuclease-free water (Qiagen, CA, USA). The relative expression levels of target genes were calculated using the Livak's $-\Delta\Delta$ CT method (Livak and Schmittgen 2001). The RT-qPCR experiment was performed in three replicates for an individual sample. The actin gene was used as a reference gene for normalization (Jiang et al. 2011).

Expressed Sequence Tag–Simple Sequence Repeats (EST-SSR) mining, primer designing, and validation by PCR amplification

To detect EST-SSR markers, transcriptome data were first assembled using Trinity assembler (Grabherr et al. 2011), and these assembled contigs were utilised to generate SSR using the MIcroSAtellite (MISA) tool (Beier et al. 2017). Primers of 18–24 bp size of EST-SSRs in microsatellite sequences were designed using Primer3 (https://primer3.sourceforge.net/) (Untergasser et al. 2007) based on the following parameters: G/C content near 50%, annealing temperature between 57 ℃ and 63 ℃, and a minimum product length of 100–300 bp. From the total, 15 pairs of SSR primers were selected randomly and synthesized (Sigma-Aldrich, MO, USA) for validation by PCR reactions (Supplementary Table 9). To validate the SSR markers, genomic DNA was extracted and purified, and PCR was carried out to detect amplification for both genotypes of peanut using designed primers. PCR was conducted using 2×PCR master mixes (Invitrogen, CA, USA), with the following profile: 1 cycle of 5 min at 94 ℃, 30 cycles of 1 min at 94 ℃, 45 s at 60 ℃ 1 min at 72 ℃, and a final cycle of 5 min at 72 ℃. The PCR products were analysed by electrophoresis on 2.5% agarose gel. The band sizes were determined against the appropriate DNA ladder (Invitrogen, CA, USA).

Table 2 Random and gene-specific primers used for validation of RNA-Seq data using RT-qPCR

Sr. No	Gene ID	Gene name	Primer sequence (forward)	Primer sequence (reverse)
1	Araip.N03N5	Rubisco methyltransferase	TGTTTACACCAGTTGACGGATGA	CTGCAAACACGCATGAAGCA
2	Araip.R9908	Trypsin-like serine protease	TGGGCTAAACCCGACAACAA	TTCTGCAAAAGACGGCTCAC
3	Araip.77S0D	Uncharacterised protein	AAGCCTCCTGCTGACAAACC	CGCAACGAAGAAAGCTCTGG
4	Araip.C41LK	Terpene synthase	TGTGGAGTACATCCATCCAACT	CACTATGACTGGAGTTTGGCTCT
5	Aradu.I4JWW	MYB transcription factor	CCCACACCAGGTGCCTTTAT	ATCTGGAACCCAACGGACAC
6	Aradu.Z1Y2A	Serine/threonine kinase	GCCTCTTCCAAACCAGCTCT	TCGCATGGTCACATCGTCAT
7	Aradu.P9J09	Cellulose synthase	AAGGCACACCGAAGTACCAA	GGTTAAGGACAGGGTTAAGGC
8	Aradu.11T0C	Transcription initiation factor	TGTGTCCCTCATTCGTGCTT	TGGTTGCGGTTGATCCTTGT
9	Aradu.VE705	WRKY family TF	CTCGCCAGTATATGGCCTCC	TTAGGGCAACTCACCGGAAC
10	Aradu.QH0IG	Cytochrome P450 protein	CTCGCCATGCTCTCTAGCTT	GTGGGTCAGTATGTTCCCCA
11	Aradu.D14Q2	Thaumatin protein	ATGTTTACACCAGTTGACGGA	TGCAAACACGCATGAAGCATT
12	Araip.DAL9A	Protein kinase	GGCTGAAAGACACTTGATGGC	TAACGGTACAGGAGGCTGAC
13	Aradu.9AI6Q	Chitinase family protein	GGGAGTTAGTGGGTTGTAGCG	GTGCAAGGAGATGAAAGGCG
14	Aradu.V83DR	Transmembrane protein	TGTCTCTGGCAGATCAACAC	AGCAATGCTTGCACGATGTC
15	Aradu.R4V51	TIR-NBS-LRR protein	TGAGTCTTTGTATCCCACTTCATCA	ACAATCGTATATAGTACGGAGGGC

Results

Sequence alignment and RNA-Seq analysis

RNA-Seq was performed using the Ion Torrent S5 system (Jain et al. 2016; Hamid et al. 2018). This study was initiated with the objective of transcriptome analysis of resistant (GPBD-4) and susceptible (JL-24) genotypes of peanut involved in plant-pathogen interactions. Sequencing of cDNA libraries from all the samples viz. RC, RI, SC, and SI produced a total of 86,380,930 reads. The Ion S5 sequencing technology was used to obtain a read length of 150–250 bp in the generated libraries. An average read length of 156 bp was obtained during this process. Various tools were used to remove and trim the undesired products and to maintain the quality of the data. Details of the RNA-Seq run are summarised in Table 1. Only aligned and mapped reads were considered for subsequent analysis, which includes uniquely mapped reads for SI, RI, SC, and RC with an average matching rate of 60.36%.

DEGs analysis

Significant fold-change in the up- and down-regulated genes in infected tissues compared to the corresponding controls was found for both genotypes of peanut via the Cufflinks tool. With FDR < 0.05, p-value < 0.01, and Log2 fold-change ≥ 1, deferentially expressed transcripts were obtained in RI/RC as well as SI/SC. In total, 212 and 99 transcripts were up and down-regulated, respectively, when RI was compared with RC, i.e., the difference was noted within 24 h upon infection in the resistant variety (Supplementary Table 1). However, considerably fewer transcripts were up-regulated (18) compared to those down-regulated (257) in the case of SI with respect to SC (Supplementary Table 2). This indicates that resistance-related genes were induced upon infection in the resistant variety leading to the up-regulation of ~ 200 genes compared to that in the susceptible variety. The FDR value cut-off was set < 0.05, to achieve higher accuracy and significant genetic differences in RI and SI compared to their respective controls.

The correlation of distribution in fold-change with the gene number among the four sample libraries is presented in Fig. 3. Genes with more than an eight-fold difference between RI/RC mainly encoded chitinase, Glutathione S-Transferase (GST), polygalacturonase, terpene synthase, cytochrome P450 superfamily protein, pectinesterase, cysteine synthase, MLO-like protein for defence response, Serine/Threonine kinase family protein, F-box protein, oxidoreductase, GH3 auxin-responsive promoter,
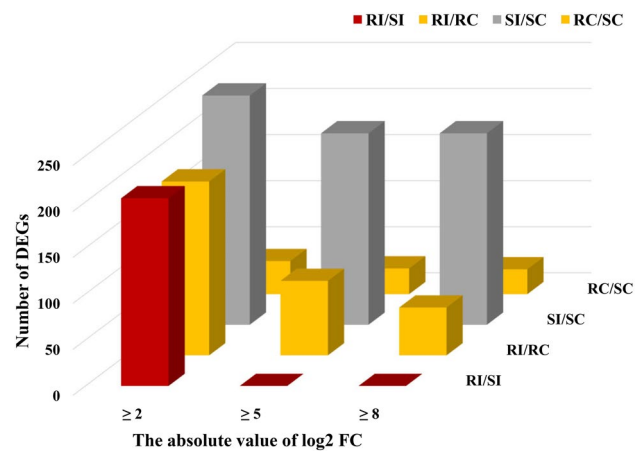
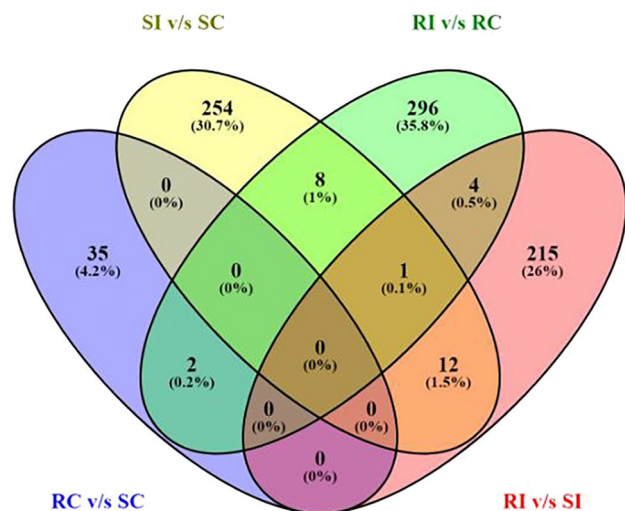**Fig. 3** The Fold change wise distribution of DEGs under the comparison of four different samples

Fig. 4 Venn diagram showing the distribution of unique and common DEGs among control and infected stages of susceptible and resistant variety

and WRKY family transcription factor (Supplementary Table 1). These highly expressed DEGs were expected to play a crucial role in the defence mechanisms during fungal pathogen infection in *A. hypogaea*.

The distribution of unique and regular DEGs for the four sample types is shown in Fig. 4. In total 35 (4.2%), 254 (30.7%), 296 (35.8%), and 215 (26%) genes were discovered that were expressed diversely in RC v/s SC, SI v/s SC, RI v/s RC, and RI v/s SI, respectively. Eight (1%) genes were found to be common between SI v/s SC and RI v/s RC, 12 (1.5%) between SI v/s SC and RI v/s SI, two (0.2%) between RI v/s RC and RC v/s SC, and four (0.5%) between RI v/s RC and RI v/s SI. Eight DEGs associated with the GO terms 'U-box superfamily protein', 'Pentatricopeptide

repeat (PPR) protein', 'Phosphorylase protein', and 'Chitinase family protein' were common between RI v/s RC and SI v/s SC. A detailed discussion of the comparative enriched GO analysis between resistant and susceptible genotype is presented in the next section.

These DEGs represented a total of 747 non-redundant genes that were distributed across the ten chromosomes of peanut (Fig. 5). A mapping approach was adapted to develop closely linked markers for the rust resistance gene in peanut, where major Rust_QTL was found to be on the A03 chromosome (Mondal and Badigannavar 2018). It is interesting to note that in the present study, chromosome A03 carried possible defence-related protein-coding genes (Aradu. EZY28, Aradu.X29NW, Aradu.K5XM1, Aradu.2X14D, and Aradu.639I9) which were differentially expressed in RI/RC.

During pathogen infection of plants, the immune system of the plant relies on its ability to recognize foreign molecules followed by signal transduction, and it responds by involving many genes in different defensive pathways. DEGs related to plant defence mechanism were classified into six different groups; PR genes, defence-related (R) genes, signalling molecule-related genes, transcription factors, genes involved in secondary metabolic pathways, and photosynthesis-related genes (Table 3).

Expression analysis of PR genes related to cell wall modification during biotic stress

A well-known phenomenon in legumes is the differential expression of PR genes under different biotic and abiotic stresses (salinity, drought, wounding and cold stress) (Liu and Ekramoddoullah 2006; van Loon et al. 2006). The plant PR genes are involved in attacking pathogens by either the degradation of fungal cell wall components or modulating the osmotic balance upon fungal infection. The numbers shown in the bracket following gene name indicates its fold change. It was observed that the expression of polygalacturonase (8.38-fold) and chitinase proteins (8.58-fold) were up-regulated in the RI genotype. The hydrolysis of glycoside bonds in fungal cell wall polymers is catalysed by glycoside hydrolase (GH). The glycoside hydrolases gene family contains PR2 genes producing ß-1, 3-glucanases (8.25-fold) that hydrolyse ß-1,3-D-glucosidic links in ß-1,3-glucans of the fungal cell wall, and it was observed that these genes were up-regulated in the RI sample compared to in the RC sample. Cellulose synthase (8.57-fold) transcript was found to be highly expressed in the resistant genotype. This enzyme is involved in the synthesis of cellulose, a major component of the plant cell wall, which acts as a physical barrier to prevent pathogen invasion. Moreover, DEGs encoding Thaumatin (PR-5) protein (8.96-fold) were significantly up-regulated in the RI genotype compared to SI.

Differentially expressed defence mechanism-related R genes and defence-related hormone biosynthesis genes

In the resistant genotype, the expression of the defence-related genes, such as cytochrome P450 (9.17-fold), was up-regulated, which catalyses the oxidation of many substrates via molecular oxygen. DEG-encoding peroxidase (POD) (− 13.47-fold) was down-regulated with a distinct expression pattern in the susceptible genotype. Other defence-related genes, such as GST family protein and MLO-like protein, were up-regulated in the RI sample compared to the SI sample (Supplementary Table 3). Different R genes, such as nucleotide binding-leucine-rich repeat (NB-LRR), F-box, and MLO-like protein were found during DEG analysis (Table 3). In peanut rust interaction, the transcripts with the highest and most exclusive up-regulation were F-box protein (8.79-fold) followed by MLO-like proteins (8.25-fold) which play an important role in defence response in the infected sample of the resistant genotype. NB-LRR protein

Fig. 5 The total number of DEGs present on each chromosome of the peanut plant. A total number of DEGs on genome-A (*A. duranensis*) and genome-B (*A. ipaensis*). The *X*-axis represents different chromosomes. *Y*-axis represents number of genes on each chromosome
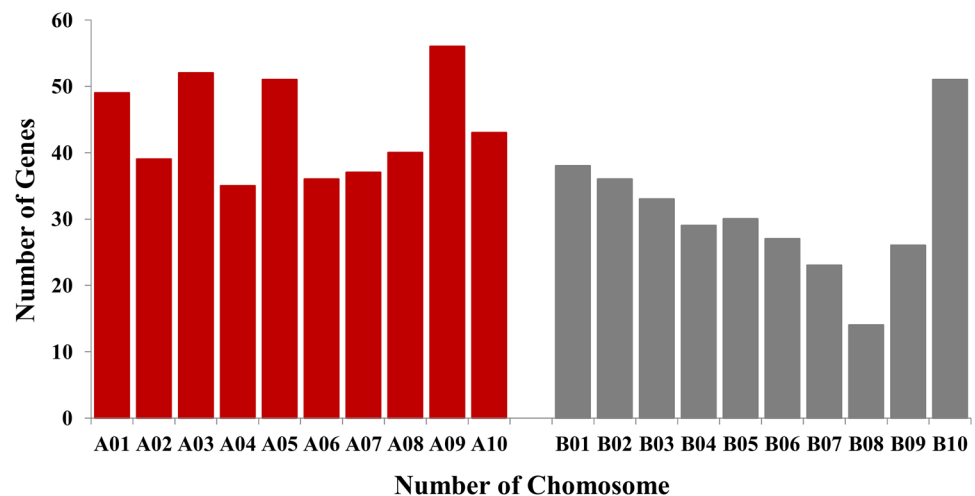
Table 3 Selected DEGs of resistant variety of peanut plant related to plant defense against pathogen

Gene name	Gene length	log2FC (RI/RC)	Description
Aradu.P0G7F, Aradu.23UZB	2111, 3087	8.38, 6.20	Polygalacturonase (glycoside hydrolase)
Aradu.FUK65, Aradu.KH972	3942, 11941	1.54, 8.25	Beta glucosidase (glycoside hydrolase)
Aradu.9AI6Q, Aradu.118NW	2021, 2499	8.58, 6.29	Chitinase protein
Aradu.BZH82, Aradu.FPU8X	13832, 3695	8.57, − 3.35	Cellulose synthase
Aradu.D14Q2	9705	8.96	Thaumatin protein
Aradu.N8G7F	3910	8.25	MLO-like protein
Aradu.K5XM1, Aradu.6HJ87, Aradu.QH0IG	2656, 3775, 2648	9.17, 6.15, 3.40	Cytochrome P450 protein
Aradu.E6KMV, Aradu.51L6N	1523, 1104	8.35, − 3.36	Glutathione S-transferase
Aradu.PP2DC, Aradu.SJ15T	3578, 2980	8.79, 6.10	F-box protein
Aradu.R4V51	3197	3.34	TIR-NBS-LRR
Aradu.LYT7G, Aradu.6M72C, Araip.DAL9A	3797, 7841, 3361	8.55, 6.74, − 3.72	Protein kinase protein
Aradu.Z1Y2A, Aradu.X29NW	5824, 5075	8.43, 1.64	Serine/threonine kinase
Aradu.F623P	7038	− 3.37	Leucine-rich repeat protein
Aradu.RG31X	4603	9.24	Ethylene-responsive transcription factor
Aradu.I4JWW, Araip.9P5VU, Aradu.85BTF	5857, 2225, 1754	8.69, 3.68, 7.85	MYB transcription factor
Aradu.VE705	1634	8.24	WRKY transcription factor
Aradu.YNN2E	3139	3.43	GATA transcription factor
Aradu.U2NBF, Aradu.S4DGV	9499, 2083	9.10, 7.09	Heat shock protein
Aradu.PU456, Aradu.8JG2E	7467, 3560	8.08, − 3.28	Terpene synthase
Aradu.BM2KZ, Araip.SX3RK	8741, 4227	1.28, − 3.70	Caffeate *O*-methyltransferase (COMT)
Aradu.GZ2X7, Aradu.P7UBS, Araip.SP6BX	4129, 3393, 2213	1.66, − 3.43, − 3.70	Pentatricopeptide repeat (PPR) protein
Aradu.X6AKD	1064	8.17	Chlorophyll a/b binding protein
Aradu.B1CT2	978	1.43	Thiamine thiazole synthase

p-value < 0.01, Negative (−) value of log2FC indicates down regulation of DEGs

(3.34-fold) was up-regulated in RI compared to RC. Transcripts responsible for defence-related plant hormones were differentially up-regulated in resistant genotype compared to the susceptible genotypes with different fold-changes. Compared to RC, the transcript levels of Jasmonic acid (JA) biosynthesis genes, such as 12-oxophytodienoicacid reductase (1.43-fold) were generally up-regulated in RI, while lipoxygenase was down-regulated in SI when compared to SC.

Regulation of transcription factors (TF) and plant signalling molecule genes in response to infection

Transcription factors, such as ERF, WRKY, MYB, and BHLH play an important role in plant immunity by regulating the expression of defence-related genes. In the present study, the TFs such as ethylene-responsive TF (ERF) (9.24-fold), MYB TF (8.69-fold) and WRKY TF (8.24-fold) were overexpressed in RI compared to RC, whereas bZIP TF and basic helix-loop-helix (bHLH) DNA-binding protein and WRKY family TF were down-regulated in SI compared to SC. Transcription factors are involved in the activation of protein kinase and mitogen-activated protein kinase (MAPK) cascade for the defence mechanism (Qiu et al. 2008). Genes coding for signal transduction-related proteins,

such as protein kinases and Serine/Threonine kinase, are upregulated in the resistant infected genotype compared to the susceptible infected genotype (Supplementary Tables 3, 4).

Differentially expressed secondary metabolite genes and regulation of photosynthesis-related genes

The secondary metabolite-related transcripts, such as caffeoyl-CoA 3-O-methyltransferase (COMT) (1.28-fold) and terpene synthase (8.08-fold) were up-regulated in RI compared to RC. In the case of susceptible genotype, caffeoyl-CoA 3-O-methyltransferase (COMT) (− 12.39-fold) and terpene synthase (− 12.79-fold) were down-regulated in SI than in SC, indicating that the susceptible genotype is not able to produce sufficient secondary metabolites, such as terpenes and flavonoids, to defend against pathogens. In the present study, DEGs of photosynthesis-related genes, including various chlorophyll a/b binding protein domains (8.17-fold) and thiamine thiazole synthase (1.43-fold) were up-regulated in RI compared to the RC genotype. However, few photosynthesis-related genes were affected negatively in the resistant variety as well, because pentatricopeptide repeat (PPR) protein (− 3.43-fold) transcript expressions were down-regulated in the RI genotype compared to RC

genotype. Nevertheless, in the susceptible genotype (both SI/SC), the similar gene (PPR protein) was found to be down-regulated at a greater level (− 13.61-fold) in infected resistant compared to control resistant genotype.

Enriched GO analysis by WEGO software for the comparison of resistant and susceptible genotypes

The GO classification by WEGO software (Ye et al. 2006) was used to identify the difference in functional categories between infected resistant (RI) and infected susceptible (SC) compared to their controls (RC and SC), respectively. DEGs set. The results of the comparative analysis of the GO terms between the resistant and susceptible genes are shown in Supplementary Fig. 1. In total, 603 genes of RI/RC and 514 genes of SI/SC were assigned with one or more GO terms. GO annotation in three major groups were found to produce a total of 1117 unigenes (Supplementary Table 5). In the comparative GO analysis of RI/RC and SI/SC, different GO terms were identified within the cellular component. Membrane (GO: 0016020), cell (GO: 0005623), and cell part (GO: 0044464) are the top three groups of cellular components. In the cellular component, GO terms, such as membrane part and protein-containing complex, were higher in number in RI/RC compared to SI/SC. In the case of molecular function, catalytic and transporter activity (GO: 0003824 and GO: 0005215, respectively), and binding activity (GO: 0005488) were found to be the three major groups, while transcription regulator activity and signal transducer activity were highly expressed in RI/RC than in SI/SC. During the comparative GO analysis of resistant and susceptible varieties, the metabolic and cellular processes (GO: 0008152 and GO: 0009987, respectively) and localization (GO: 0051179) were the top three groups in the biological process category as well as were highly expressed in RI/RC than in SI/SC.

Gene Ontology analysis of DEGs using the REVIGO tool

REVIGO software was used to accomplish GO enrichment analysis for differently expressed genes of all four samples (Supek et al. 2011). A total of 311 GO terms were assigned and the distribution of percentages of three major groups were as follows: 46.3% for molecular functions (MF) (144 GO terms), 42.77% for biological processes (BP) (133 GO terms), and 10.93% for cellular components (CC) (34 GO terms) (Supplementary Fig. 2). Generated GO terms of these three major groups are described in Supplementary Table 6. This mainly includes BP-like defence response to fungus (GO: 0050832), chitin catabolic process (GO: 0006032), SOS response (GO: 0009432), and response to wounding (GO: 0009611). This indicates the plant's direct response

towards fungal infection concerning protecting itself from the damage caused by the pathogen. Among the biological process category, based on the abundance of transcripts, protein phosphorylation was the main functional group followed by intracellular signal transduction and lipid metabolic processes, indicating their role in important signalling pathways, such as MAPK signalling pathways, which result in the production of catabolic enzymes to attack the pathogen. Within the cellular component category, based on gene expression, GO terms related to the membrane, integral component of the plasma membrane, *N*-acetyl transferase activity, and phosphatase activity were highly expressed in the given order, respectively. Whereas, MF related to transcription factor activity (GO: 0003712), GST activity (GO: 0004364), peroxidase activity (GO: 0004601), metal ion transmembrane transporter activity (GO: 0046873), and terpene synthase activity (GO: 0010333) were important functional groups involved in secondary metabolite production and the genetic regulation of important defence pathways.

Gene function analysis was performed in a systematic manner using the KEGG pathway database (Kanehisa and Goto 2000). KEGG analysis of the present study revealed a total of 558 genes that were allocated to 60 pathways (Supplementary Table 7). The main groups of transcripts belonged to metabolic pathways (64, 11.46%), followed by the biosynthesis of secondary metabolites (41, 7.34%) and carbon metabolism (27, 4.83%). DEGs were also analysed by the KEGG pathway to identify defence-linked regulatory mechanisms. Defence-related pathways, such as the MAPK signalling pathway (23, 4.12%), phenylalanine metabolism (17, 3.04%), plant hormone signal transduction (3, 0.53%), and plant-pathogen interactions (25, 4.48%) were the most enriched pathways of RI/RC that were found to be up-regulated during DEGs analysis, whereas such enriched pathways were down-regulated in SI/SC.

RT-qPCR of DEGs to confirm RNA-Seq analysis

A total of 15 transcripts were arbitrarily selected to design primers for RT-qPCR, which were used to confirm the reliability of the sequencing result. The RT-qPCR analysis showed that out of a total of 15ss transcripts used, 13 transcripts completely matched with the data obtained through RNA-Seq. For example, the expression of the Serine/Threonine kinase family protein, which is involved in the plant-pathogen-related response, was up-regulated in RI plants. The difference in terms of fold-change obtained from the data of RNA-Seq was 8.42-fold, while with RT-qPCR, it was 4.34-fold as observed in RI vs RC. Out of 15 random transcripts, six were related to pathogen defence response pathways and represented similar results in both analyses. However, similar expression tendency was not found in two randomly selected transcripts, i.e. GATA transcription factor

and terpene synthase. The actin gene transcript was used as an endogenous control for normalizing the relative gene expression of transcripts (Supplementary Table 8). Comparative analysis of data obtained through both techniques had a positive correlation of 0.82. The values of log2 fold-change were also found to be consistent in expression. Supplementary Fig. 3 and Supplementary Table 8 depict correlation among RNA-Seq and RT-qPCR data.

Frequency and distribution of EST-SSRs in *Arachis hypogaea*

Specific filters were used to remove low-quality reads from initial generated data, which resulted in more than 73.34 million raw reads. The obtained reads were assembled into 257,823 contigs, which fell in a range of 419 to 2951 bp in length. Finally, 4511 EST SSRs were classified from 3983 sequences containing SSR (Table 4). The successful design of a total of 2892 primer sets was achieved using Primer3 software. To validate the designed primers for SSR, 15 primer sets were selected randomly for PCR amplification (Supplementary Table 9). All the randomly selected markers of both genotypes were successfully amplified, and amplicons were confirmed by 2.5% agarose gel electrophoresis (Supplementary Fig. 4). However, 2.5% gel was found to be inefficient for discrimination of the allelic variant of groundnut. Therefore, further confirmation is essential to recognise the allelic variants responsible for defence responsive mechanisms in groundnut. Even distribution was not observed in the proportion of different SSR unit sizes. In this study, tri-nucleotide repeats (67.32%) were the most abundant motif followed by dinucleotide (20.88%), single nucleotide (8.37%), tetranucleotide (2.15%), hexanucleotide (0.70%), and pentanucleotide (0.55%), respectively (Fig. 6). The average genome SSR was 5.4 kb in size. $(AAG/CTT)_n$ had the highest frequency of 19.06% in a genome compared to all other types of repeat motifs. Additionally, $(AG/CT)_n$ and $(ATC/ATG)_n$ with 14.14%, and 12.74%, respectively, were found in greater amounts. The RNA-Seq data of *A. hypogaea* were used to design EST-SSR primers. Details of

Table 4 Summary and statistics of identified EST-SSRs in *Arachis hypogaea* RNA-Seq using Trinity and MISA

Parameters	Value
Analysed RNA-Seq sequences for SSR	72,142
Analysed sequences size (bp)	30,256,167
Identified total SSRs from sequences	4511
Total sequences containing SSR	3983
Total sequences with more than 1 SSR	452
Total SSR found in a compound formation	292
Primers designed from SSR	2892

specific primers are provided in Supplementary Table 9. For the application of EST-SSR primers, allelic variation needs to be established between the two varieties (i.e. resistant and susceptible) as a prerequisite for EST-SSR primers to be used for varietal selection.

Exclusively expressed genes in resistant and susceptible varieties of *Arachis hypogaea*

Overall, it was observed that four different defence-related genes; ERF (9.24-fold), MLO-like protein (8.25-fold), F-box protein (8.79-fold), and Thaumatin (8.96-fold) were exclusively expressed in the resistant variety during fungal infection, which helped it to sustain under biotic stress. Some important defence-related genes, such as lipoxygenase (− 10.78-fold) and pectin methyl-esterase inhibitor protein (− 12.01-fold), were found to be exclusively down-regulated in a susceptible variety during infection. Down-regulation of such defence-related genes in susceptible genotype could be the reason for disease development.

Discussion

Plants have well-established defence mechanisms against pathogen infection, such as physical barriers of the cell wall to prevent pathogen invasion, secondary metabolites that are toxic to the pathogens, and specific molecular pathways for protection (Zhang et al. 2017). Major defence mechanisms observed in peanut plants as a result of fungal infection are shown in Fig. 7. These defence mechanisms include, recognition of pathogen effector molecule by plant and lead to activation of TFs, PR proteins, oxidative enzymes and defence-related genes such as R-gene, GST, chitinase and cytochrome P450. In the present study, RNA-Seq technology was used to determine changes in the expression of genes among the two selected genotypes of peanut infected with *P. arachidis*.

Increasing the expression of PR proteins specifies the beginning of systemic acquired resistance to various pathogens. Such proteins have an antifungal activity to various pathogenic fungi. Glycoside hydrolases (GHs) (PR-2 genes) produce ß-1,3-glucanases that hydrolyse the glycosidic bonds of fungal cell wall polymers (Garnica et al. 2013). In the case of the soybean plant, ß-1,3-glucanases level was doubled during an infected resistant variety during rust infection caused by *Phakopsora pachyrhizi* fungal pathogen (Soria-Guerra et al. 2010). In this study, up- and down-regulation of GH genes encoding defence-related enzymes, such as chitinase, were found in resistant and susceptible genotypes, respectively, during infection. Thaumatin belongs to PR protein class-5 and causes transmembrane pores in fungal cell membranes

Fig. 6 The frequency distribution of the EST-SSRs identified in peanut transcriptome data. **a** Distribution of the total number of EST-SSRs in different motif types. Di-, tri-, tetra-, penta-, hexa- and compound nucleotide repeats were analyzed. **b** Proportion distribution of selected motifs of trinucleotide repeats
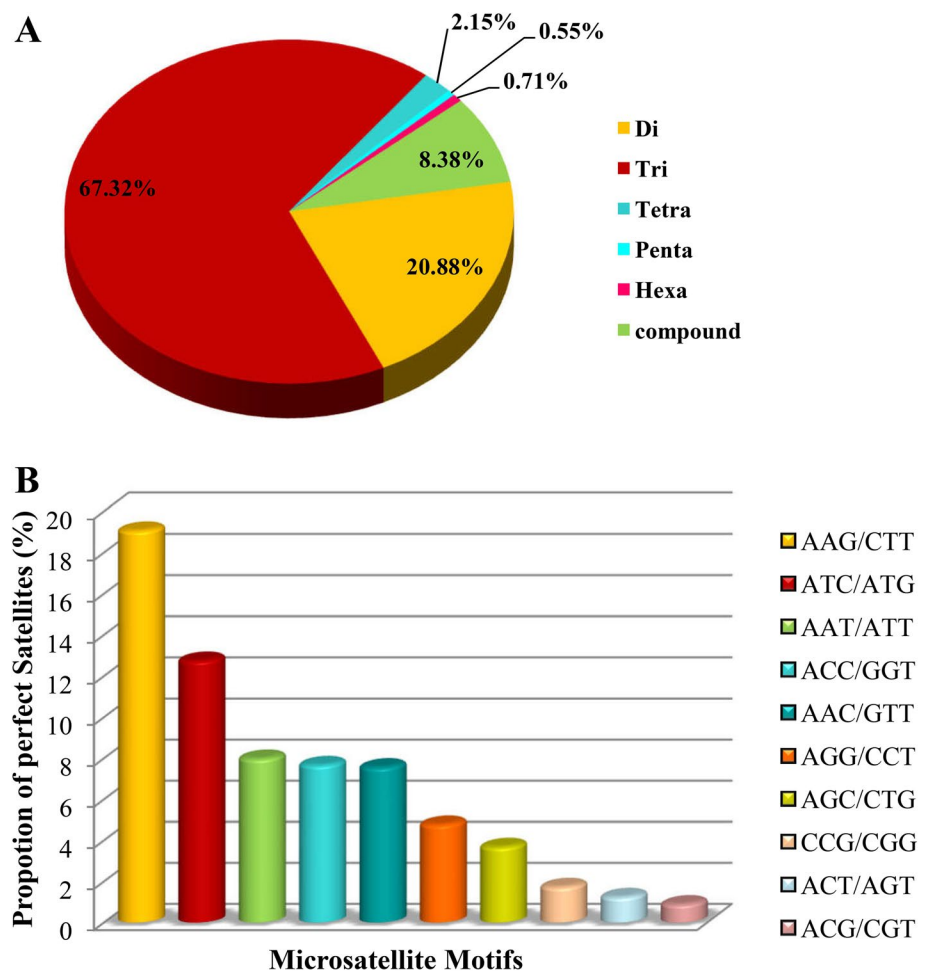
and acts as a permatin and hence has antifungal activity (Abad et al. 1996). Transcriptome analysis of a *Glycine max* also revealed an expression of the thaumatin gene for defence mechanism against *Phakopsora pachyrhizi* infection (Tremblay et al. 2010). Pectin methylesterases (PMEs) catalyses the demethylesterification of the homogalacturonan domains of pectin in the plant cell wall. Their activity is regulated by PME inhibitors (PMEIs), which function in plant responses to fungal infection (Liu et al. 2018).

Different defence-related genes, such as GST, cytochrome P450, and peroxidase were up-regulated in the resistant peanut genotype compared to the susceptible genotype in biotic stress. The GST enzymes play an important role in grass pea by protecting cells from secondary metabolites produced in response to rust pathogen attack (Garnica et al. 2013). The up-regulation of cytochrome P450 gene has been observed in infected *Glycine tomentella* during rust infection caused by *Phakopsora pachyrhizi* fungi. This cytochrome P450 is involved in the production of phyto-oxylipins, which play a critical role in plant defence response (Soria-Guerra et al. 2010). In this study, a similar trend of cytochrome P450 gene

up-regulation was found in the infected resistant sample compared to control resistant sample.

R genes encode proteins that interact with avirulence (Avr) effector proteins to induce resistance responses called effector-triggered immunity (ETI), which leads to hypersensitive response (HR) to restrict pathogen growth in plant cells (Lee and Yeom 2015). In general, it was found that R genes, such as F-box protein, MLO-like protein, and TIR-NBS-LRR class protein were highly up-regulated in the resistant variety (Liu et al. 2013a). F-box genes are involved in the regulation of plant hormone signalling pathways (Auxin, gibberellins, ethylene and JA) and disease resistance (Yu et al. 2007). R genes play a role in defence mechanism during wilt infection in castor crop, rust infection in common bean and wheat crops (Kapadia et al. 2015; Ayyappan et al. 2015; Chandra et al. 2016). We found induction PR genes such as beta-1,3-glucanase, GST and chitinase. PR genes are induced by salicylic acid (SA) signalling pathway and finally, lead to programmed cell death (Tremblay et al. 2010). Genes associated with the JA biosynthetic pathway were found to be up-regulated in the RI genotype, including the gene 12-oxophytodienoic acid reductase (Aradu.
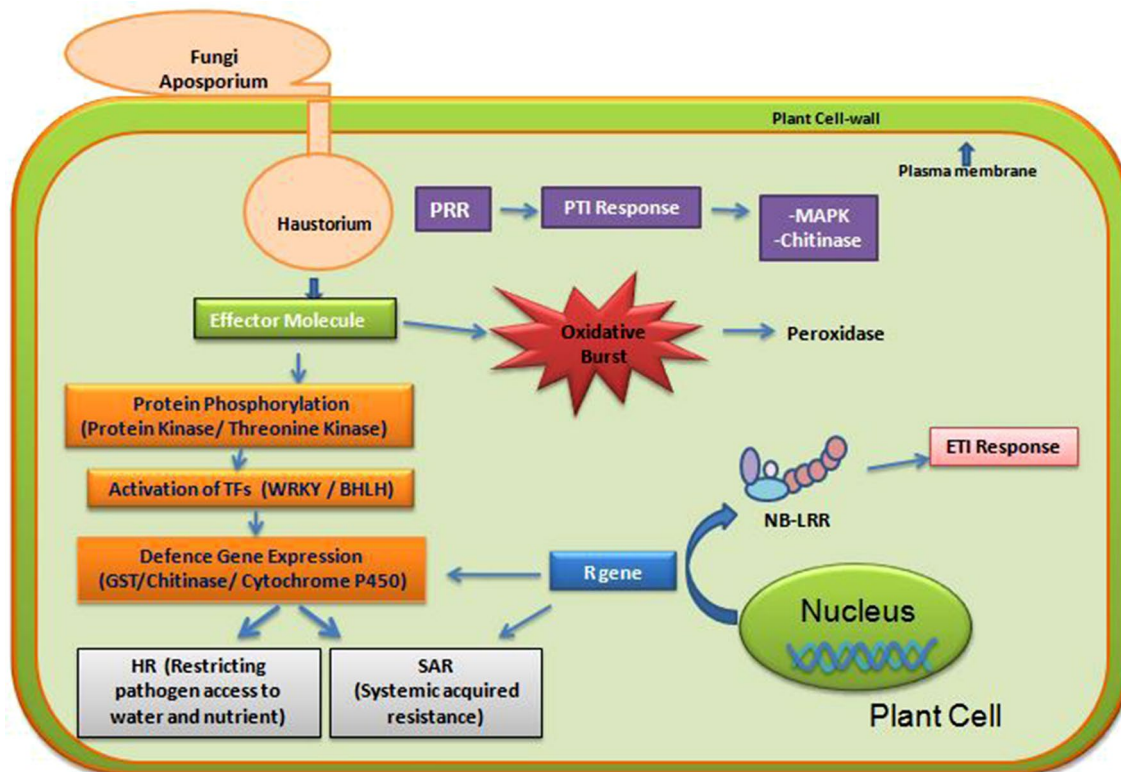
Fig. 7 Major defence mechanisms observed in peanut plants as a result of fungal infection. In peanut plants, three different defence mechanisms were found to be highly predominant in response to fungal infection. Fungal pathogen invades the plant cell with the help of haustorium to get access of water and nutrient. Pathogen effector molecule is recognized by the plant immune system, which activates protein kinase cascade followed by activation of transcription factors like WRKY and expression of defence related genes like, GST, Chi-tinase, and Cytochrome P450. Another defence mechanism results in oxidative burst leading to the production of enzymes such as peroxidase. In the second mechanism, plant cell expresses R-gene for production of NB-LRR protein, which leads to Hypersensitive Response and Systemic Acquired resistance. While in the third mechanism, Pathogen effector molecules are recognized by the host surface receptor proteins called pattern-recognition receptors (PRRs) which increase the MAPK activation

U86RL). A similar trend of 12-oxophytodienoic acid reductase gene expression was observed in the *Anemone coronaria* plant during rust disease, caused by the basidiomycete *Tranzschelia discolor* fungi (Laura et al. 2015). While during the infection, the SI genotype exhibited the down-regulation of lipoxygenase-like genes (Aradu.AS232), which actively participate in the biosynthesis of JA. Lipoxygenases (LOXs) play an important role in plant defence against fungal infection by the production of defence-related components and stomata closing (Canonne et al. 2011; Mhaske et al. 2013).

The transcription factors ERF, WRKY, MYB, and bZIP are involved in disease resistance by regulating the synthesis of phytoalexin (antimicrobial) compounds (Mao et al. 2011; Alves et al. 2014). WRKY genes were found to be up-regulated in wheat when infected with *Puccinia triticina*, causing leaf rust infection (Chandra et al. 2016). ERF gene expression is linked to the regulation of ethylene and JA dependent defence response genes (Shafiei et al. 2007; Heyman et al. 2018). Several genes and TFs such as WRKY, MYB, bHLH, bZIP, and NAC were actively expressed in early defence

responses in common bean-rust interaction (Ayyappan et al. 2015). In the present study, the MYB transcription factor was up-regulated (8.69-fold) in RI compared to in the RC genotype (Supplementary Tables 1). In plants, genes involved in signalling mechanisms play an important role in effecting early defence response (Chandra et al. 2016). We observed a high up-regulation of such genes, including protein kinase and serine/threonine kinase related transcripts (Aradu.6M72C, Aradu.LYT7G, and Aradu.ZTA1W). In this study, we found a higher expression of genes related to secondary metabolites, such as caffeate O-methyltransferase and terpenoids in infected resistant (GPBD-4) samples as compared to control, which may become important markers for the screening of resistant varieties in the defence response of plant against the pathogen. A similar trend of COMT gene expression was observed during rust infection in anemone plant (Laura et al. 2015). During biotic stress, the plant photosystem is suppressed, which leads to the down-regulation of photosynthesis-related genes during pathogen infection. The down-regulation of photosynthesis-related genes, such

as chlorophyll a/b binding proteins and ribulose bisphosphate carboxylase, was found in the common bean (*Phaseolus vulgaris*) during fungal infection (Jain et al. 2016). Simultaneously, in the present study, photosynthesis-related genes, such as thiamine thiazole synthase and pentatricopeptide repeat (PPR) superfamily protein, were found to be down-regulated at a greater level in the infected susceptible genotype compared to the infected resistant genotype.

The RT-qPCR analysis indicated that the expression patterns of the chitinase family and disease resistance genes were similar to those of the transcriptome sequencing data. We hypothesized that these are important genes regulated in response to the fungal pathogen (Supplementary Table 8). The cellulose synthesis gene that plays a central role in determining the mechanical properties of plant cell walls was up-regulated in the resistant variety during RT-qPCR and had the same expression pattern in RNA-Seq analysis (Kesten et al. 2017; Hamid et al. 2019).

RNA-Seq is a cost-effective, rapid and efficient approach to develop SSR markers in various plant species, EST-SSRs identified in this study are likely to have polymorphism within genes related to fungal resistance. These molecular markers may also assist in the construction of a peanut genetic map and diversity analysis. Overall, these two techniques were found to be supportive of RNA-Seq analysis. Earlier studies on EST-SSR mining have been reported from peanut seed transcriptome data (Zhang et al. 2012), and the data obtained from the database for stress response in *A. hypogaea* (Bosamia et al. 2015). Biotechnology can play an important role in developing new varieties through marker-assisted selection. Gene expression studies through NGS has made specific genome sequence information available, and this enables the identification and development of genome-wide markers (Onaga and Wydra 2016; Tulsani et al. 2020). Such molecular markers and gene discoveries may assist in developing *P. arachidis* pathogen-resistant peanut varieties.

Conclusion

The transcriptome profile of resistant and susceptible genotypes of peanut plants against *P. arachidis* was studied by RNA-Seq technology. DEGs were found to be related to the regulatory pathway of metabolism and defence-related activity during biotic stress. GO and KEGG analysis of DEGs revealed essential genes and their pathways responsible for the defence response to fungus. A resistant variety was found to withstand biotic stress due to the up-regulation of exclusively expressed defence-related genes (MLO-like protein, ERF, thaumatin, and F-box). On the other hand, the defence-related genes (lipoxygenase enzyme and pectin methyl-esterase inhibitor protein) were exclusively down-regulated in the susceptible variety during infection. Results of RT-qPCR

analysis validated the observations obtained from RNA-Seq data, while EST-SSRs mining is useful for QTL mapping, and crop improvement through marker-assisted breeding. This investigation helped to identify the varietal differences and candidate genes responsible for the plant defence mechanism against *P. arachidis* infection.

Compliance with ethical standards

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