DC-DC-FP2-5.FP2-5-11 - Sources of resistance in the existing breeding germplasm will be identified for incorporation in the elite cultivar/variety.

- 1. Identification of new sources of resistance to foliar pathogens of barley.
- 2. The FIGS subsets of net blotch, GCP subset, low input association mapping panel (LI-AM), and the high input barley association mapping panel (HI-AM) were screened independently with a mixture of 20-isolates of net blotch and 17-isolates of spot blotch under controlled conditions.
- 3. In order to identify new sources of resistance to net blotch, a FIGS subset consisting of 96 barley accessions was screened with a mixture of 20-isolates of net blotch collected from different agro-climatic regions of Morocco. Of the 96 accessions, 30 accessions of barley were found to be resistant to net blotch. Similarly, the same FIGS subsets of 96 accessions of barley was also challenged with spot blotch. Of the 96 accessions, 17 accessions of barley were found to be resistant to spot blotch. In addition, LI-AM and HI-AM panels were also screened with a mixture of 17-isolates of spot blotch and 54 and 69 accessions were found resistant, respectively (Table 1).

Table 1. Response of different FIGS subsets, GCP and AM-panels to spot blotch (SB) and net blotch (NB) at seedling stage.

Name of the subset	# of accessions	Resistant to net blotch	Resistant to spot blotch
FIGS- Net blotch (NB)	96	30	17
GCP subset	136	26	21
LI-AM panel	336	-	54
HI- AM panel	320	-	69

4. The barley accessions with novel resistance to multiple diseases will be incorporated into the barley breeding program of ICARDA and NARS partners.