While traditional varieties (landraces) already provide benefits to farmers for climate change adaptation, there is still the opportunity to further improve them through breeding. Our research aims to produce a new population from Ethiopian landraces that can be used as material for gene discovery, as well as advanced pre-breeding germplasm to improve grain yield and quality.

The final goal is to produce a so-called ‘nested association mapping’ (or NAM) population, which is a way to maximize the diversity within the initial set of varieties to create lines that perform well over time. Based on the molecular analyses performed on our landrace collection (see Factsheet 5), we selected 53 landraces that showed the maximum diversity. Each line was then independently crossed with an elite cultivar (called Assasa), acting as a common parent (see Fig. 1).

Fig. 1 - Scheme for the development of a NAM population
The progeny of each crossing is a hybrid that has both the Assassa and a landrace genome. To generate molecular variation, we performed other crossings among the progeny and selected around 400 seeds from each crossing. In order to stabilize the genomic diversity obtained with these seeds, we self-pollinated each individual plant.

Our progress

• At the end of the process we have obtained a very large family. From the original 53 landraces we now have around 10,000 stable lines that are ready for further breeding or to be distributed to farmers according to the Ethiopian law (Fig. 2 and Fig 3).

• Some of the lines from the NAM population have shown an outstanding performance when compared to the original 53 landraces. This could be because of the ‘hybrid vigour’ effect. While widely studied and exploited in maize, this characteristic is poorly known in wheat.

Looking ahead

The breeding lines resulting from this research can be an extraordinary asset for the Ethiopian agronomic system. They can be used as a pool where we can look for lines ready to distribute to farmers, as well as a tool to increase our understanding of wheat biology. Furthermore, once the phenotypes and genotypes of these lines are characterized, the NAM population will be a precious resource for the international scientific and breeding community.

Next steps will also include advanced transcriptomic approaches to better understand ‘hybrid vigour’.

Fig. 2 - Crossing between 53 accessions and Assasa

Fig. 3 - Evaluating plant performance

Fig. 4 - This wheat plant shows an uncommonly big spike – with 29 heavy spikelets and 36 fertile tillers. This could be the result of ‘hybrid vigour’.