Genetic Diversity and utilization of the wild cotton germplasm

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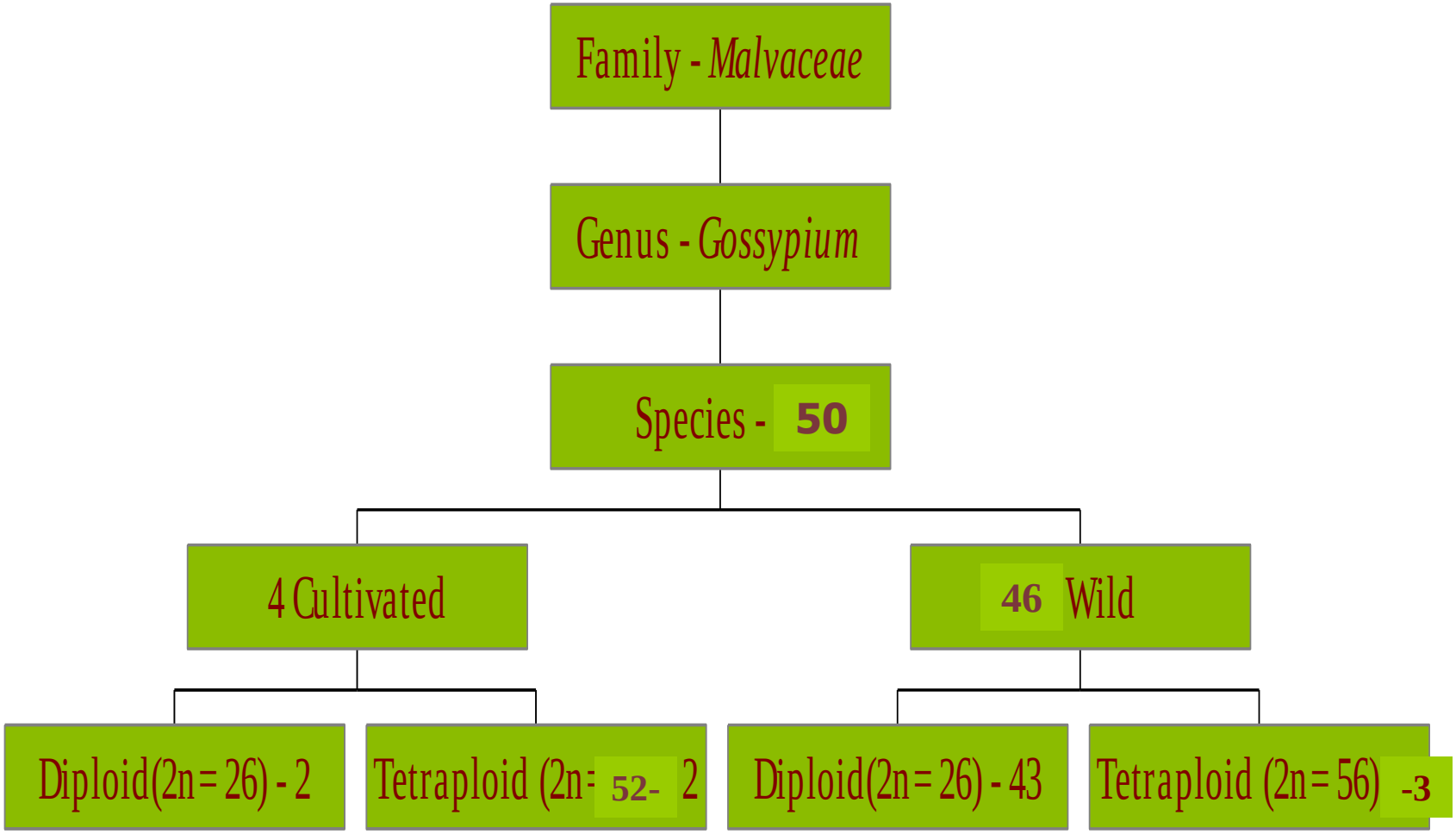
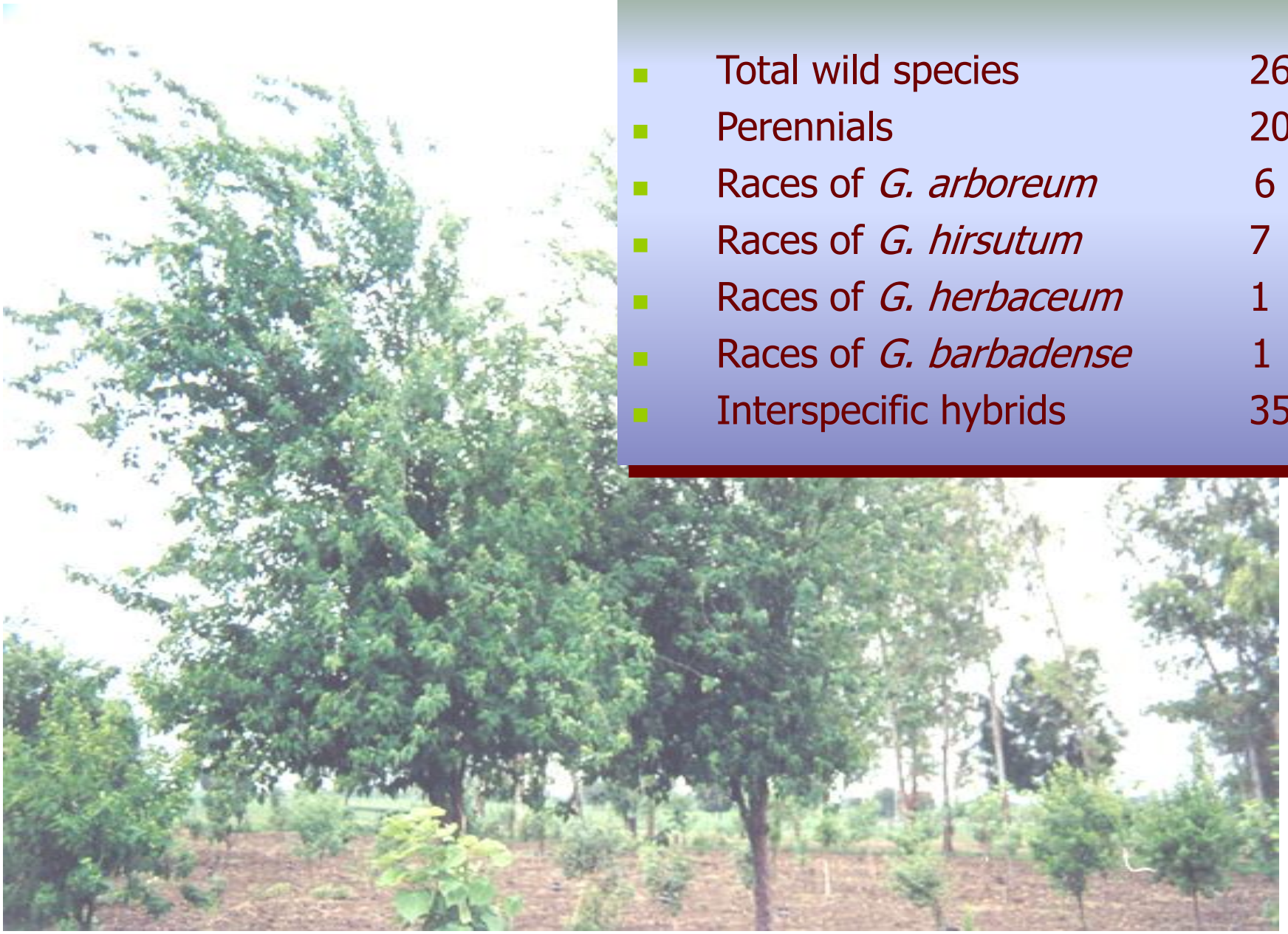
CLASSIFICATION OF *GOSSYPIUM* SPECES



SPECIES OF *GOSSYPIUM* GROUPED BY GENOME

Genome	2n number	Total species	Species	Geographical origin
A	26	2	*G. herbaceum, G. arboreum*	Asia
B	26	3	*G. anomalum, G. triphyllum, G. capitis-viridis*	Africa
C	26	2	*G. sturtianum, G. robinsonii*	Australia
D	26	13	*G. thurberi, G. armourianum, G. harknessii, G. klotzchianum, G. davidsonii, G. aridum, G. raimondii, G. gossypioides, G. lobatum, G. trilobum, G. laxum, G. turneri, G. schwendimanii*	N. America, S. America, Galapagos Islands
E	26	8	*G. stocksii, G. somalense, G. areysianum, G. incanum, G. benadirense, G. bricchettii, G. vollesenii, G. trifurcatum*	Africa
F	26	1	*G. longicalyx*	Africa
G	26	3	*G. bickii, G. australe, G. nelsonii*	Australia
K	26	13	*G. anapoides, G. costulatum, G. cunninghamii, G. exiguum, G. enthyle, G. condonderriense, G. merchantii, G. nobile, G. pilosum, G. populifolium, G. pulchellum, G. rotundifolium, G. sp. nov*	Australia
AD	52	5	*G.hirsutum, G.barbadense, G.tomentosum, G.mustilinum, G.darwinii*	N. America, S. America, Hawaii

SPECIES GARDEN OF CICR, NAGPUR, INDIA



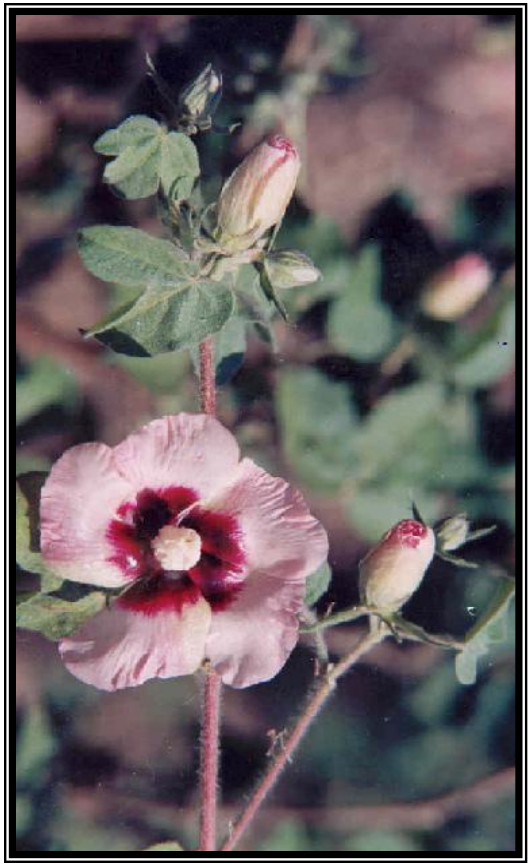
- Total wild species 26
- Perennials 20
- Races of *G. arboreum* 6
- Races of *G. hirsutum* 7
- Races of *G. herbaceum* 1
- Races of *G. barbadense* 1
- Interspecific hybrids 35

G. anomalum

Diploid species

Genome – B_1

Distribution - Africa



G.davidsoni

Diploid species

Genome – $D_{3\text{-}d}$

G.klotzchianum

Diploid species

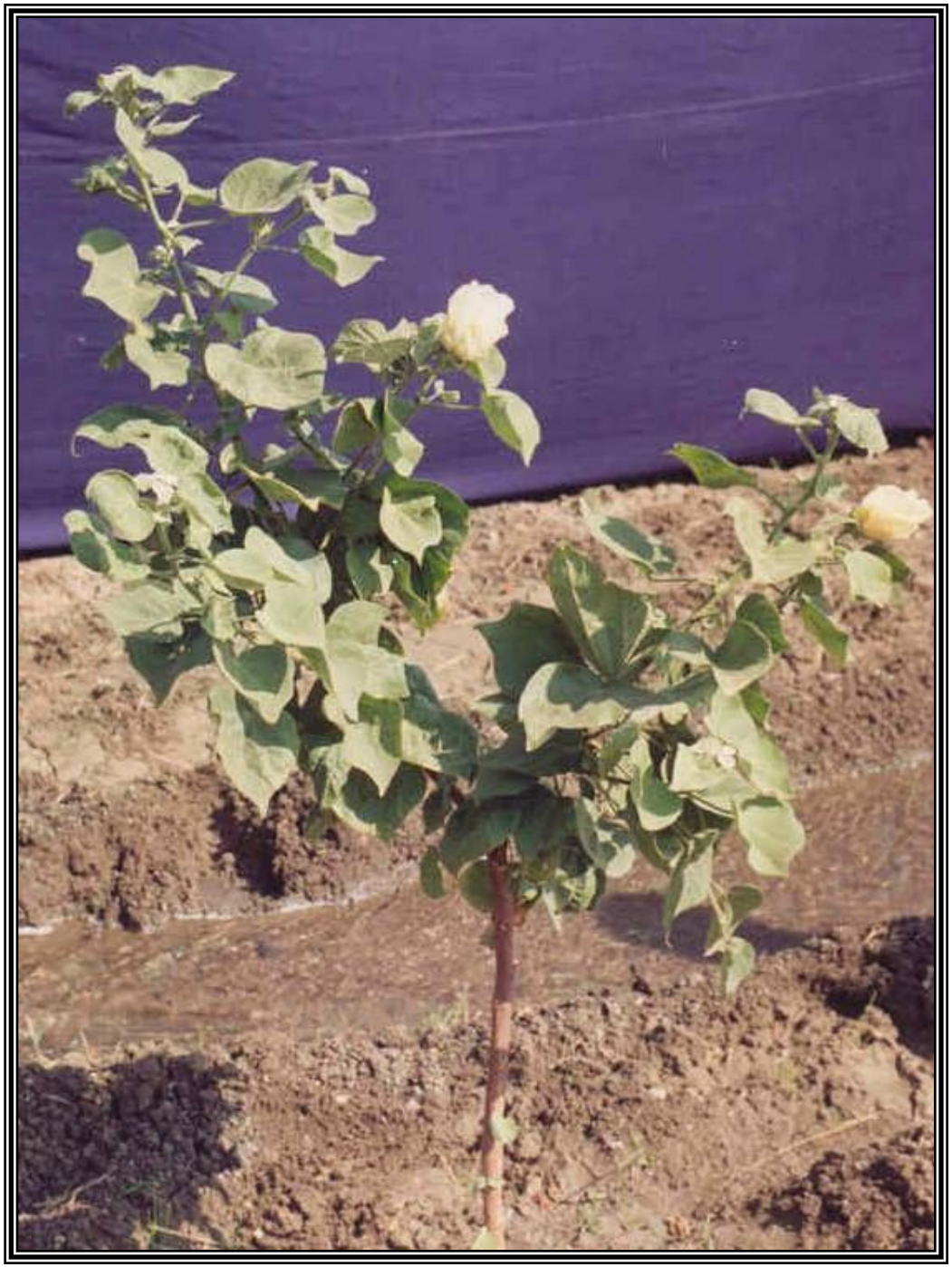
Genome – $D_{3\text{-}k}$

G.raimondii

Diploid species

Genome – D_5

Distribution – America

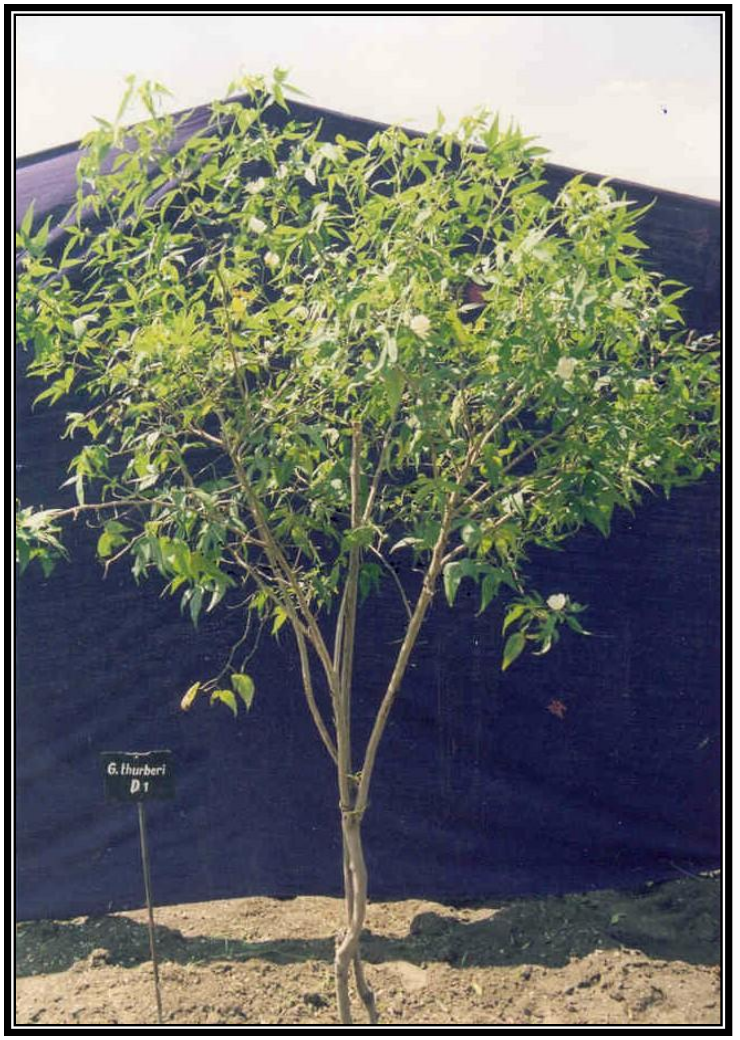


G. thurberi

Diploid species

Genome – D_1

Distribution – America



G. trilobum

Diploid species

Genome – D_8

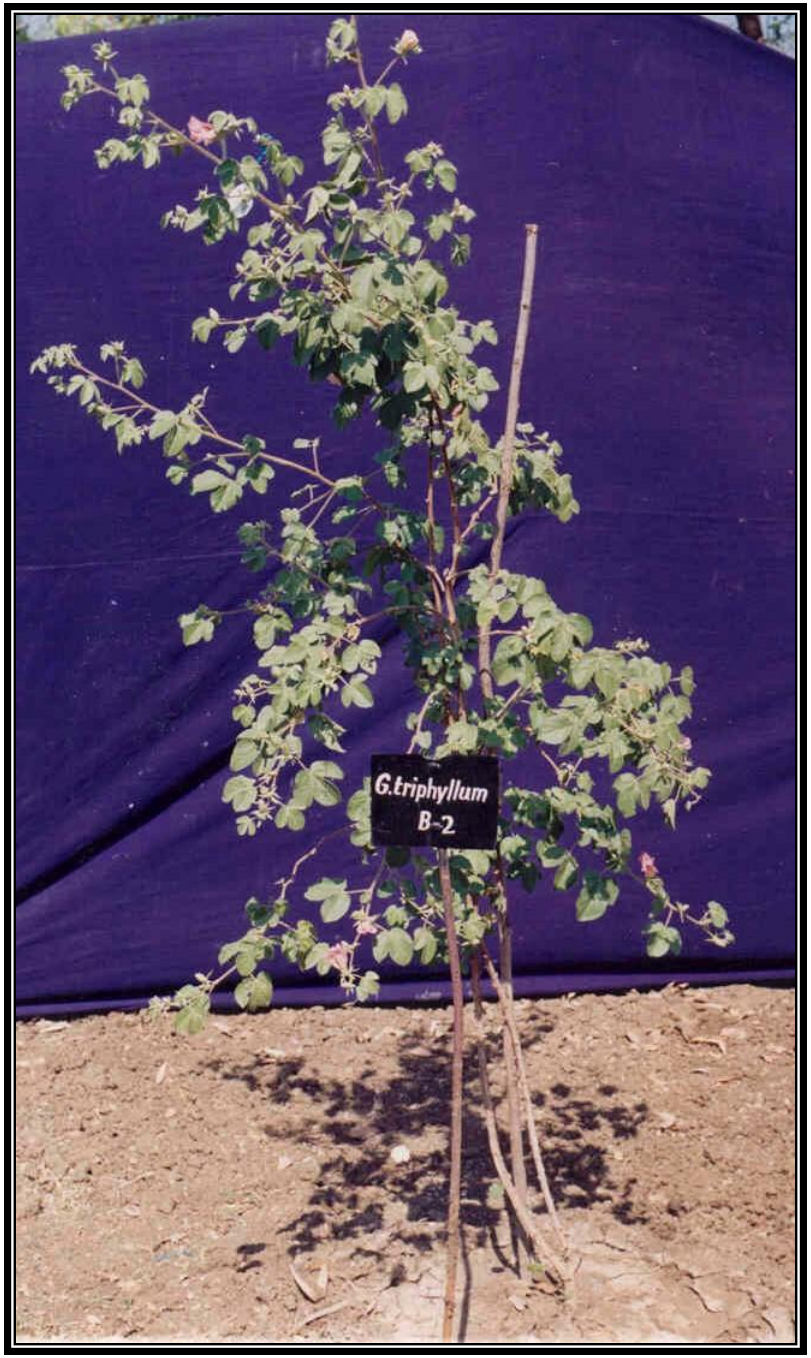
Distribution – America

G. triphyllum

Diploid species

Genome – B_2

Distribution – Africa



G. arboreum race Cernuum

North-eastern Hilly Region of India

Utilization of wild species and introgressed derivatives in converting existing varieties and hybrids

Crossing program is attempted involving a wide array of sources of resistance to major biotic and abiotic factors, better fiber properties, & Gossypol free oil. Till date several crosses were affected between the cultivated species using about 13 wild species & 9 races as pollinators and vice versa.

Utilization of Wild Species

- **Difficulties in the use of species arise from chromosome structural differences and differences in chromosome complements between wild diploids and the tetraploids.**
- **Fertility relationship among the species are highly variable and only about two thirds of the interspecific hybrids produce fertile F1's.**
- **Even though interspecific hybridization presents considerable problems, its use offers intriguing possibilities.**

Barriers

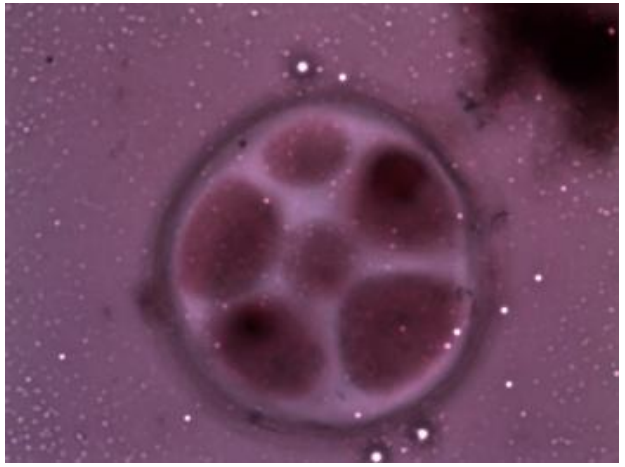
Several barriers, which operate at various levels, prevent the successful gene transfer from wild to cultivated species.

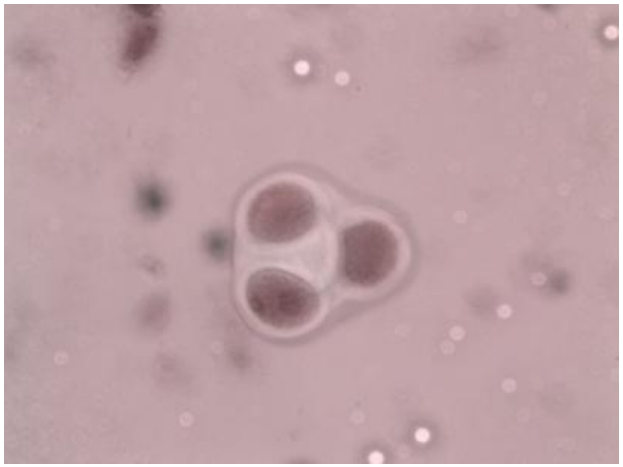
Several pre-zygotic and post – zygotic barriers are known to limit the production of hybrids between distantly related species.

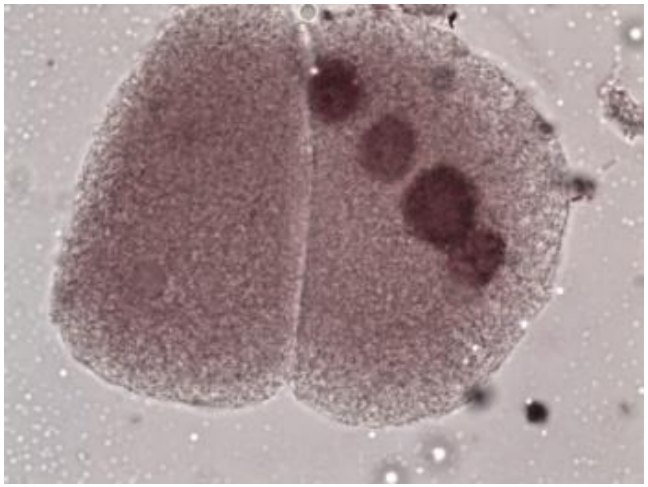
So far, it is the species from the primary and secondary gene pool which have been utilized in direct hybridization while the use of species from the tertiary gene pool has been very limited owing to their low level of genetic recombination.

Basic cross- compatibility

Abnormalities observed in interspecific crosses







Six Genetic Stocks with unique traits have been registered with the National Bureau of Plant Genetic Resources , New Delhi

Ideal plant type

MSH 99 SP 6

- **Zero monopodia**
- **Erect plant type**

JASSID TOLERANT COMPACT PLANT TYPE INTROGRESSED DERIVATIVES

Jassid Tolerant
NISC lines

Susceptible
LRA5166

NISC 40

NISC 43

NISC 44

MSH 53 – A DARK BROWN LINTED INTROGRESSED DERIVATIVE
Yield : 113g/pl, FL : 20.8mm,
FS : 17.2g/tex, Tolerant to Jassids

Development of Mapping Population and introgressed lines

F2 mapping population for the derivatives of wild species established

Sr.No	Derivative	Number of F2 Plants
1.	*G. herbaceum* x *G. longicalyx*	557
2.	*G. arboreum* race indicum x *G. davidsonii*	212
3.	*G. arboreum* x *G. thurberi*	53
4.	AK 8401 x *G. davidsonii*	34

Introgressed tetraploid Upland Cotton lines

- **Rai lines**(*G. hirsutum* , *G. raimondii*)

129 lines, based on single plant selection, were evaluated for biotic, abiotic stresses and yield.

- **Multi Species Hybrid derivatives (MSH)**

(*G. hirsutum* , *G. raimondii*, *G. barbadense* , *G. thurberi)*

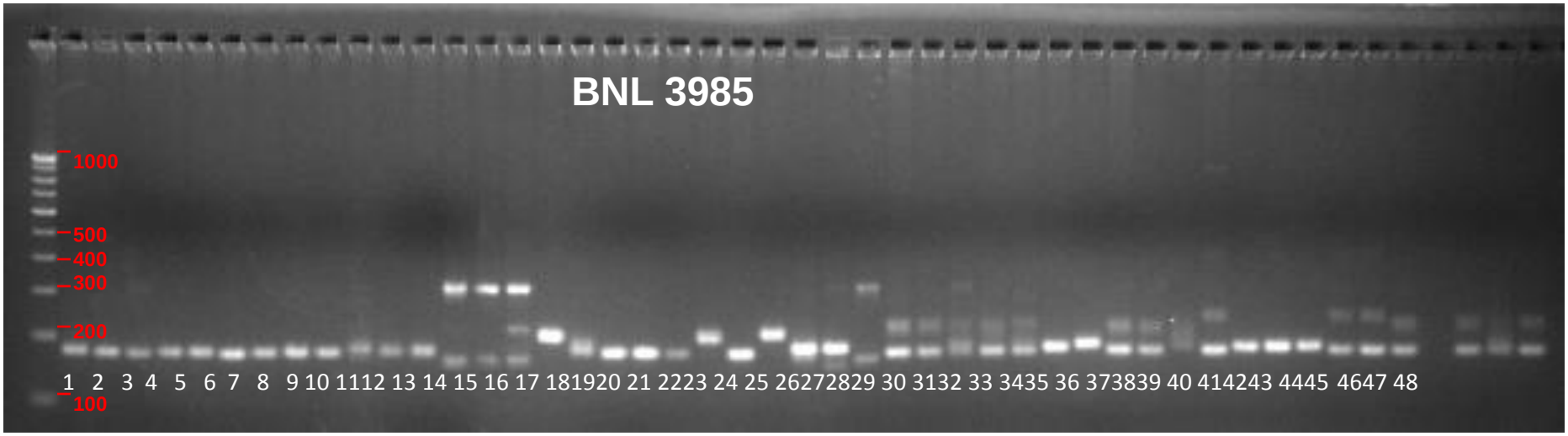
179 lines lines have evaluated for biotic, abiotic stresses and yield.

Cultures showing Jassid Tolerance which are being used by the breeders

- NISC 261
- NISC 289
- NISC 291
- NISC 219-12
- NISC-297

Genetic Diversity:

- **A total of 413 Simple Sequence Repeat (SSR) markers were screened using a set of 48 samples including 20 wild species of cotton, 15 races of cultivated species and synthetic polyploids to identify informative markers for genetic diversity assessment.**
- **24 % (103/413) markers showed polymorphism.**



Modified rapid method for extraction of DNA from the wild species

- **At the molecular level, isolation of DNA from cotton which is high in secondary isolated compound sometimes is problematic and the yield of DNA is often low and the quality can be poor.**
- **A modified rapid method for extraction of DNA from the wild species of Gossypium was also standardized while working with SSR markers for genetic diversity among wild species and introgressed derivatives.**

Sincere Thanks are due to

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THANK YOU