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REVIEW

Host pathogen interaction and resistance screening of groundnut to stem rot disease caused by *Sclerotium rolfsii*

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Abstract Recently, soil borne diseases are posing a greater threat to groundnut production. Stem rot of groundnut is a soil-borne disease caused by the necrotrophic pathogen, *Sclerotium rolfsii*. Yield losses from major groundnut growing countries of 20–80% have been reported depending on disease intensity. Chemical and cultural practices are used to manage this disease, the soil borne nature of the pathogen and wide host range make it difficult to manage this disease by chemical and cultural methods alone. Additionally, host plant resistance is the most preferred option as it is cost-effective and an environmentally sustainable approach. Sources of resistance are reported from both cultivated species, *Arachis hypogaea*, and inter-specific derivatives. Spatial distribution and sensitivity of pathogen to environmental factors pose challenges to field evaluations. Although different methods of phenotyping are available, progress in breeding stem rot resistant cultivars is slow, given the challenges in using these phenotyping tools to identify quantitative disease resistance loci. Recently developed oxalic acid assay (OAA) is a robust method to distinguish plants that can easily succumb to this pathogen.Attempts were made to understand the biochemical and anatomical mechanisms and to identify genomic regions contributing towards resistance to stem rot disease. This review provides an overview of stem rot disease in groundnut, with a focus on host resistance and its application in breeding resistant cultivars.

Keywords Groundnut · Stem rot · Soil borne · Necrotrophic · Resistance · Breeding

Abbreviations

OAA	Oxalic acid assay
PPO	Polyphenol oxidase
POD	Peroxidase
PAL	Phenylalanine ammonia lyase
QTL	Quantitative trait loci
ICG	ICRISAT groundnut germplasm
ICGV	ICRISAT groundnut variety

Background

Groundnut (*Arachis hypogaea* L.), native to South America, is cultivated in more than 100 countries in the world (Desmae et al. 2019). Globally, it is grown in an area of 30.5 million hectares (M ha) with annual production of 54.2 million tonnes (Mt) (FAOSTAT 2023). Groundnut is considered as a rich source of protein, oil and several nutrients such as vitamin E, calcium, potassium, magnesium, phosphorus, zinc, iron, riboflavin, thiamine and niacin (Shasidhar et al. 2017). Kernels hold about ~ 25% protein, ~ 50% oil

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and ~ 15% carbohydrates (Janila et al. 2016). About 100 g of kernels provide 5 g of dietary fibre and 567 kcal of energy (Variath et al. 2017). Resveratrol, a polyphenol antioxidant present in groundnut, has been shown to protect against viral infections, cancer, heart disease, and degenerative neurological disease (Kumar et al. 2013). Groundnut-based products, particularly the confectionery types, are in high demand in the international market (Variath et al. 2017). Approximately 95% of the world's groundnut production occurs in Asia and Africa, where farmers with little resources produce the crop under rain-fed conditions with minimal inputs, resulting in low output (Janila et al. 2013). Low production is linked to inaccessibility to seeds of better cultivars, poor soil fertility, insufficient crop management measures, coupled with attack by various insect pests and diseases.

Disease-causing pathogens impact groundnut crop at different phases of growth, thus lowering the production (Ghuge et al. 1981; Ghewande et al. 1983). Collar rot, stem rot and dry root rot are the important soil borne diseases (Singh and Oswalt 1992). Soilborne pathogens impose significant yield losses in groundnut due to the close association of the pods with the soil (Thiessen et al. 2012). Among soilborne diseases, stem rot of groundnut caused by *Sclerotium rolfsii* is a global concern. This fast-spreading disease of groundnut is present in the tropics, subtropics, and warm temperate zones across the globe. Stem rot disease has resulted in significant crop losses in Bolivia, China, Egypt, Uganda, Vietnam, Taiwan, and Thailand (Kasundra et al. 2016). Changes in farming practices and climate have led to an increase in the disease's prevalence in several regions during the past decade (Kun-rong et al. 2018). Consequently, yield reductions of 5 to 25% have been reported under normal conditions (Mayee et al. 1988), and losses exceeding 80% have occurred in heavily infected fields under favourable weather conditions (Mehan et al. 1990). Huge economic losses are being incurred due to the stem rot disease in diverse crops, with groundnut sustaining the highest losses among all agricultural crops (Kator et al. 2015). In the twentieth century, in the USA, the groundnut crop incurred a loss of 10–20 million U.S dollars due to this disease (Kator et al. 2015).

Sclerotium rolfsii, is a ubiquitous necrotrophic fungal pathogen, has a wide host range of around 500 plant species, including groundnut (Aycock et al. 1966). The host range is as wide as including species from 100 families, infecting crops such as tomatoes, chillies, potatoes, sweet potatoes, carrots, crucifers, cucurbits, onion, cotton, soybean, sunflower legumes, wheat, and groundnuts (Hossain 2000). Billah et al. (2017) described the pathogenicity of *Sclerotium rolfsii* on different host species. It is challenging to control this pathogen in the infested soil as it can colonize either a living or a dead plant tissue (Thiessen et al. 2012). Chemical and cultural techniques have been the primary means of controlling this disease (Porter et al. 1982). However, chemical-based control is not encouraged due to economic reasons, environmental safety, and concerns on fungicide resistance in the target pathogen (Biswas and Sen 2000; Pant et al. 2001; Patibanda et al. 2002; Rudresh et al. 2005). The pathogen's persistence in soil and the presence of a large host range (approximately 500 species) frequently hinder the efficiency of chemical and cultural management strategies for stem rot disease (Shew et al. 1987). Disease management can be more effective by combining cultural methods with the development of resistant cultivars (Shew et al. 1984).

It is difficult to screen for stem rot resistance in the field because of the pathogen's uneven spatial distribution, sensitivity to temperature, humidity, soil type, cropping method, and host response in artificially inoculated circumstances (Shew et al. 1984). An efficient and repeatable screening technique to identify genotypes that are resistant to stem rot disease is required. Reports on greenhouse screening technology are also available, however, results have varied between the same genotypes tested in field and controlled conditions. Although several phenotypic screening methods are available, limited success has been achieved in identifying stable sources of resistance. Understanding the genetic control of stem rot disease and the use of novel genomic technologies is the key to identifying resistant sources. Studies are reported on the genetic control and the genomic regions associated with stem rot disease resistance in groundnut.

The pathogen and pathogenesis

The pathogen thrives in tropical, subtropical and warm temperate regions of the world, particularly in the United States, South and Central America, Africa, India and the European countries bordering the

Mediterranean region (Kator et al. 2015). The pathogen rarely occurs at temperatures below 0 °C and causes diseases such as blight, wilt, foot rot, collar rot, and stem rot (Punja 1985). The fungus produces sclerotia, which germinate under favourable conditions to produce the mycelium. Initially, the sclerotia are white to cream coloured, and later turn dark brown to black at maturity (Bekriwala.et al. 2015). They remain viable for several years in soil, potting media, or on plant debris. The mycelium could be killed at 0 °C, but sclerotia can thrive at temperatures as low as −10 °C (Ferreira and Boley 2018). The sclerotia can survive even when they are buried at 15–30 cm soil depth.(Punja 1988).

Several factors influence the growth, survival and pathogenicity of *S. rolfsii* including temperature, high humidity, aeration, and light (Bera et al. 2016b). Hyphal growth occurs at temperatures ranging from 8 to 40 °C, with optimum growth and sclerotia production occurring between 27 and 35 ℃ (Bera et al. 2016b). Punja (1985) described, specific soil conditions influence also impact fungal survival, it thrives in a pH of 3–5; sclerotia germination and mycelial growth are favoured in moist aerobic conditions. Infections of host is further enhanced when there is organic matter near plants. The influence of the stated factors on the pathogen's survival has been very well described by Punja (1985).

Stem rot disease cycle

As the main inoculum for the pathogen, sclerotia that are freely present in the soil or in combination with plant detritus are dispersed to uninfested areas by wind, water, animals, and soil (Kator et al. 2015). When the weather conditions favour, the sclerotia germinate at 25–35 °C by eruptive or hyphal germination to produce a white mycelium (Punja et al. 1984) that appears to be hyaline, branched, septate with clamp connections (Bekriwala et al. 2015) The amount of mycelium produced by germinating sclerotia is influenced by volatile chemicals, decaying plant tissues, and soluble nutrients in the soil (Punja and Grogan 1981). The groundnut plant canopy provides a warm and moist conducive environment for the infection of the pathogen (Shokes et al. 1998). The first infection of the host begins when white mycelium attacks the base of the stem. A dense white fungal mat with sclerotia on lower stems and the soil surface would be formed by the abundance of thick, massive hyphal cells on infected tissues (Punja and Grogan 1981). Mycelial growth from infected plants, plant debris, or sclerotia can spread the disease, but the movement of infected plant material or soil infested with sclerotia causes the disease to spread over great distances and recur in subsequent seasons (Punja 1985) (Fig. 1.).

Host–pathogen interaction

Infection begins when the mycelium contacts the host. The fungus takes two to ten days to form a mass of mycelium on the plant surface before penetrating the host cells (Kator et al. 2015). The mycelium grows as a dense network along the surface of the stem base. Mycelial aggregates (appressoria) are formed from the hyphal tips, which assist in entering the host tissue. An appressorium grows to form an infection peg to puncture the host cells to seek its entry into the host (Smith et al. 1986). Natural openings such as stomata and lenticels, wounds on the plant surface, the cuticle could be the entry sites into the host (Bera et al. 2016b; Rajasekhar et al. 2019). Histopathological works have declared that the fungus, being necrotrophic, causes tissue necrosis in advance of entering the host tissue, and piercing occurs later by means of appressoria (Higgins 1927; Milthrope 1941; Rajasekhar et al. 2019). Penetration into the host tissues occurs due to the cell wall degrading enzymes namely oxalic acid, pectic acid, polygalacturonase and cellulase which are released by the fungus. They act synergistically to cause separation and death of the cells (Bateman and Beer 1965; Aycock et al. 1966; Punja and Damini 1996). Thus, depicting the intra- and intercellular nature of the fungus through invasion within and in between the cells by the dissolution mechanism (Smith et al. 1986; Rajasekhar et al. 2019).

Oxalic acid is the principal metabolite and the primary pathogenicity factor of stem rot disease (Bateman and Miller 1966; Bateman and Beer 1965; Aycock et al. 1966). Oxalic acid chelates the calcium of the middle lamella of the cell walls to form calcium oxalate crystals; it also degrades the lignin present in cell walls, thus dissolving the structural components of the cells resulting in tissue maceration (Punja 1985; Bateman and Beer 1965; Kuan and

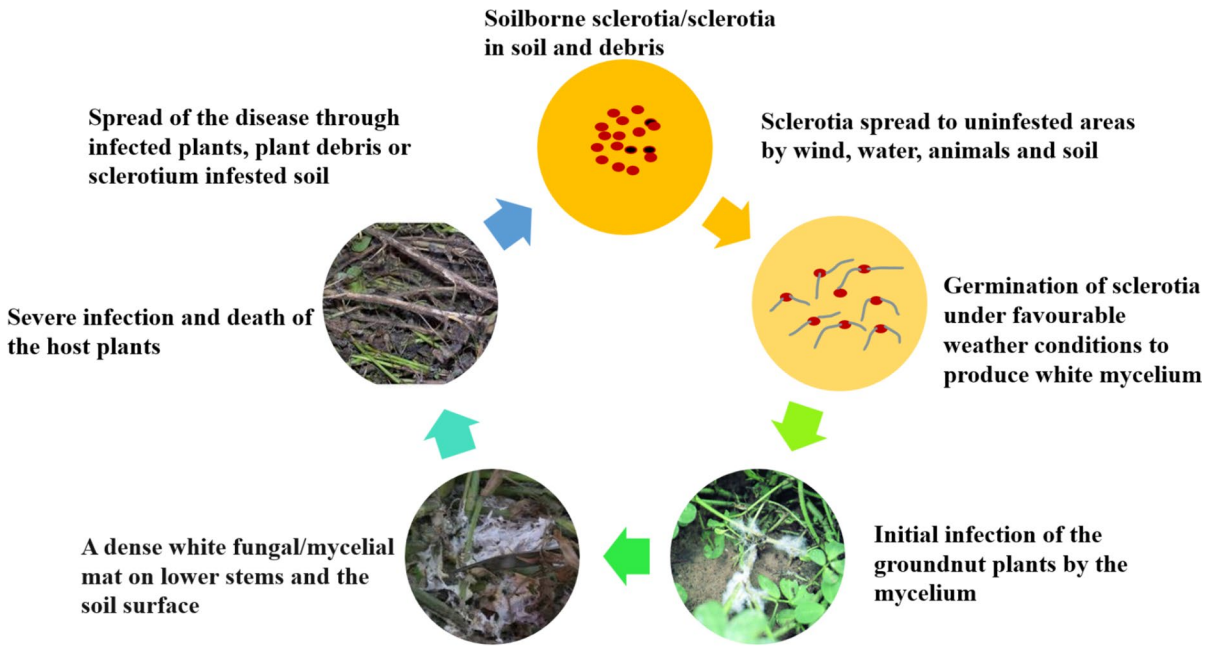

Fig. 1 Spread of the disease, Pathogenesis and disease cycle of *Sclerotiumrolfsii*

Tien 1993). The pathogen seeks its nutrition from the macerated tissues (Aycock et al. 1966). Thus, interfering with the translocation of water and minerals in the xylem vessels, consequently the wilting, yellowing and necrosis of the host plant (Bateman and Beer 1965; Yadeta and Thomma 2013).

Symptomatology

In Groundnut, the pathogen first targets the stem portion but can spread to the root, leaf, flower and pod of the plant (Bera et al. 2016b). The leaves on one or more branches may start to yellow and wilt, seem slightly decolourised, and ultimately turn brown. On each plant, a few branches may survive without infection. Groundnut plants, when infected in dry weather with a combination of high temperature, humidity, and wet condition, become totally rotted in the stem region except for the xylem (Backman and Brenneman 1984). The presence of mycelia can be observed at the collar region, and the production of sclerotia that resembles a mustard seed is visible. Mehan et al. (1995a) reported that, leaves are often small with a mild brown coloration when stems are partly girdled, but wilting does not occur. Subrahmanyam et al. (1992) reported the symptoms of pod rot include scattered black spots or large blackened regions on pod surface. Typically, the discolouration is superficial, but it can spread into the pod, thus causing kernel discolouration and reducing the kernel size. Occasionally, the diseased kernels exhibit a distinctive bluish-grey testa discolouration known as blue-damage (Subrahmanyam et al. 1992).

Host-resistance and defence mechanisms against stem rot in groundnut and other crops

The mechanism of resistance to *Sclerotium rolfsii* in groundnut may be due to structural, biochemical/metabolic, genetic factors, that may act alone or synergistically and cannot be clearly demarcated (Shew et al. 1987; Wynne et al. 1991). Characterization of components of resistance to stem rot pathogen in groundnut should differentiate between disease escape due to canopy type (phenological suppression) or those from structural barriers or the actual active responses of the plant to pathogen infection (metabolic resistance) (Shew et al. 1987). Phenological suppression of disease was best detected in field plots where differences in canopy structure were most fully expressed

(Fuller et al. 1984). Conversely, screening in highly conducive environments in the greenhouse negated the effect of crop canopy, allowing detection of metabolic resistance only (Fuller et al. 1984; Hunter et al. 1981).

Phenological and structural defence

The plant morphological features such as non-succulent stems for resistance to stem rot, hard pod shells for resistance to pod rot (Mehan et al. 1995a) and plant growth habit (Blad et al. 1978) can contribute to resistance to *S.rolfsii* in groundnut. *S. rolfsii* resistance may be phenologically associated with the canopy type in groundnut (Shokes et al. 1998). The growth habit and early maturity of the Spanish bunch cultivar, Chico and open/upright canopy of Virginia cultivars contributed to resistance to *Sclerotinia minor* (Chappell et al. 1995). Different mechanisms of suppression of *Sclerotinia sclerotiorum*, which is also a necrotrophic soil–borne pathogen, were detected in field and greenhouse evaluation of beans (Fuller et al. 1984; Hunter et al. 1981; Schwartz et al. 1978).

Anatomical defence

The internal anatomical features in plant species could contribute to resistance against plant pathogens. Formation of tyloses, specialized xylem ingrowths that can prevent colonization and spread of the pathogen to the upward plant parts just at the time of infection could be a resistance mechanism against *S. rolfsii* in CS 319, a known stem rot resistant cultivar of groundnut (Sujit Kumar 2015). Impermeable layer of phellogen deposited by lignified or suberized plant tissues (Aycock et al. 1966) with higher levels of calcium (Bateman and Beer 1965; Punja 1985), phenolic compounds or oxalic acid oxidase (Franceschi and Horner 1980), and tissues that contain protein inhibitors of endo polygalacturonases (Albersheim and Anderson 1971) can offer resistance to *S. rolfsii* invasion and infection.

Biochemical/metabolic defence

A hypersensitive reaction (HR) is incited upon pathogen attack, which protects the plants by strengthening their cell walls through deposition of phenolic compounds, synthesis of enzymes, phytoalexins and accumulation of pathogenesis related (PR) proteins (Nandi et al. 2013; Bosamia et al. 2020). Defence responses are frequently activated in the plant's surrounding and even distal uninfected parts, resulting in systemic acquired resistance (SAR) (Yu et al. 1997). Induction of systemic acquired resistance by enhanced activity of chitinases and β-1,3-glucanase (which hydrolyses the β-1,3-glucans, an important biopolymer seen in the fungal cell walls) against *Rhizoctonia* species in bean plants was demonstrated by Xue et al. (1998). SAR upon treatment with *Sclerotium rolfsii* was demonstrated in four cultivars of groundnut (A100-32, Georgia Green, Ga-07 W and York) by Jogi et al. (2016) and J-11, GG-20, TG-26 and TPG 41 by Nandini et al. (2010). Reports infer that increase in the content of oxidative enzymes notably polyphenol oxidase (PPO) and peroxidase (POD) as well as the ones responsible for phenolic biosynthesis such as Phenylalanine ammonia lyase (PAL) involved defence reactions in plants (Chen et al. 2010). Results of increased activity of POD, PPO, chitinase and β-1, 3-glucanase were observed by Nandi et al. (2013) in cowpea when inoculated with *S. rolfsii.* POD, PPO, PAL and phenol are involved in cowpea resistance against *R. solani* and in tea against *S. rolfsii* (Bhagat and Chakraborty 2010). Phenolics are fungitoxic in nature which brings certain morphological changes that cause cytoplasmic disorganization and reduced protoplasm content of the fungal hyphae. Besides, they also increase mechanical strength of the host cell wall (Nandi et al. 2013). Saraswathi et al. (2012) reported in their chromatographic technique studies, the presence of 10 phenolic acids in healthy plants. Sugars are the precursors of phenolics (Vidyasekaran 1978). They actively inhibit pectinolytic and cellulolytic enzymes, which are important for the pathogen (Bateman and Miller 1966). A study conducted by Mahatma et al. (2018) to analyze the metabolic profile of groundnut genotypes under *S. rolfsii* infection revealed distinguished metabolic patterns of sugars in control and inoculated plants. Succinic acid, pentitol, scopolin, D-glucose and D-turanose, myo-inositol, fructose and mannitol were found in excess in control

plants, however, D-ribopyranoside, thymol, pentadecanoic acid and octadecanoic acid were abundant in the inoculated plants at 24 h after inoculation than that of control. The stem rot resistant groundnut genotypes CS 319 and CS 19 had greater levels of glucose, sucrose, and phenolics such as cinnamic acid, caffeic acid, and salicylic acid.

Evaluation of *S. rolfsii* disease resistance in groundnut

For improving genetic resistance to diseases by breeding, availability of resistant sources and reliable disease screening methods are prerequisites. A reliable and repeatable screening method ensures the identification of resistant sources and for screening the segregating populations to exercise selection decisions. Multi seasonal and muti-locational disease trials that also assess the genotype and environment (G X E) interaction of disease reaction would further enhance the reliability of lines selected for disease resistance. To transfer the disease resistance trait from resistant sources to an elite high yielding genotype, the availability of an efficient phenotyping technique is essential (Pande et al. 1994) or trait associated markers are necessary. Different phenotypic screening methods have been practiced for assessing stem rot disease in groundnut (Cui et al. 2020; Luo et al. 2020). Phenotyping techniques for diseases in plants in general include screening in field, glasshouse and laboratory methods.

The field screening for stem rot disease reaction requires a disease sick/inoculated plot that needs to be developed by application of inoculum and measuring the inoculum load. In sick plot, the disease development depends on several factors such as, type of inoculum, presence of organic matter on soil surface, quantity of inoculum and depth of inoculum (Pande et al. 1994). Hence, the development of artificially inoculated plots requires application of sufficient inoculum load. Bera et al. (2016a, 2016b) have standardized a phenotypic technique for screening of stem rot disease in groundnut under field conditions in inoculated plots. The essential components of the screening technique are multiplication of the pathogen, field preparation and sowing of the plant material, selection of appropriate measure of disease reaction (disease mortality, severity score and time, stage of the crop for inoculum application, maintenance of optimum temperature and moisture conditions and evaluation of the disease parameters (Bera et al. 2016b). The most favourable temperature and the recommended time for phenotyping is 15–35 ℃ (Bera et al. 2016b) and 40–45 days after germination (Pande et al. 1994) respectively. Regular irrigations should be applied to the field to maintain sufficient soil moisture conditions to ensure pathogen growth. For disease evaluation/assessment, Shokes et al. (1998) reported a scale of 1–5 for disease severity assessment under greenhouse and field conditions. The scale is denoted by 1 = healthy plants (resistant), 2 = stem lesions only (moderately resistant), 3 = ≤ 25% of the stems wilted or dead (moderately susceptible), 4 = 26–50% of stems wilted or dead (susceptible) and 5 = > 50% of stems wilted or dead (highly susceptible).

Stem rot disease screening studies at the field level have been taken up by various researchers in inoculated plots and disease incidence varied with the market types of groundnut, planting dates, growth stages and the maturity duration of the crop. The Valencia market types were reported to have the highest susceptibility (Cooper 1965; Branch and Csinos 1987). The Spanish bunch types were more susceptible compared to the Virginia types, while the Runner type cultivars have depicted more disease resistance than the other market types (Cooper 1965). Susceptibility of host plants and disease severity was observed to be the highest in the early planted genotypes and during the early stages of the plant growth (0–45 days after sowing), while a decrease in susceptibility was noticed in the late planted genotypes and with the increasing age of the plant (Brenneman and Hadden 1996; Gorbet et al. 2004; Bekriwala et al. 2015). Conversely, Pande et al. (1994) reported that, susceptibility was not observed to be reduced with plant maturity.

Screening of germplasm for stem rot resistance has revealed clear genotypic/varietal differences in groundnut (Muheet, et al. 1975; Branch and Csinos 1987; Shew et al. 1987; Bera et al. 2014). Disease evaluation studies on heterogeneous plant material over different locations, seasons and years with varying soil types have shown significant differences in resistance responses. Shokes et al. (1998), Mehan et al. (1995a, b), Bera et al. (2014), Revankar et al. (2018), reported that post rainy and summer screening in Vertisols recorded higher disease incidence, the

resistant cultivars identified from such screening were late maturing, semi-spreading Virginia bunch types with non-succulent stems and hard pod shells.

When carrying out pot screening, the factors such as pot size, soil mixture, amount, and method of application of inoculum, optimum temperature, humidity and moisture conditions determine optimum disease development (Bera et al. 2016b). Besides, the disease assessment method is also important. Pande et al. (1994) developed a greenhouse screening method for evaluation of groundnut genotypes for stem rot reaction, the inoculum was applied by spreading it on the soil surface which was followed by covering it with groundnut leaf debris. This inoculation method ensures pathogen conducive warm and humid micro-environment for maximum disease development. Nevertheless, characterization of components of resistance and identification of breeding lines with stable resistance, genotypes and segregating populations must be evaluated in field, micro plots, and greenhouse environments (Shew et al. 1987). Groundnut germplasm from gene banks and improved germplasm from breeding programs reported for resistance to stem rot disease are summarized in Tables 1 and 2.

On the other hand, laboratory assays would prove beneficial for obtaining rapid, and repeatable results. The crop diseases in which oxalic acid secretion of the pathogen happens to be the principal pathogenicity factor, indirect assay using oxalic acid solution by the replacement of the actual pathogen provides a fast-screening method. Indirect assays using oxalic acid have been demonstrated in common bean for white mould (Kolkman and Kelly 2000; Chipps et al. 2005); in *Jerusalem artichoke* for stem rot (Sennoi et al. 2021) and in groundnut, for *Sclerotinia minor* using detached stems (Brenneman et al. 1988; Melouk et al. 1992; Bennett et al. 2015) leaflets (Hollowell et al. 2003), whole plant (Cruickshank et al. 2002; Goldman et al. 1995), in groundnut for *S. rolfsii* (Kiranmayee et al. 2024; VeerendraKumar et al. 2024). This method of screening is more efficient and is complementary to the glasshouse and field screening methods and has high throughput.

In case of groundnut stem rot, Bailey, a partially resistant line to stem rot disease was released in 2008 by North Carolina Agricultural Research Service (Isleib et al. 2011). NC 2, a partially resistant cultivar was released in 1953 (Cook 1981).NC 3033, a resistant line, was identified and used as a parent in crossing programs to develop resistant breeding lines (Beute et al. 1976; Shew et al. 1985). The resulting breeding lines from these crosses exhibited partial resistance to stem rot disease in the field and glasshouse screening tests. Till date, cultivars with high resistance to stem rot disease are not available. Hence, there is a need to identify better resistant sources for breeding resistant cultivars.

Resistance to soil-borne pathogens including stem rot of groundnut has been attributed to polygenic control and additive gene action (Bera et al. 2016a). Polygenes are thought to oversee partial resistance, which is analogous to horizontal resistance (Bera et al 2016a). Smith et al. (1989) have studied the reaction of selected groundnut breeding lines for stem and pod rot diseases and reported that resistance to these diseases is heritable, thus creating a scope to further improve the resistance of these lines.

Dodia et al. (2019) examined stem rot disease resistance in an F2 mapping population (TG–37A x NRCGCS 85) of groundnut and reported three polymorphic SSR primers (DGR294, DGR470 and DGR510) between the resistant and susceptible bulks. The first study on the discovery of stem rot disease resistance QTL was performed using linkage mapping and QTL mapping approach, which has been published by Bera et al. (2016a) in an F2 population (GG 20×CS 19) and a major QTL, identified as *qstga01.1* on linkage group one, and was contributed by the resistant parent CS 19 was identified through this study. Dodia et al. (2019) also performed linkage analysis and QTL mapping in a bi-parental population (TG37A×NRCG-CS85), a main-effect QTL could not be detected, but they identified 44 major epistatic QTLs with a phenotypic variation ranging from 14.32 to 67.95%. A QTL on a physical map length of 5.2 Mb was identified on B04 comprising of 170 different genes. Developing diagnostic markers for selection of the candidate QTLs can be useful in breeding for stem rot resistance. Integrating phenotyping methods with molecular markers linked to identified QTLs would accelerate the advancement of stem rot resistance breeding programmes in groundnut. Genomic predictions (GP) can also be utilized for the use in resistance breeding programs targeting the improvement of stem rot disease resistance genotypes.

Table 1 Stem rot resistant sources identified, utilized in groundnut breeding programs so far through field studies

Field screening		
Genotypes that are resistant/moderately resistant identified from the study	Type of plant material (germplasm, improved germplasm etc.)	References
TxAG-3, Tx-798716 and Tx-4798396	Breeding lines (improved germplasm)	Smith et al. (1989)
NC 2	Germplasm lines	Cook (1981)
NC 9, VA 81B	Bunch type groundnut cultivars	Brenneman et al. (1990)
Interspecific hybrids and their derivatives 326, 988, 1019, 1024, 1065, 1267 and 1364	Interspecific derivatives	Mehan et al. (1995a)
ICGVs 86,034, 86,124, 86,252, 86,388, 86,590, 86,606, 86,635, 87,160 and 87,359	Interspecific derivatives	Mehan et al. (1995a)
ICGV 87165 and ICGV 86590	Spanish bunch elite lines	Krishnakanth et al (1999)
Toalson and Mass-selected populations from Sunbelt Runner Toalson	Mass selection population; F6-F9 generations	Brenneman et al. (1990)
Florida MDR 98 and C-99R	Florida MDR 98—three-way cross made C-99R- selection line from a cross	Gorbet and Shokes (2002a); Gorbet and Shokes (2002b)
Dh 8	Groundnut cultivar	Krishnakanth et al. (2003)
ICGV-91167, Y-1024, JL-80 and CSMG-84–1	Advanced breeding lines and released cultivars (improved germplasm)	NRCG Annual report (2003–04)
NRCGCS-168, NRCGCS-151, NRCGCS-25, NRCGCS-19 and NRCGCS-157	Interspecific derivatives	NRCG Annual Report (2003–2004)
TCG 1525, P 1269710, NCAC38, Hory-anawadim ND 8–2, SS 34 m, VRR 472, Talson, P 1268559, NCAc 18,019 and RR 5290	Germplasm accessions, advance breeding lines and released cultivars	Ashok et al. (2004)
Gorgia–03L	A cross between 'Georgia Browne' and VA-C92R. Pedigree selection within (F.sub 2), (F.sub 3) and (F.sub 4) segregating population	Branch (2004)
NRCGCS-15, NRCGCS-272, NRCGCS-286, NRCGCS-300, NRCGCS-306, NRCGCS-307, NRCGCS-311, NRCGCS-315, NRCGCS-319, NRCGCS-327, NRCGCS-334, NRCGCS-343, NRCGCS-347 and NRCGCS-350	Interspecific derivatives	NRCG Annual Report (2005–2006)
CS-19	Interspecific derivatives	Bera S K et al. (2005)
PBS-30033 and PBS-22028	Breeding lines	NRCG Annual Report (2006–2007)
Georgia-07W	A cross between ' 'C–99R' x 'Georgia Green'	Branch and Brenneman (2008)
NRCGCS-365, NRCGCS-387, NRCGCS-394, NRCGCS-398 and NRCGCS-399	Interspecific derivatives	DGR Annual Report (2008–2009)
Florida-07	Released cultivar	Gorbet and Tillman 2009
NRCGCS-85, NRCGCS-124 and NRCGCS-180	Interspecific derivatives	Bera S K et al. (2011)
GG-11 and GG-13: moderately resistant,	Spreading type groundnut cultivars	Rakholiya, K.B and Jadeja, KB (2010)
NRCGCS-86, NRCGCS-21 and NRCGCS-222	Interspecific derivatives	Bera S K et al. (2010)
NRCGCS-319	Advanced breeding lines	Thirumalaisamy et al. (2014)
NRCGCS-47, NRCGCS-99, NRCGCS131 and NRCGCS-319	Interspecific derivatives	Bera S K et al. (2014)

Table 1 (continued)

Field screening		
Genotypes that are resistant/moderately resistant identified from the study	Type of plant material (germplasm, improved germplasm etc.)	References
NC 2, NC Ac 18,016, NC Ac 18,416, ICG 319 15,233, ICG 15234, ICG 15235, ICG 15236, ICGV 96590 and ICGV 87160 (ICRISAT); NRCGCS 47, NRCGCS 99, NRCGCS 131 and NRCGCS 319 (DGR, Junagadh, India); Southern Runner, Toalson, Pronto, Georgia Browne, Sunbelt, Runner, Tamrun 96, Georgia-10R and Georgia-05E (USA)	Germplasm lines and improved germplasm (elite breeding lines)	Nigam (2015)
Six segregant lines (21, 77, 109, 25, 165 and 36)	165 segregants derived from TAG 24 and R 9227	Santoshkumar et al. (2011)

Table 2 Stem rot resistant sources identified, utilized in groundnut breeding programs so far through glasshouse studies

Glass house Screening		
Genotypes that are resistant/moderately resistantidentified from the study	Type of plant material (germplasm, improved germplasm etc.)	References
GG-11, GG-13	Groundnut cultivars	Rakholiya K B (2009)
NRCGCS-47, NRCGCS-99, NRCGCS-31 and NRCGCS-319	Interspecific derivatives	Bera S K et al. (2014)
NRCG-CS-319, NRCG-CS-19	Interspecific derivatives, and registered groundnut cultivars	Thirumalaisamy P P et al. (2014)
ICGV 86699, ICGV 91114 and ICGV 89280	Advance breeding lines (improved germplasm)	Divya Rani et al. (2017)

ICG : ICRISAT Germplasm; ICGV : ICRISAT Groundnut Variety; ICGS : ICRISAT Groundnut Selection; NRCG : National Research Centre for Groundnut; TxAG/Tx : Texas Groundnut; NC : North Carolina line; VA : Virginia line, Dh : Dharwad; JL : Jalgaon; NCAc : North Carolina Accession; GG : Gujarat groundnut

Candidate genes governing stem rot resistance

Jogi et al. (2016) conducted a study to identify differentially expressed genes during the early infection stage of *S. rolfsii* in four cultivars of groundnut namely, A100-32, Georgia Green, Ga-07 W and York. The identified genes from the study were responsible for induction of systemic acquired resistance (SAR) upon treatment with *Sclerotium rolfsii*. Upregulation of genes related to defence enzymes namely peroxidase, phenyl ammonia lyase, salicylic acid, β-1,3-glucanase and chitinase was observed in the resistant cultivar, York. Nogiya et al. (2021) observed that the resistant groundnut genotypes, CS319, GG17, and GG31, when infected with *S. rolfsii*, exhibited upregulation of genes involved in polyamine biosynthesis. In contrast, the susceptible genotype TG 37A showed increased expression of genes related to ethylene biosynthesis and amine oxidase. Several transcription factors, receptor like kinases and jasmonic acid pathway enzymes were involved in the profound expression in groundnut stem rot resistant genotypes (Bosamia et al. 2020). Although some of the studies mentioned here have aided in understanding the resistance mechanisms at the RNA/genes level, further studies are essential to characterize and validate the unknown genes and to fully understand the function of the identified genes so as to apprehend the early host–pathogen interaction.

Conclusion and future prospects

The increasing groundnut yield losses caused by stem rot disease over the last decade necessitated

management of the disease to plug the losses. Chemical and cultural control methods are employed to manage the stem rot disease, however, host–plant resistance to stem rot disease in groundnut is an economically viable and environmentally sustainable option, and it deployed together with other management methods. To exploit the potential of host-resistance, research groups have made progress in understanding the biology of pathogen, mode of infection, spread, and interaction with a wide range of hosts. Studies have shown that oxalic acid, pectic acid, polygalacturonases and other cell wall degrading enzymes are the components that can constrain invasion of pathogen. Tissue section studies to establish the entry points and the path taken by the pathogen to kill the host cells will help in understanding of host-plant interaction, and the host-plant resistance mechanism, genetics and mode of inheritance. In the USA moderately resistant stem rot cultivars are developed and made available to the growers. Source of resistance (of varying degree) have been reported in the cultivated species as well as several inter-specific derivatives. The sick plot screening is effective under favourable weather conditions; however it is expensive and is low throughput given the spatial variation of the pathogen in the soil. Although stem rot resistant sources have been identified their use in breeding is limited given that the expensive sick plot screening and lack of high throughput phenotyping tools. The Oxalic Acid Assay (OAA) is a lab based high throughput method that allows for screening a large number of lines in the breeding program, and thus can be used to reduce the number of lines that can be moved to sick plot screening, thus optimizing the resources.

To overcome current limitations, there is a need to standardize phenotyping protocols and explore diverse sources of resistance, including wild *Arachis* species and interspecific derivatives. Pre-breeding efforts should focus on transferring resistance into elite cultivars without compromising the yield. Molecular breeding strategies, such as QTL mapping, marker-assisted selection, and genomic prediction, hold great potential for accelerating the development of resistant cultivars. Additionally, omics approaches such as transcriptomics, proteomics, and metabolomics can provide deeper insights into resistance mechanisms and help identify novel candidate genes. Given the nature of the disease, the genomic prediction and machine learning can be explored for use in developing stem rot resistant cultivars to strengthen groundnut breeding pipelines.

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