



ISBN 978-85-66836-16-5

TRANSCRIPTOME ANALYSIS OF RESISTANT AND SUSCEPTIBLE COWPEA NEAR ISOGENIC LINES INFECTED WITH ROOT-KNOT NEMATODE<sup>1</sup>/ Análise do transcriptoma de isolinhas resistentes e suscetíveis de feijão-caupi infectadas com o nematoide das galhas. J. R. P. SANTOS<sup>1</sup>; A. NDEVE<sup>1</sup>; B. HUYNH<sup>1</sup>; W. C. MATTHEWS<sup>1</sup>; S. WANAMAKER<sup>2</sup>; T. J. CLOSE<sup>2</sup>; P. A. ROBERTS<sup>1</sup>. <sup>1</sup> Department of Nematology, University of California, Riverside, CA 92521, USA / <sup>2</sup> Department of Botany and Plant Sciences, University of California, Riverside, CA 92521, USA. E-mail: jansen@unb.br

Cowpea (*Vigna unguiculata* L. Walp.) is protein-rich legume crop, particularly important in Africa, Latin America, Asia and United States. This crop is notable for its high adaptability to extreme temperature conditions, poor soil fertility and water deficit. However, its production is severely limited by biotic and abiotic constraints, including root-knot nematode (RKN) infection. To address this issue, we analyzed the transcriptome profile of two cowpea near-isogenic lines, CB46 Null (homozygous susceptible) and CB46 72-1-3 (homozygous resistant). RNA sequencing of root tissues was performed 3 and 9 days after RKN inoculation (DAI), and sequence reads were aligned to common bean whole genome, resulting in about 19,000 unique genes mapped to the reference genome. Comparison between inoculated and non-inoculated plants at both time points revealed a total of 239 DEGs in the susceptible line and 1969 DEGs in the resistant line. Overall, most of the genes were up-regulated in both lines, mostly at 3 DAI compared to 9 DAI for the susceptible line and at 9 DAI compared to 3 DAI for the resistant line. Genes related to abiotic stress, hormone signaling (ethylene and jasmonic acid (JA)), cell wall, beta glucanase, proteolysis, R genes, PR-proteins, redox state, peroxidases, glutathione-S-transferase, signaling, transcription factor (ERF and MYB) and heat shock proteins were significantly up-regulated at 3 DAI, with few genes related to specific hormone signaling (abscisic acid (ABA) and ethylene), signaling, transcription factor (WRKY), and secondary metabolites being down-regulated for the susceptible line. In the resistant line, genes related to hormone signaling (auxins, ABA, ethylene), cell wall, proteolysis, PR-proteins, abiotic stress, peroxidases, signaling and transcription factors (ERF, WRKY, MYB, DOF) were down-regulated at 3 DAI, while significant up-regulation was observed for genes related to hormone signaling, cell wall, beta glucanase, proteolysis, PR-proteins, signaling, abiotic stress, redox state, peroxidases, glutathione-S-transferase, transcription factors (ERF, bZIP, WRKY, MYB), heat shock proteins and secondary metabolites at 9 DAI. Among the genes assigned to defense, only one gene belonging to resistance gene family, a TIR-NBS-LRR, was up-regulated in the resistant line. The expression analysis provided insights into gene modulation during infection, including both defense responses to limit parasitism and effector-targeted host genes.

**Keywords:** *Meloidogyne incognita*; RNA-Seq; Resistance; *Vigna unguiculata*.

<sup>1</sup> Grant information: USAID, California Dry Bean Advisory Board, California Agricultural Experiment Station and CAPES Foundation.