Abstract No: 214 Life Sciences

## ASSESSMENT OF BLAST DISEASE DAMAGE IN FINGER MILLET FARMER FIELDS: A PRELIMINARY INVESTIGATION

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Blast is a serious disease in finger millet (*Eleusine coracana*) worldwide. The objective of the present study was to estimate blast disease damage in finger millet farmer fields in Sri Lanka. Four randomly selected fields in two agroecological zones DL1b and DL2 were screened. Fields located at DL1b include, one at Anuradhapura which was 2 months after planting (F1), a field at Ampara, which was 4 months after planting (F2) and a field at Puttlum which was 2.5 months after planting (FIV). Fields located at DL2 include one at Puttlum which was 1.5 months after planting (FIII). Variety 'Oshadha' was cultivated in FI and FIV whereas traditional varieties were grown in FII and FIII. Three independent researchers visually estimated disease incidence (DI) percentage and disease severity (DS) percentage in three 1 m<sup>2</sup> plots per field. A detailed analysis was carried out using samples of 30 plants from FIII and FIV using a 1 to 9 DS scale based on lesion counts. The DS was 5%, 5%, 30% and 23% and DI was 84%, 0%, 100% and 100%, respectively, in the Fields I, II, III and IV. Seed broadcasting was practiced in three out of the four fields studied (FI, FIII and FIV) where the average plant density was 99/m<sup>2</sup>, twice higher than in field where transplanting was practiced. The variety Oshadha in FI and FIV rated different DI and DS despite both fields being in DL1b; thus details of agronomic practices that directly affect disease damage need to be wellthought-out in large-scale disease assesments. Based on lesion counts FIII rated 4, and FIV rated 8, showing that visual estimations and counted data were in contrast highliging the need for more accurate protocols for field disease evaluation. Compared to the rest, FIII rated low lesion counts and lesions were  $\leq 1$  mm in diameter. Restricted lesion diameter indicates R gene mediated host resistance and the farmer variety in FIII provide genetic resources for potential putative R genes. The outcome of this study provides essential preliminary infomation for implementing an island-wide disease assessment.

Financial assistance from the National Research Council (Grant No. 18-091) is acknowledged.

**Keywords:** Agro-ecology, Agronomy, Disease incidence, Disease severity, R genes