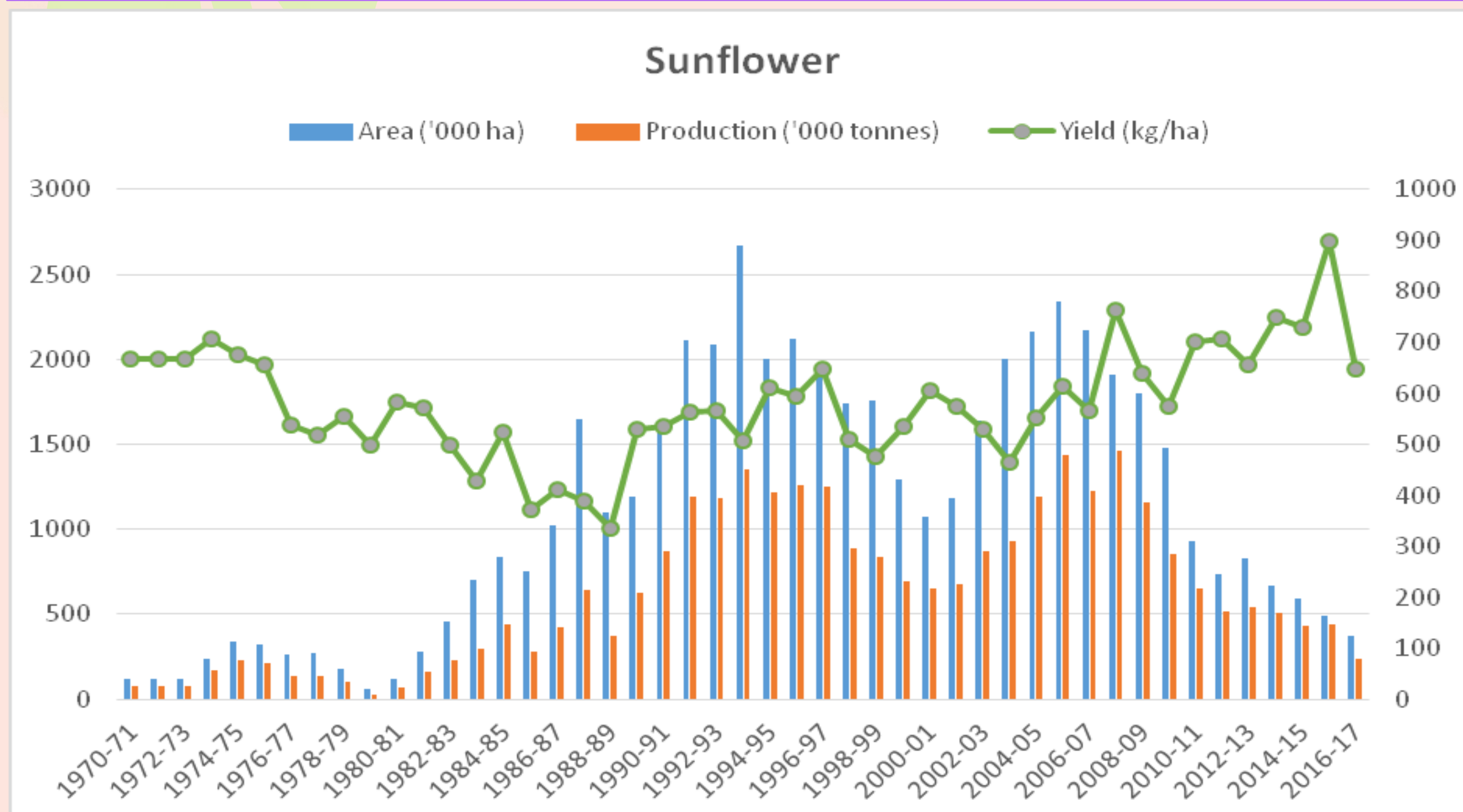


Abstract

- ❖ Major diseases of sunflower in India are leaf spot (*Alternariaster helianthi*), powdery mildew (*Golovinomyces orontii*), sunflower necrosis disease (SND) caused by tobacco streak virus (TSV) and downy mildew (*Plasmopara halstedii*) attacking crop at different phenological stages.
- ❖ Yield losses from 10 to 60% are accounted due to these biotic strusses.
- ❖ Conventional breeding, interspecific hybridization, transgenic and functional genomics approaches were followed for incorporation of resistance to various diseases.

Introduction

- ❖ Sunflower had become one of the most important oilseed crops in the Indian economy following its introduction in the country during late seventies.
- ❖ The area under cultivation had increased steeply from 0.2 m.ha in 1981-82 to 2.6 m ha in 1993-94 followed by a drastic decline since 2010 reaching 0.5 m ha in 2014-15.
- ❖ While one of the prime reasons is the competition from other remunerative crops like cotton, maize, soybean and pulses, the other reason is the vulnerability of the crop to a wide range of diseases.
- ❖ The disease situation in India is rather dynamic and there has always been a constant threat of new diseases limiting sunflower production and productivity.
- ❖ In the initial years and till 1990, the major disease was leaf spot caused by *Alternariaster helianthi*. From 1997, the crop suffered from sunflower necrosis disease (SND) caused by tobacco streak virus (TSV) and from 2006 onwards, powdery mildew incited by *Golovinomyces orontii* has assumed importance. Downy mildew which is a major disease in the tropics is localized to a single pocket in Central India. Thus, it has been a constant challenge for the breeders to identify durable sources of resistance in cultivated and wild *Helianthus* species.

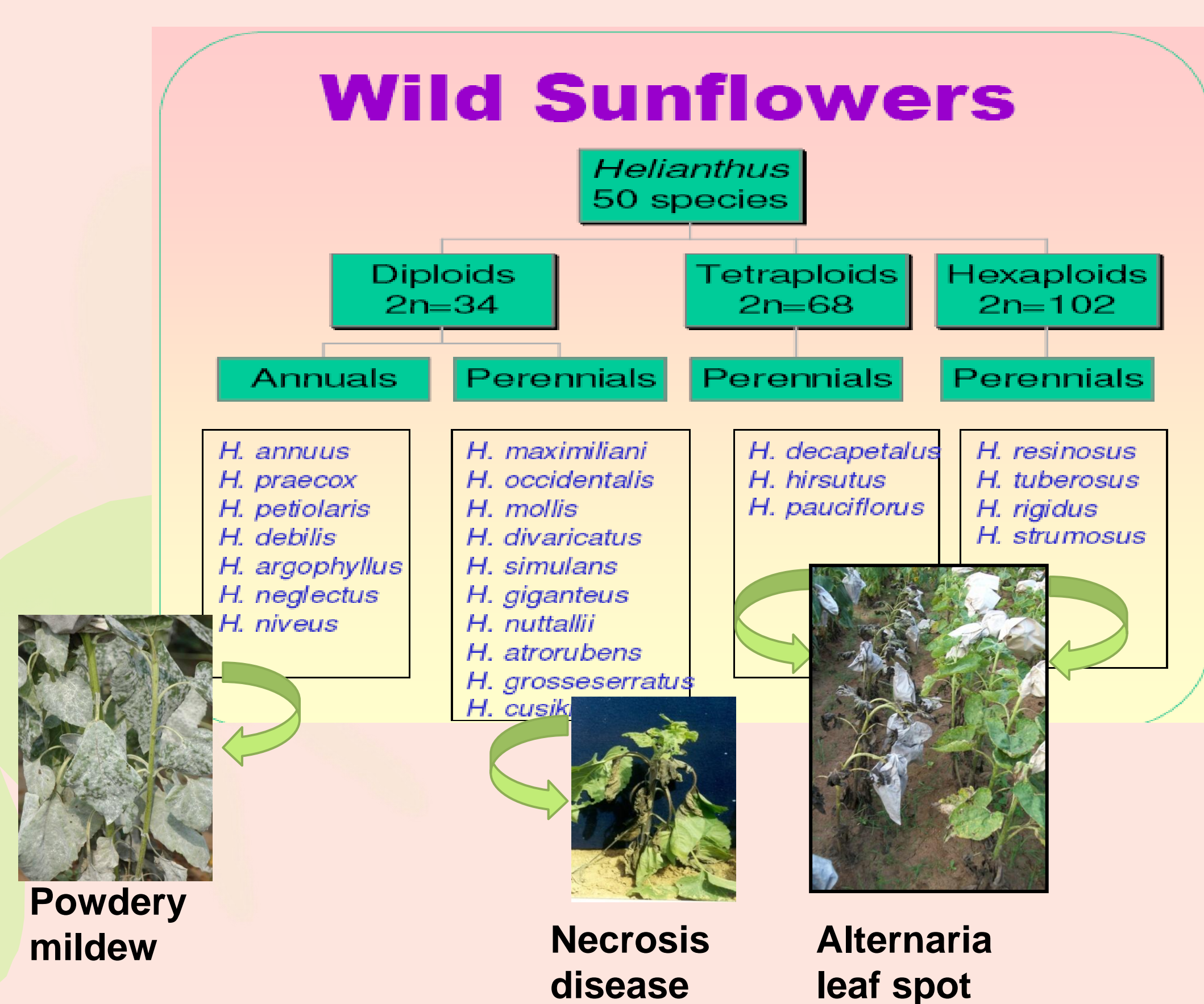


Materials and Methods

- ❖ For assessing the reaction to major pathogens, wild *Helianthus* species (42) that include both annuals and perennials of the three ploidy groups (diploid, tetraploid, hexaploid) were augmented from USDA-ARS, Ames, USA and IFVCNS, Novisad, Serbia.
- ❖ For screening against *A. helianthi*, both detached leaf and whole plant assays were followed.
- ❖ Artificial sap inoculation method was followed for screening the cultivated and wild sunflowers against sunflower necrosis disease.
- ❖ Identification of powdery mildew resistant accessions was done by the conidial dusting method from infected leaves on the healthy (test) materials.

Results and Discussion

1. Screening of wild *Helianthus* species to major diseases

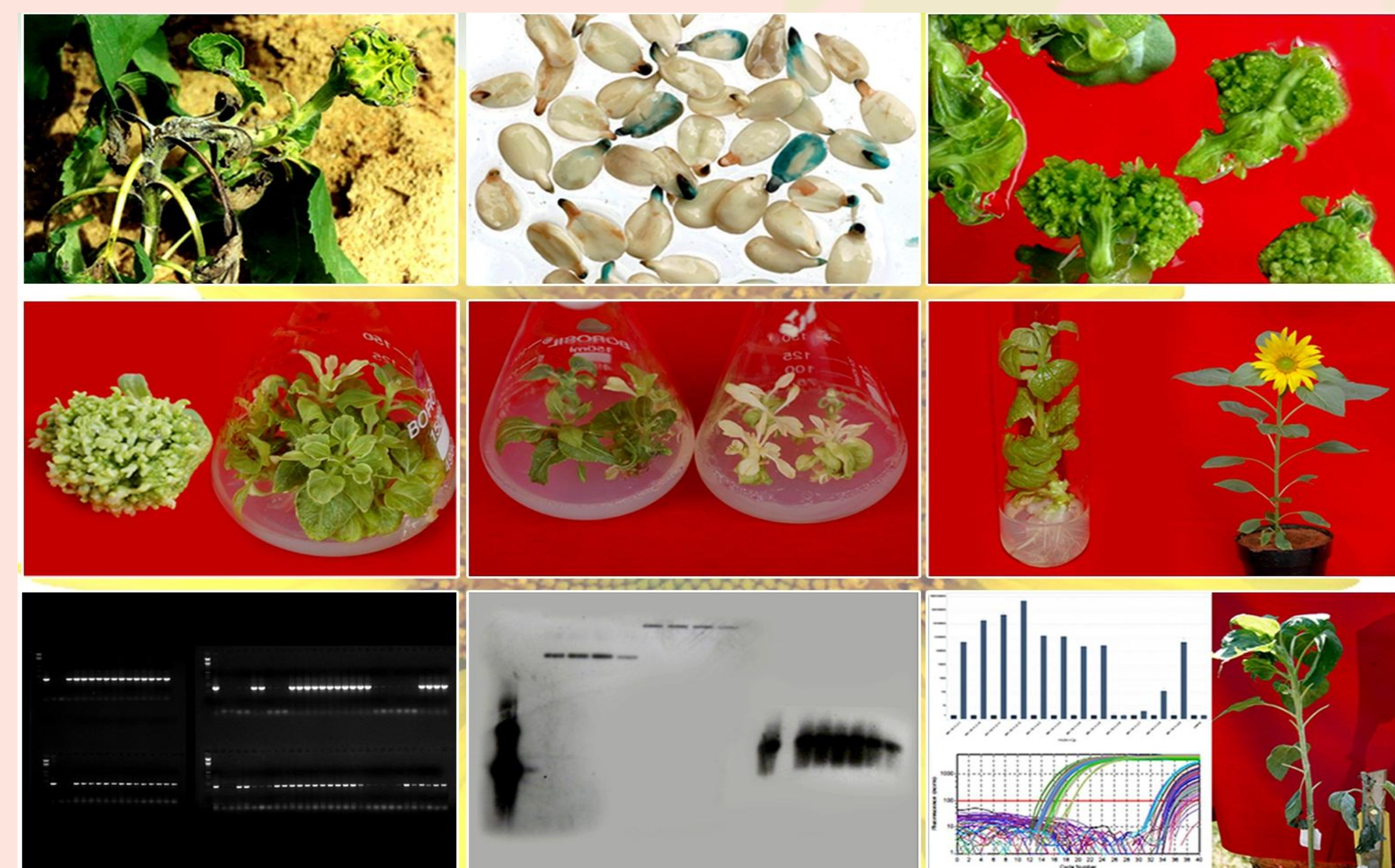


2. *Alternaria helianthi*

- ❖ Leaf blight is one of the important diseases that causes considerable yield loss. Resistance against leaf blight in the germplasm, parental lines and released sunflower cultivars is rather limited.
- ❖ Hence, screening of sunflower accessions comprised interspecific derivatives, core germplasm, pre-breeding lines, exotic lines and wild *Helianthus* species was carried out under natural field conditions over five years viz., 2003 to 2009 (Prasad et al. 2017).
- ❖ Sources of resistance to *A. helianthi* were identified in diploid perennial *Helianthus* species with limited crossability success (Sujatha et al. 1997).
- ❖ Hence, 16 stable interspecific derivatives involving perennial species such as, *H. hirsutus*, *H. tuberosus*, *H. strumosus* were obtained from USDA for assessing their reaction to the pathogen and utilization in the breeding programmes.

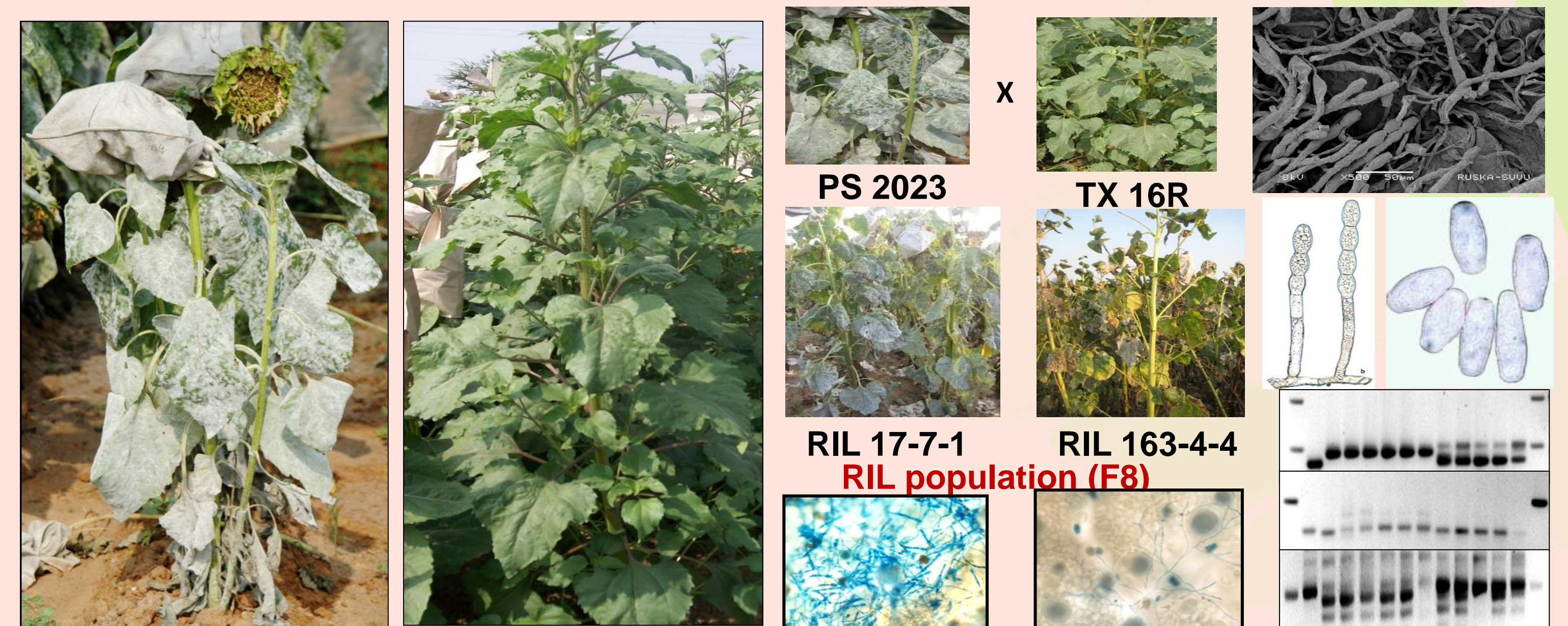
3. Sunflower necrosis disease

- ❖ Owing to lack of reliable sources of resistance to TSV, transgenic events harbouring the coat protein gene of TSV were developed for conferring resistance to SND through *Agrobacterium tumefaciens* mediated transformation using decoated mature seeds (Vasavi et al. 2018).



4. Powdery mildew

- ❖ Sources of resistance to powdery mildew are identified in diploid annual species like *H. argophyllus* and *H. praecox* and prebreeding programmes for transfer of resistance to the cultivar background is under way (Reddy et al., 2013). The donors for powdery mildew resistance including *H. praecox* (PRA 1823) were subjected to proteome and transcriptome profiling for identification of candidate gene(s) and key regulatory pathways governing resistance to the pathogen (Reddy et al., 2018).



Conclusions

- The study clearly demonstrated the potential of wild *Helianthus* species and also the advantages of integrated approaches in terms of conventional breeding methodologies and modern techniques for successful exploitation of the genetic diversity available in the wild species for the genetic improvement of sunflower.
- The advanced breeding lines possessing the vast genetic variability of the wild genomes have benefited the sunflower research programs under the All India Co-ordinated Program (AICRP) on sunflower.

References

- Prasad, M.S.L., Sujatha, M., Aivelu, K. and Sujatha, K. 2017. Crop Prot., 92, pp. 70-78.
- Reddy K.P.R., Kamakshi D., Kirti P.B., Mohan Rao C., Thakur S.S. and Sujatha M. 2018. Proteomics. doi: 10.1002/pmic.201700418.
- Reddy, K.P.R., Chander Rao, S., Kirti, P.B. and Sujatha, M. 2013. Euphytica 190: 385-399.
- Sujatha, M., Prabakaran, A.J. and Chattopadhyay, C. 1997. Helia 20(27): 15-24.
- Vasavi, S., Vijay Reddy, S., Tarakeswari, M., Revathi, T., Jain, R.K., Chander Rao S., Varaprasad, K.S.V. and Sujatha M. 2018. Plant Cell Tissue and Organ Culture doi.org/10.1007/s11240-018-1461-2.