Identification and characterisation of potential novel sources of resistance to ascochyta blight within the exotic germplasm of lentil

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Ascochyta blight (AB) caused by *Ascochyta lentis* affects gross profits and yield stability of lentil in Australia. The susceptibility of previously released resistant cultivars (Northfield and Nipper) and a future uncertainty over the resistance status of the few remaining available resistance sources, has necessitated an immediate influx of novel and diverse resistance sources into the Australian lentil breeding program. To aid in this, the potential of exotic germplasm including thirty accessions from five-wild species of lentil collected from Australian grain genebank (AGG), Horsham were screened against two highly aggressive *A. lentis* isolates (FT13037 and FT13038). The bioassay revealed two highly resistant *L. orientalis* accessions (ILWL 180 and ILWL 7) and a ten (*L. nigricans* (6), *L. odomensis* (1), *L. ervoides* (1), *L. lamottei* (1), and *L. orientalis* (1)) moderately resistant accessions. Of these, accession ILWL 180 of *L. orientalis* was the most resistant compared to the control ILL 7537. Apart from validating the symptomatic results, replicated histopathological studies was later carried out to understand the resistant mechanisms underlying lentil's defence to *A. lentis* including the assessment of spore germination percentage, germ tube length and timing of appressoria formation of highly aggressive isolate FT13037. This indicates early and rapid recognition of *A. lentis* invasion is likely a major contributor for superior resistance as observed in ILWL 180. Additional evidence of faster accumulation and notably higher levels of reactive oxygen species (ROS; hydrogen peroxide and superoxide) and phenolic compounds in response to *A. lentis* penetration at 12 hours post inoculation (hpi) compared to ILL 7537 confirmed ILWL 180 could be a potential resistant source for future lentil breeding program to develop cultivars with more durable *A. lentis* resistance.

To better understand the genetic basis of resistance, a F_5 recombinant inbred line (RIL) population (N = 140) was constructed from an interspecific cross between ILWL 180 and AB susceptible cultivar ILL 6002 using accelerated single seed descent technology. The RILs and parents were then sequenced through transcriptome sequencing and using 815 high quality single nucleotide polymorphism (SNP) markers generated, a linkage map was constructed. The map stretched 488.02 centiMorgan (cM) along eight linkage groups (LGs) with an 0.66 cM average marker-marker distance. Genetic dissection of the RIL population detected a quantitative trait loci (QTL) on LG5. The identified QTL region stretched 4.93 cM and harboured nine putative candidate genes linked to AB resistance. Of these, five candidate genes were directly related to plant defence responses. Overall, the disease symptomatology, physiological and biochemical responses, and genetic evidence of resistance against AB infection support the conclusion that a stable and novel AB resistance was identified and characterised from ILWL 180. This offers significant potential to improve AB resistance of the existing cultivars within the Australian lentil breeding program.