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# Global Challenges and Urgency for Partnerships to Deploy Genetic Resources

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The gene bank collections are believed to be "humanity's most valued assets", "repositories safeguarding agricultural heritage", and "essential to adapt agriculture to a rapidly changing environment". Yet gene banks are the ultimate source of global gene diversity, breeders seldom access this resource considering it to be of little relevance to their current breeding needs (Global Crop Diversity Trust, 2006). The *on-farm* diversity as well as genetic variability maintained in gene banks represents important reservoir in form of wild relatives, landraces and traditional cultivars that have been evolved in specific environments under particular set of climatic conditions. Several initiatives have been undertaken at global level focusing wheat pre breeding, example UK's WISP (http://www.nottingham.ac.uk/wisp/index.aspx) and CIMMYTs Seeds of Discovery (SeeD) project (http://seedsofdiscovery.org/). Despite challenges, there opportunities exist that can greatly help in successful utilisation of gene bank resources for crop breeding purposes, for example, increasing cost efficiency of high density genomics techniques/methods, availability of enormous germplasm diversity and a dynamic partnership between national and international stakeholders. These opportunities can be successfully utilized to fill the gap between diverse germplasm resources and the breeding pipelines through performing large scale coordinated pre-breeding efforts. Pre-breeding is a broad term refers to all pre-requisites of crop varietal improvement programmes. This paper presents pre-breeding efforts made at CIMMYT in collaboration with gene bank and NARS to mobilize the under-utilized diversity to breeding pipelines.

## Genotypic and Phenotypic Analysis of Gene Bank Accessions for Pre-breeding

A set of 1,500 wheat gene bank accessions including landraces, FIGS and synthetics were characterised by GBS technology at CIMMYT following a two-step complexity reduction method. Restriction was followed by amplification and sequencing using Illumina Hiseq 2500 and allele calling was performed by a proprietary analytical pipeline developed by DArT P/L (Li *et al.*, 2015, Vikram *et al.*, 2016). A core set of 200 accessions was formulated and utilized in developing wheat pre breeding germplasm resource. Core set of the Mexican wheat landrace has been formulated through using large scale genotypic and phenotypic information as well as a unique methodology explained by Vikram *et al.* (2016) to maximize the rare allelic variations (Data source: www.seedsofdiscovery.org).

## Wheat Pre-breeding Germplasm Development and Phenotypic Evaluation

A top cross population development strategy was followed for pre-breeding population development. Linked top cross population (LTP) panels were developed in such a way that each panel had a series of top cross populations in which each top cross was linked with another one via common elite parent and therefore top crosses were linked making a panel called, LTP. A total of 15000 wheat pre-breeding lines were evaluated for plant type and yellow rust in CIMMYT's El Batan research farm. For yellow rust evaluation methodology reported by Hao *et al.* (2011) was followed and visual selection for plant type was done in such a way to maintain diversity simultaneously keeping other parameters (height, flowering, yield parameters etc.) similar to adapted varieties.

## Results and Discussions

The complexity of wheat genome and a narrow genetic base (compared to its progenitors) due to its recent origin of bread wheat is a major challenge. A systematic and focused effort with clear vision in mining genes/alleles from the available genetic stocks can be the most feasible and safest approach for development of climate resilient wheat cultivars. A core reference set of 232 genotypes was selected from total of 8,000 Mexican bread wheat landraces harboring 62.87% of the rare alleles of the complete set. Interestingly, frequency of some of the rare alleles (311 alleles) rose above 0.05% in the core

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**Author for Correspondence: Email- Suk.Singh@cgiar.org* set (Fig. 1 and 2). This core reference set has already been shared with partners in India, Mexico and Kenya for evaluation under disease pressure.

For pre-breeding purpose synthetics as well as FIGS germplasm sets were also selected as allele donors. A similar strategy was followed to select accessions for use in pre-breeding. Genotypes from different genetic spaces have been selected for their deployment in pre breeding (Fig. 3). These germplasm sets can be very efficiently utilized by wheat breeders in their varietal improvement programmes. Breeders from different parts of world have been involved and trait donors will be provided to them upon request.

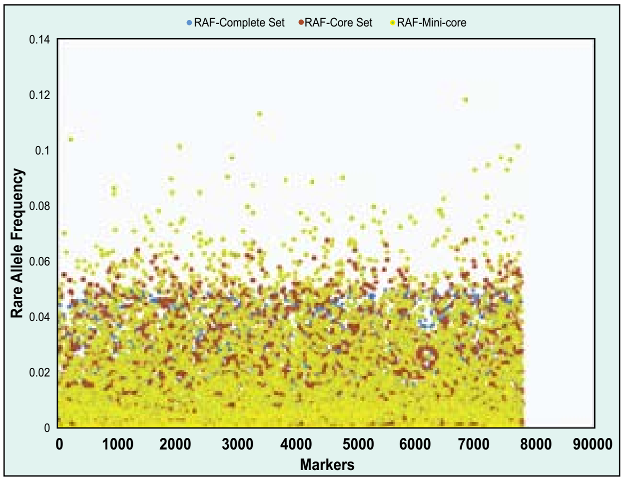

**Fig. 1. Frequency of rare alleles (of complete set) in three populations: complete set, core reference set and mini-core reference set. Rare allele frequency and individual markers (7,775 SNPs) are plotted on the Y and X axes, respectively. The figure also shows that the frequency of some alleles (which were <0.05 in the complete set) increased in core and mini-core reference sets. Details of core sets have been explained by Vikram *et al.* (2016) (Data source: www.seedsofdiscovery.org).**

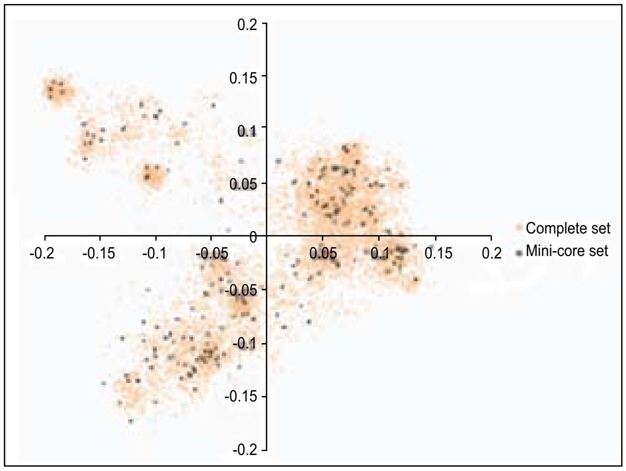

**Fig. 2. Multidimensional scaling graph showing the relative distribution of complete and mini-core reference set accessions of Mexican hexaploid landraces (Data source: www.seedsofdiscovery.org).**

Two complimentary pre-breeding strategies were followed, one incorporating general diversity and other one to introduce trait based diversity. International wheat pre breeding nurseries are being shared with the NARS in different countries (Fig. 4). Preliminary evaluation results identified disease resistant genotypes as compared to the local checks (CIMMYT, Unpublished).

A comprehensive strategy is being followed in CIMMYT's wheat pre-breeding initiative (www.seedsofdiscovery.org) for leveraging gene bank and derived resources for achieving short-, medium- and long-term impacts. The global wheat community has encouraged these ongoing largescale-unique efforts and breeders from South Asia and other parts of world are welcomed to leverage resource and deliver impact. The wheat landrace core sets/pre breeding germplasm resources have been shared with NARS/ARIs in Mexico, India, Iran, Pakistan, China, Kenya and USA. Efforts are made to enhance partnerships among stakeholders for maximizing the resource leverage and ensure impact.

## Conclusion

An extra ordinary support of Mexican government to CIMMYT's Seeds of Discovery-wheat project enabled sequencing of nearly 40% CIMMYT's wheat GeneBank, large scale phenotypic characterisation (Data Source: www.seedsofdiscovery.org) and establishes a wheat pre breeding pipeline for the wheat breeders in Mexico

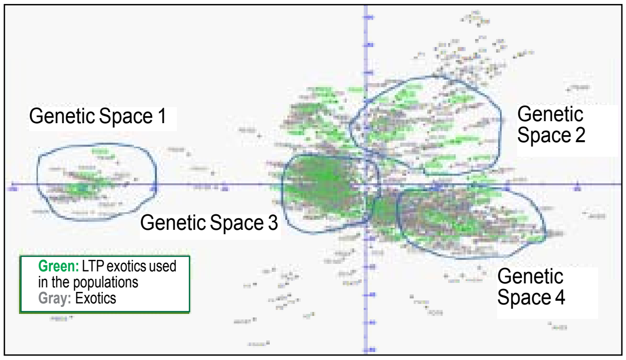

**Fig. 3. Principal component graph showing distribution of exotics (gray) in different genetic spaces and selected accessions (green) from them. Exotics include landraces, FIGS and synthetics (Data source: Sehgal *et al.*, 2015).**

**Fig. 4. Wheat pre-breeding nurseries planted at NARS site in Mexico (Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias-INIFAP, Mexico) and India (Borlaug Institute for South Asia-BISA, India)**

**Fig. 5. Pre-breeding lines developed after selecting for heat-drought-plant type-diseases, available for breeders upon request**

and abroad. Partnership among national and international organizations is urgently required to leverage these resources for expanding the genetic base of cultivated wheat, thereby delivering high impact at the farmer field level.

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