**Activity:** Quantification of Foc colonization through qPCR in resistant and susceptible cultivars grown under elevated CO2

**Objective**: Real-time quantification of Foc causing Fusarium wilt disease in chickpea under elevated atmospheric CO2

**Materials and methods**: The chickpea seedlings of susceptible cv. JG 62 and resistant cv. WR 315 were grown in open top chambers at different CO2 concentrations [ambient (~380 ppm) and elevated ( 550 ppm and 700 ppm). Seven day old seedlings were inoculated with Foc and samples were collected 7, 14 and 21 days of post inoculation. The sequence specific primers for quantification of Foc were designed using 18S sequences of FOC. qPCR was carried out using pure gDNA and a standard curve was generated by plotting the cycle threshold value (Ct) versus the logarithm of the concentration of each serial dilution of DNA in a 10 fold over a 7-log range from 10 to 1 × 10−4 ng/μL. The quantification of Foc in chickpea was quantified using DNA of infected plant samples through real-time PCR.

**Results and interpretation**: A good correlation was observed between Ct values and DNA concentration of standard. The slope of linear regression curve was −3.27 with the correlation coefficient R2 = 0.99 demonstrating the PCR efficiency of 101.87%. Standard curve obtained in this study indicated that the nominated primer was highly specific over a linear series of magnitude. The fungal colonization and disease development was found to be similar in ambient and higher CO2 concentration (700 ppm) but delayed at 550 ppm. In ambient condition, the fungal DNA reached to the minimum detection limit 0.097 ng in 1.0 ng of host plant DNA after two weeks of Foc inoculation. In case of elevated CO2 concentration of 550 ppm and 700 ppm, the fungal colonization was 0.022 ng and 0.096 ng respectively, at similar time point.

**Next steps**: Study needs to be repeated to confirm the findings.