



Optimum Hybrid Maize Breeding Strategies Using Doubled Haploids

Andrés Gordillo^{1,2} and Hartwig H. Geiger¹

¹University of Hohenheim

Institute of Plant Breeding, Seed Science, and Population Genetics

70593 Stuttgart, Germany

²AgReliant Genetics LLC, Lebanon, IN

Outline

- **Introduction**
- ***In vivo* induction of maternal haploids**
- **DH-line based breeding schemes**
- **Software MBP for optimizing the allocation of breeding resources**
 - **Features**
 - **Selected results**
- **Summary and conclusions**

Applications of the DH technology

- **Marker-trait association studies**
 - **Marker-aided introgression of genes**
 - **Genetic engineering**
 - **Molecular cytogenetics**
 - **Hybrid breeding**
- **The DH technology has become an indispensable tool of modern maize research and breeding**

Advantages of DH lines in hybrid breeding

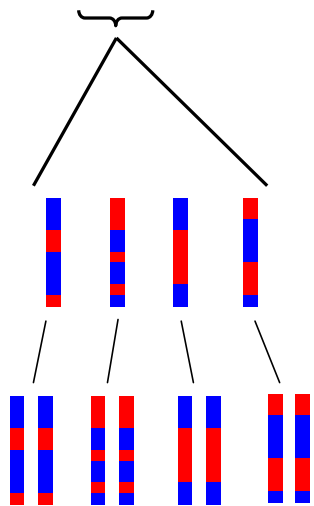
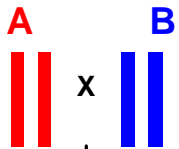
- **Maximum genotypic variance in line-*per-se* and testcross trials**
- **High reproducibility of early-testing results**
 - **Increased selection gain**
- **Complete homozygosity from the very first generation**
 - **Perfect compliance with DUS criteria for variety protection, short “time to market”**
 - **Reduced nursery expenses, simplified logistics**
 - **Facilitates marker-assisted selection and backcrossing**

In vivo induction of maternal maize haploids

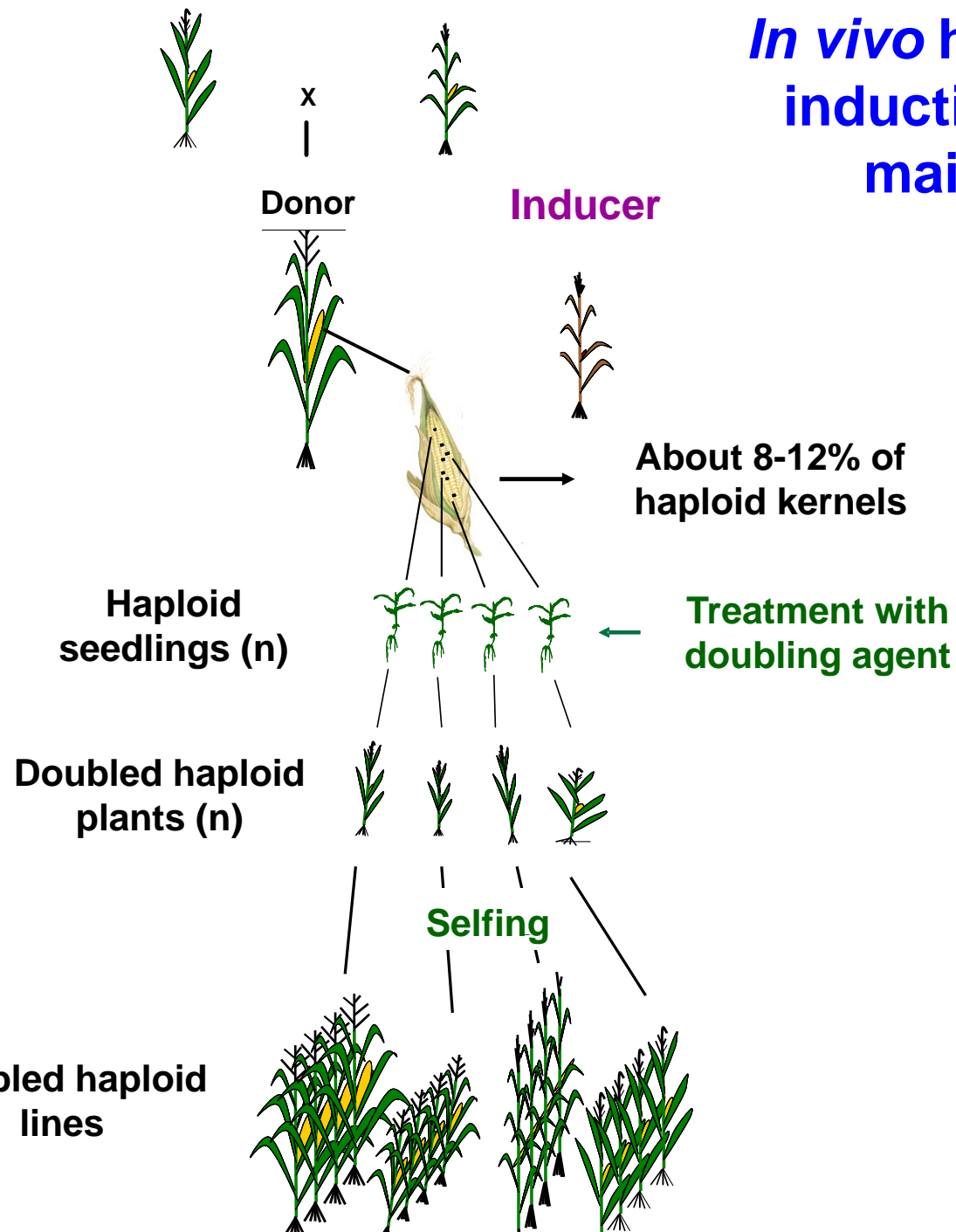
For review see Geiger (2009) in Handbook of Maize. Springer, New York

- Pollination of maize plants with specific genotypes called **inducers**, which leads to kernels with a **haploid embryo** and a regular triploid endosperm
- Widely used for line development in commercial hybrid maize breeding
- Increasingly used in research
- Only **moderate influence of donor genotype and induction environment** compared to *in vitro* haploid induction

Inbred Inbred



In vivo haploid induction in maize



Haploid-identification markers (1)

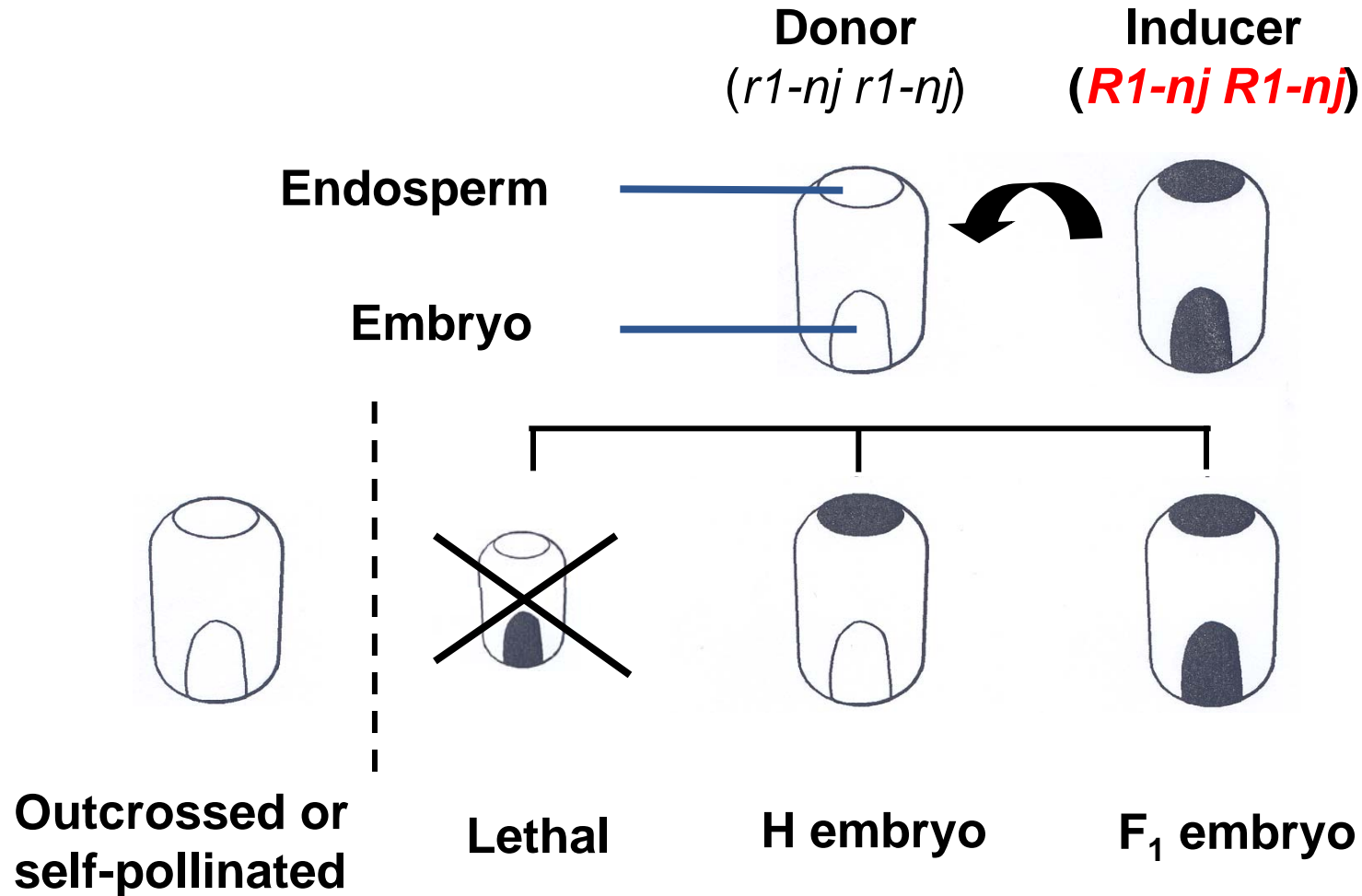
Markers expressed before chromosome doubling

- Dominant **grain color** marker gene ***R1-nj***
(in conjunction with mutant pigmentation genes ***A1*** or ***A2***, and ***C2***)
 - Causes **pigmentation** in the aleurone (**endosperm**) and in the **scutellum** (embryo tissue)
 - Needs donor with colorless seeds
 - Expression may be suppressed by **inhibitor genes** (e.g. ***C1-l***) carried by the female parent
- Dominant color marker genes expressed in the primary **root** and coleoptile (e.g. ***PI1*** in conjunction with ***B1***)

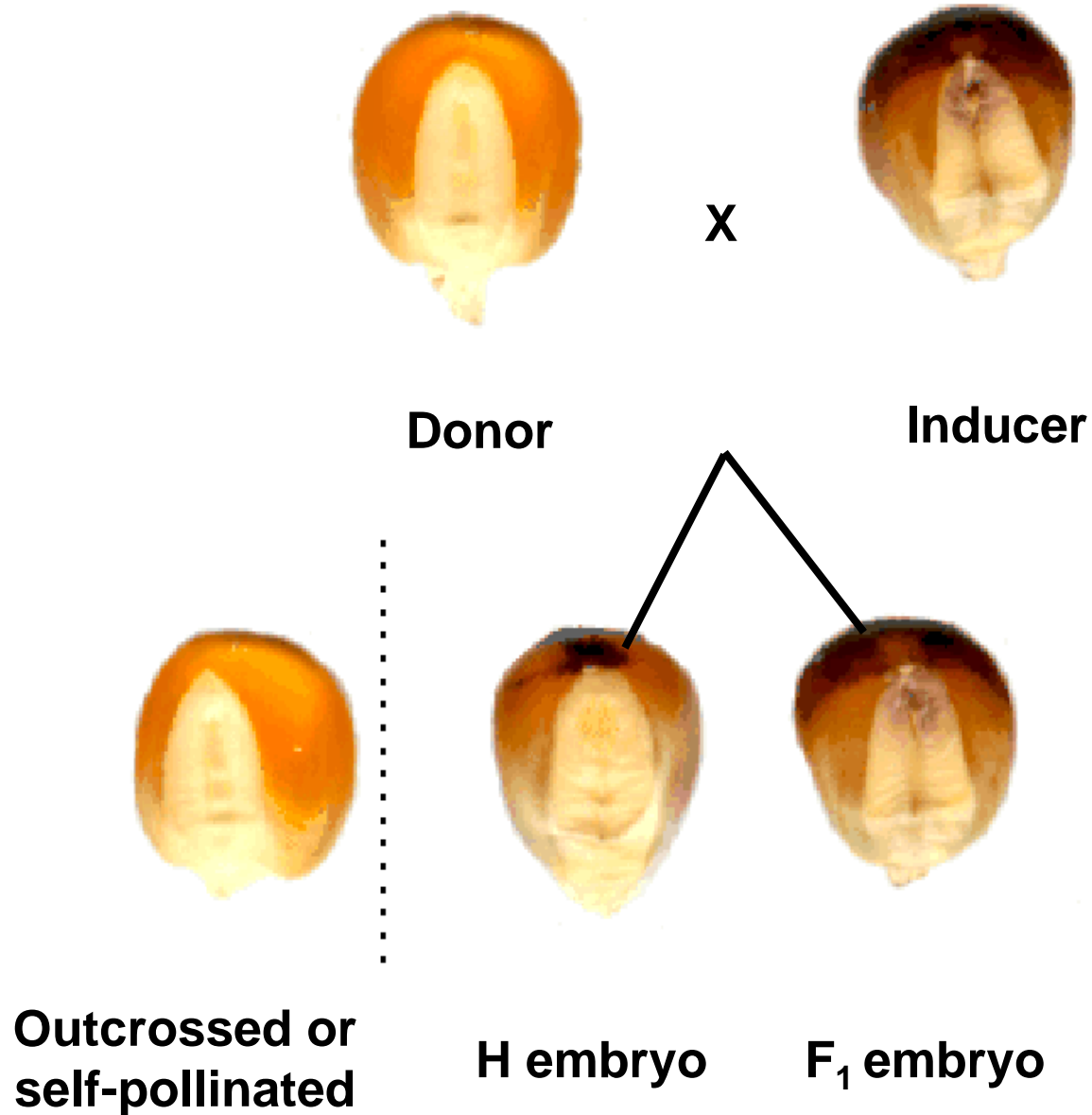
Haploid-identification markers (2)

„Red crown“ marker *R1-nj*

(After Röber 1999)



„Red crown“ marker *R1-nj* (3)



Chromosome doubling

- Immersion of seedlings in **colchicine** (Gayen *et al.* 1994, Deimling *et al.* 1997, Eder and Chalyk 2002)
 - 70 – 80% of the seedlings survive
 - 10 – 40% of the surviving plants produce selfed seed
- Due to **high toxicity of colchicine**, most breeding companies are interested in less hazardous substances
 - **Herbicides**, e.g. Pronamid, APM, Trifluralin, Oryzalin
 - **Nitrous oxide gas** (Kato 2002)

-> not suited for large-scale haploid induction

Seedling ready for reducing the root and clipping the tip of the coleoptile



Transplanting colchicinated juvenile plants into the field



Photo F.K. Röber

DH-line observation nursery

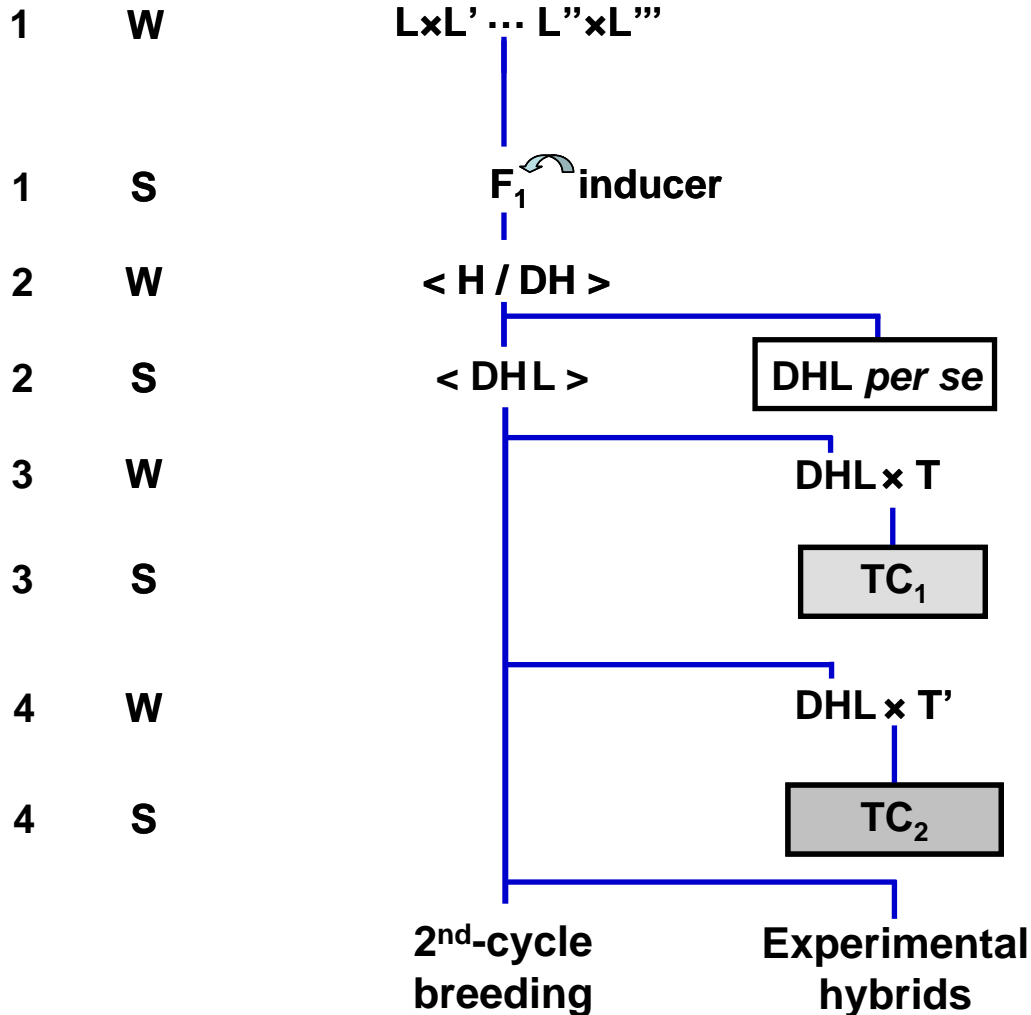


Photo W. Schmidt

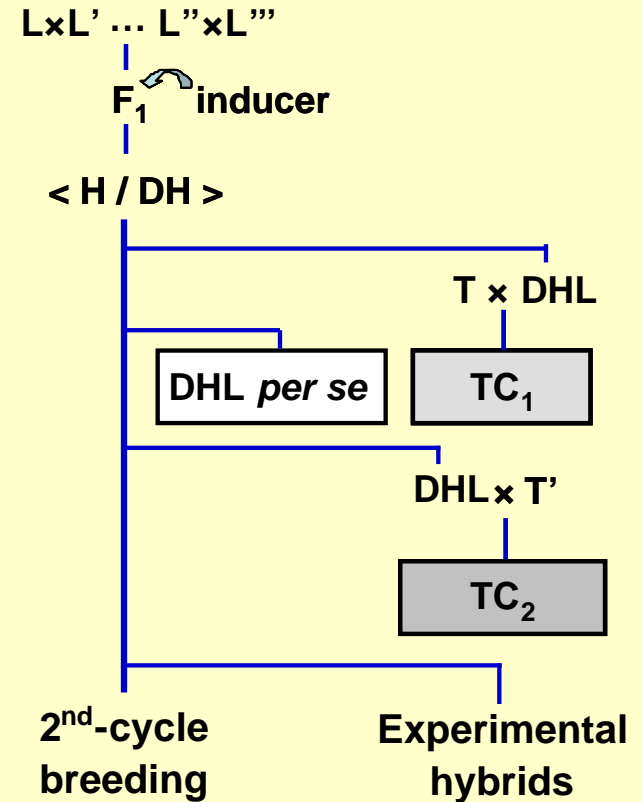
Two-stage line development (LD) schemes

Year Season

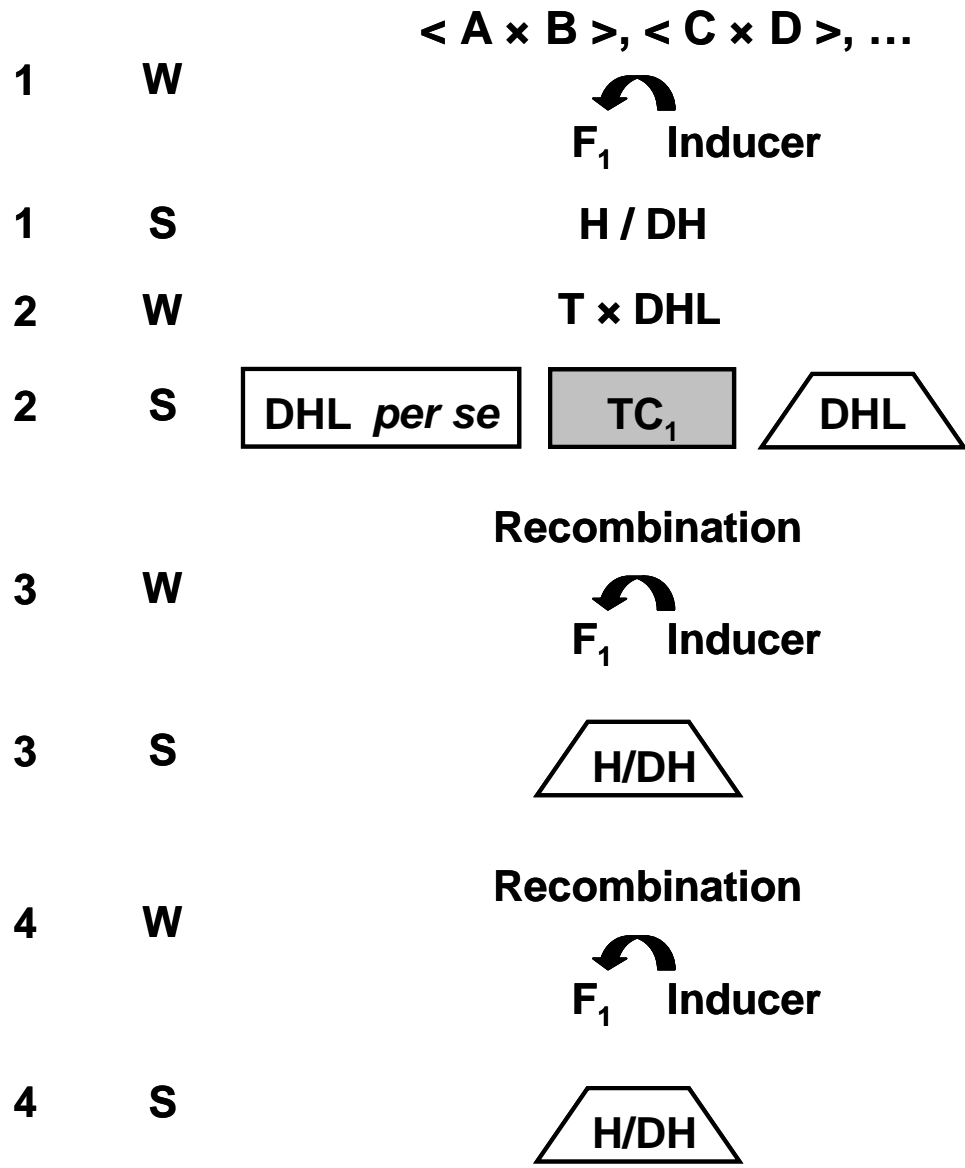
Standard scheme



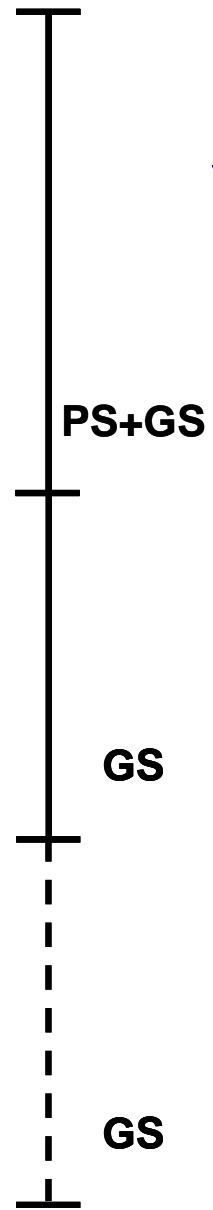
Accelerated scheme



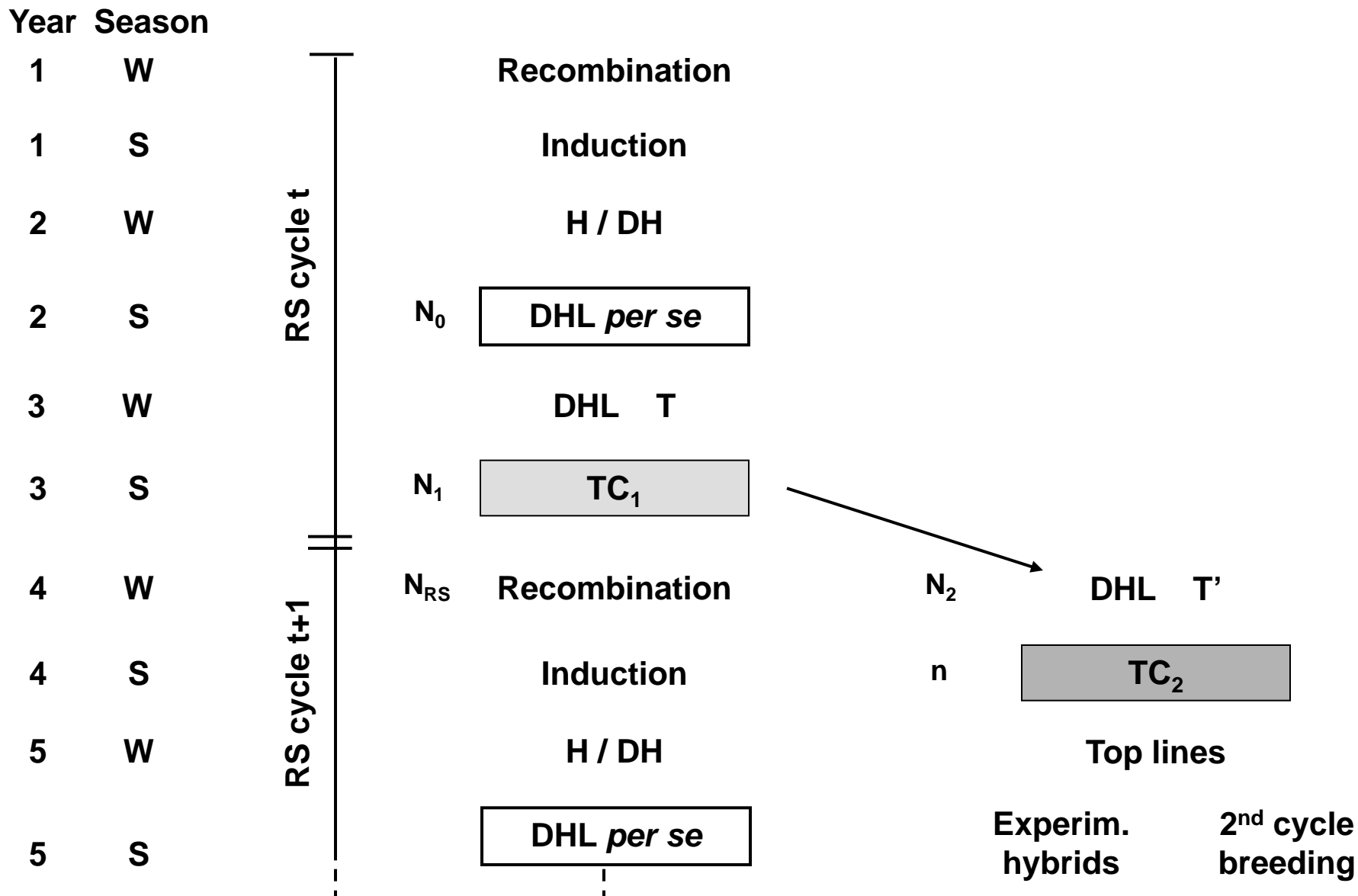
Year Season



Integration of genome-wide selection (GS)



Integrated recurrent selection (RS) and parent line development (LD)



MBP (Version 1.0)

Software for optimizing **M**aize **B**reeding **P**lans based on DH lines

(Gordillo & Geiger 2008)

- Maximizes the expected **genetic gain per year** for a given **annual budget** and a limited relative annual **loss of genetic variance**.
- Allows to optimize **1-, 2-, and 3-stage testcross selection** procedures for alternative breeding schemes.
- Allows the user to specify the **tester type** (e.g. pure line, single cross, population) for each testcross selection stage separately.
- Accounts for detailed **monetary costs** of each individual breeding step.

MBP is applicable to :

- Line development (**LD**) in hybrid breeding
- Recurrent selection (**RS**)
- Integrated **RS/LD** approaches
 - **RS is treated as an integral part of LD**
- Interlinking successive staggered breeding cycles

MBP: Quantitative genetic and operational input variables

- **Estimates of variance components and genetic correlation coefficients**
- **Haploid induction parameters**
- **Costs of the individual breeding steps**
- **All variables are based on data from collaborating breeding companies and can be varied by the user according to his genetic, technical, and financial resources.**

MBP: Gain criterion

The gain criterion is the expected genetic gain in **GCA** for an **index** composed of the testcross performance for grain **yield** and **dry matter content**.

- **Arbitrary index weights may be chosen by the user.**

Selected MBP results: 1. General program specifications

- Annual budget: **US \$ 750,000**
- Proportion of lines pre-selected for *per se* performance: **50%**
- **Single-cross tester(s)** at all selection stages
- Yield trials: multiple locations, unreplicated
- Three finally selected lines per LD cycle ($N_{LD} = 3$)
- Annual loss of genetic diversity restricted to 2%
- Gain criterion:
 $I = \text{Grain yield (Qx/Ha)} + 2.5 \text{ Dry matter content (\%)}$

MBP results: 2. Standard vs. accelerated two-stage LD scheme

Scheme	N_{LD}	Optimum allocation ^a						Genetic gain for yield (kg ha ⁻¹)	
		N_1	N_2	T_1	T_2	L_1	L_2	per cycle	per year
Standard (4 ys)	3	3573	57	1	7	5	20	812	203
Acceler. (3 ys)	3	5680	79	1	6	3	19	786	262

^a N, T, L = Number of DH-lines, testers, and locations, respectively
Indices refer to test stages 1 and 2

Note: In the Accelerated Scheme, the *per se* evaluation of DH lines is not before but in parallel to the TC_1

→ 7146 vs. 5680 lines are evaluated *per se* in the standard vs. accelerated scheme, respectively

- High-input, short-cycle breeding procedures maximize the genetic gain **per year**.

MBP results: 3. Standard vs. accelerated 1- and 2-stage RS

Annual loss of genetic variance restricted to 2%

Scheme	Optimum allocation							Genetic gain for yield (kg ha ⁻¹)	
	N_{RS}	N_1	N_2	T_1	T_2	L_1	L_2	per cycle	per year
1-stage RS:									
Stand. (3 years)	43	2481	-	2	-	6	-	504	168
Acceler. (2 years)	57	3900	-	1	-	8	-	442	210
2-stage RS:									
Stand. (4 years)	32	3821	225	1	3	4	12	624	156
Acceler. (3 years)	39	5574	274	1	3	3	12	576	192

- The accelerated version is more efficient than the standard scheme.
- One-stage RS is superior to two-stage RS.
- In the most efficient RS scheme more than 50 DH lines need to be recombined to comply with the loss-of-genetic-variance restriction.

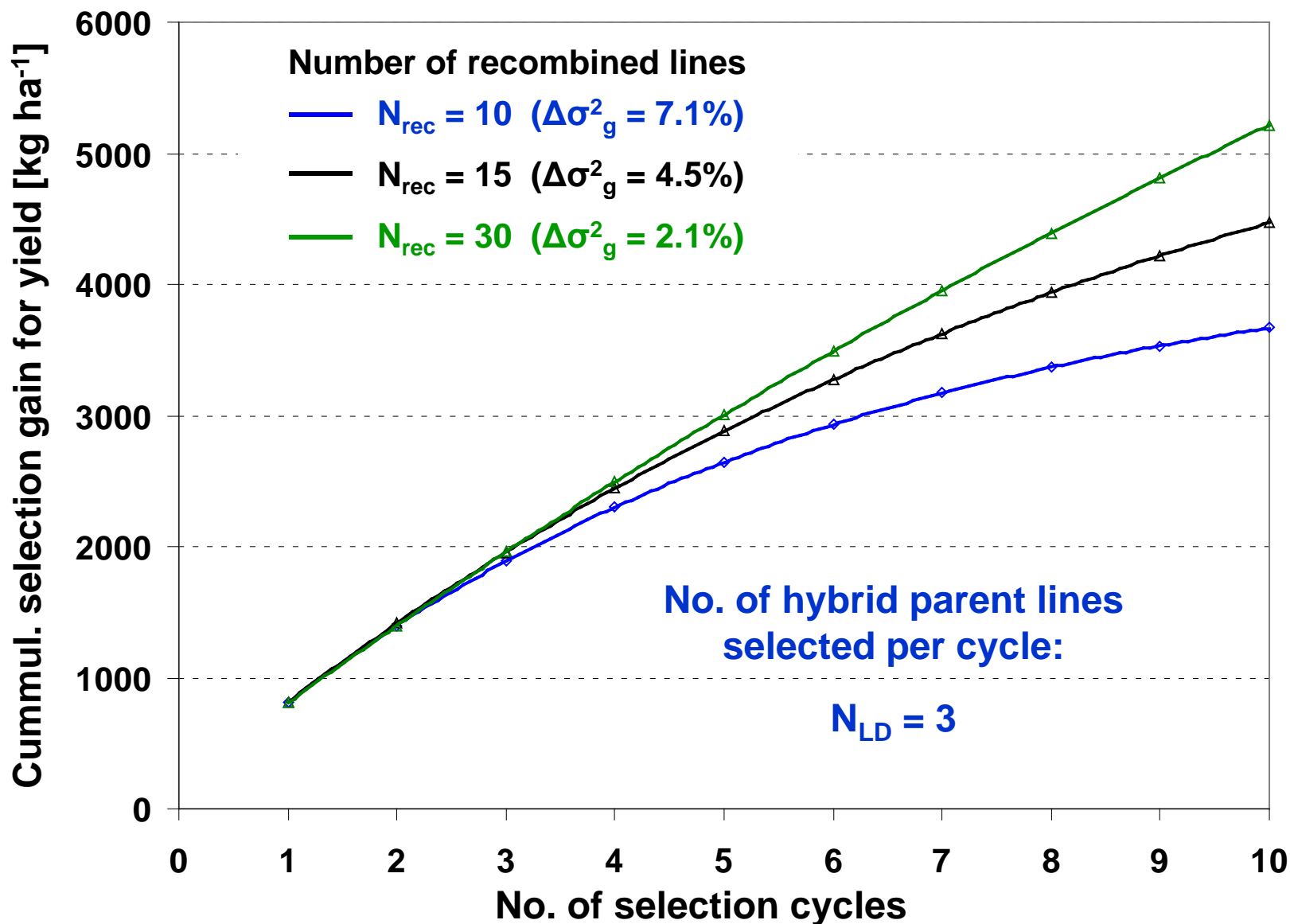
MBP results: 4. Integrated RS/LD standard breeding scheme; influence of the weights for RS and LD

- One-stage testcrossing in RS
- Two-stage testcrossing in LD
- Annual loss of genetic variance restricted to 2%

$W_{RS} : W_{LD}$	N_{RS}	N_{LD}	Optimum allocation						Genetic gain for yield (kg ha ⁻¹) per year	
			N_1	N_2	T_1	T_2	L_1	L_2	G_{RS}	P_{LD}
0 : 1	34	3	3573	57	1	7	5	20	143	204
0.5 : 0.5	32	3	3805	153	1	4	4	14	155	202
1 : 0	32	3	3831	225	1	3	4	12	156	199

- Weights given to RS and LD, respectively, considerably influence the optimum allocation but hardly affect the maximal genetic gain per year.

MBP results: 5. Influence of population size on the long-term progress in line development



Summary and Conclusions (1)

- *In vivo* techniques of haploid induction have become standard tools in maize breeding and research.
- Major **advantages** of DH lines in hybrid breeding include
 - maximum genetic variance from the very first generation
 - perfect compliance with DUS criteria
 - **short time to market**
 - **simplified logistics**
 - reduced expenses for selfing and maintenance breeding.

Summary and Conclusions (2)

- **Genome-wide selection** can effectively be integrated in DH-line based breeding schemes.
- A software package “**MBP (version.1.0)**” has been developed to optimize the allocation of breeding resources and to determine the relative merits of alternative breeding schemes.
- High-input, short-cycle, breeding schemes are expected to provide maximal **annual** genetic gain.

Summary and Conclusions (3)

- The long-term genetic gain in LD builds up on the cumulative genetic gain from RS.
 - It is advisable to weight RS higher than LD when optimizing *combined RS/LD* breeding schemes
- Increasing the weight for RS leads to a considerable increase in the gain from RS, while it hardly affects the gain in LD.
- **Sizable numbers of selected DH-lines need to be recombined** to preserve enough genetic diversity for subsequent breeding cycles, **especially in case of short-cycle (accelerated) schemes!**

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