**Phenotypic data**

Phenotyping in this study was done in five separate experiments. For all experiments, two plants were grown in plastic containers measuring ~ 3.8 cm in diameter, which were arranged in racks containing 98 containers per rack. Each container of two plants was considered an experimental unit.

The first experiment consisted of 68 wheat accessions that included 10 accessions of common wheat (*Triticum aestivum* L., 2*n* = 6*x* = 42, AABBDD), 42 accessions of durum wheat (*T. turgidum* ssp*. durum* (Desf.) Husnot., 2*n* = 4*x* = 28, AABB), two accessions of makha wheat (*T. aestivum* ssp. *macha* Dekapr. et MenAbde, 2*n* = 6*x* = 42, AABBDD), two accessions of club wheat [*T. aestivum* ssp*. compactum* (Host) MacKey, 2*n* = 6*x* = 42, AABBDD], eight accessions of cultivated emmer wheat [*T. turgidum* ssp*. dicoccum* (Shrank) Shubl*,* 2*n* = 4*x* = 28, AABB], three accessions of wild emmer wheat [*T. turgidum* ssp*. dicoccoides* (Körn. Ex Asch. & Graebner) Aarons, 2*n* = 4*x* = 28, AABB], and one accession of the diploid goatgrass *Aegilops speltoides* ssp*. ligustica* Tausch (2*n* = 2*x* = 14, SS) grown in a total of six replicates arranged in a completely randomized design (CRD). The second experiment included 184 hard red spring wheat (HRSW) accessions and consisted of three replicates. The third experiment consisted of 510 durum wheat accessions and was planted in a total of three replicates in a CRD. The fourth experiment included three replicates of 13 wheat accessions (ArinaLrFor, Jagger, Julius, LongReach Lancer, CDC Landmark, Mace, Norin61, Spelta, CDC Stanley, SY Mattis, Fielder, Glenn, Rollag) that had reference genome assemblies available at pseudochromosome level. The fifth experiment consisted of 20 accessions (Amery, Grandin, Hope, RL 1527, Shinchunaga, 17, 184 P.2.A.1.F, Aussie, Criollo, ND 407, II-11401-4B-9T-3B-3T, Sr 13, Deir Alla, Khosti, II-19865-58M-100Y-104C, G 319-33-0-C2-E20, 3085, G-29-14-0-3-1-0, C 10444, Timstein) which were selected based on results from previous experiments, and it consisted of five replicates grown in a CRD.

Fully expanded secondary leaf of each plant was infiltrated with ≈25 μL of a liquid culture containing the SnTox1 protein using a 1 mL syringe with the needle removed. The boundaries of the infiltration sites were marked with a permanent marker before the water-soaking disappeared. All plants were kept at 21 °C in a growth chamber and leaves were evaluated on the fifth day after infiltration.

An expanded scoring scale, which included seven categories (0, 0.5, 1.0, 1.5, 2.0, 2.5, and 3.0), was used to rate SnTox1 sensitivity levels. A score of 0 was used to represent no visible necrosis or chlorosis. A score of 2.0 was used if the infiltrated area had highly visible chlorosis with no visible necrosis. A score of 3.0 was used if extensive and severe necrosis was visible throughout the entire infiltrated area with complete tissue collapse and shriveling or narrowing of the leaf within the infiltrated region. Scores of 0.5, 1.5 and 2.5 were used if the sensitivity levels were intermediate between the ranges of 0 – 1.0, 1.0 – 2.0 and 2.0 – 3.0, respectively. Lines with scores ≤ 1.0 were considered as insensitive and lines with scores > 1.0 were considered as sensitive.