IHAR-PIB contribution into the sustainable use of pesticides and integrated pest management

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Identyfikator

The Institute was **founded in 1951** for research in breeding and seed production of arable, vegetable and ornamental crops.

IHAR responsibilities were changing over decades. At present IHAR mandate of responsibilities ranges from fundamental research for plant breeding to germplasm conservation, enhancement and utilization, development of production technologies of field crops and technologies of certified seed prodution, etc...

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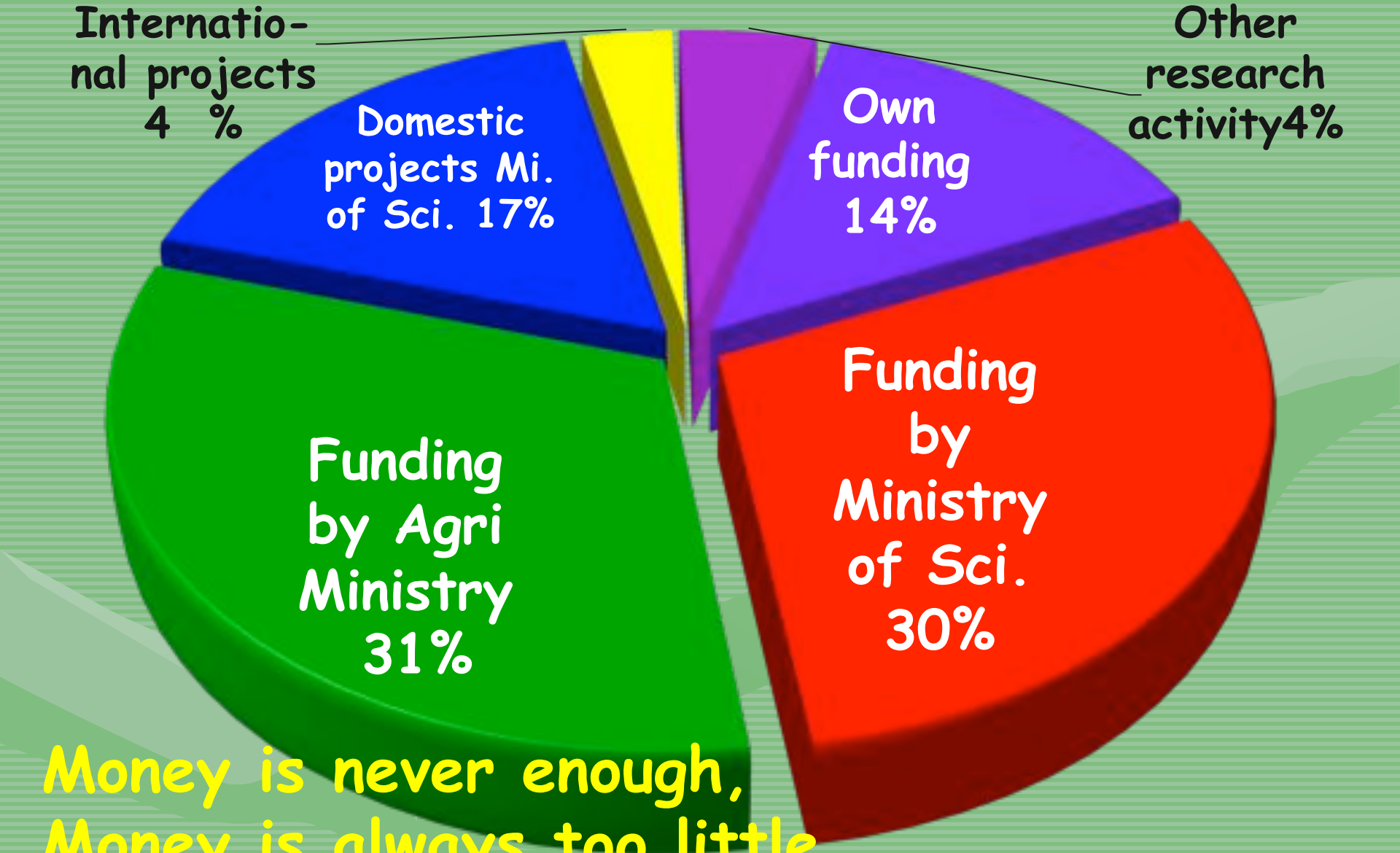
The Institute subordinates to the Ministry of Agriculture and Rural Development

EMPLOYMENT as of 31 December

POSITION	INSTITUTE	Exp. Stn.	TOTAL
2010			
Titular Professors	10		10
Asoociate Professors	21		21
Adjunct Professors	64		64
Research Assistants	50		44
Total research personnel	145		145
Technical personnel	148	26	174
Administrative personnel	66	30	96
Auxiliary personnel	71	104	175
TOTAL	430	160	590

430 (Institute)+160 (Exp.Sta.)+550 (PB Co. Ltd) =1180 empl.

IHAR-PIB budget 2010



Money is never enough,
Money is always too little …,
especially in research institutions.

Comment 1

IHAR-PIB research programs are oriented on sustainable and low input (organic) agricultural production systems with utilization of biological potential of crop plant.

Comment 2

Plant resistance is an important component regardless of IPM concept

&

especially if IPM is perceived or defined as not a single pest control but rather as a combination of components and practices plant resistance bears on IPM effectiveness.

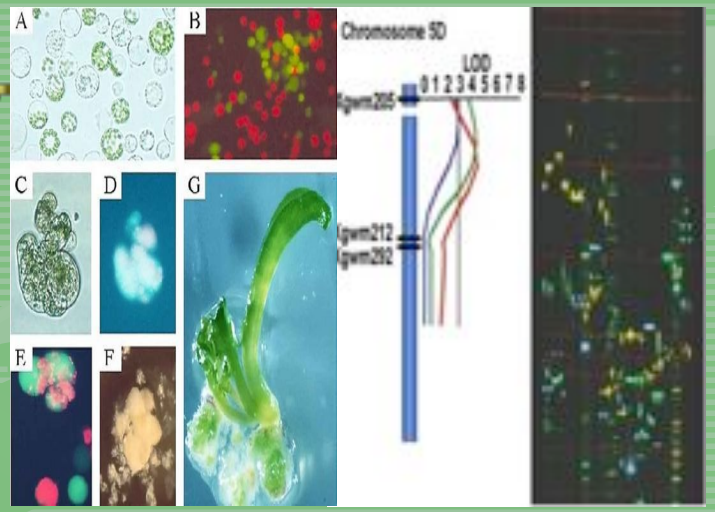
Programs and pieces of research related to IPM

IHAR-PIB R & D activities
Research programs

Statutory research = 170 projects

I. Development & enhancement of plant germplasm and implementation of new strategies into plant breeding.

Head: Prof. dr hab. E. Arseniuk

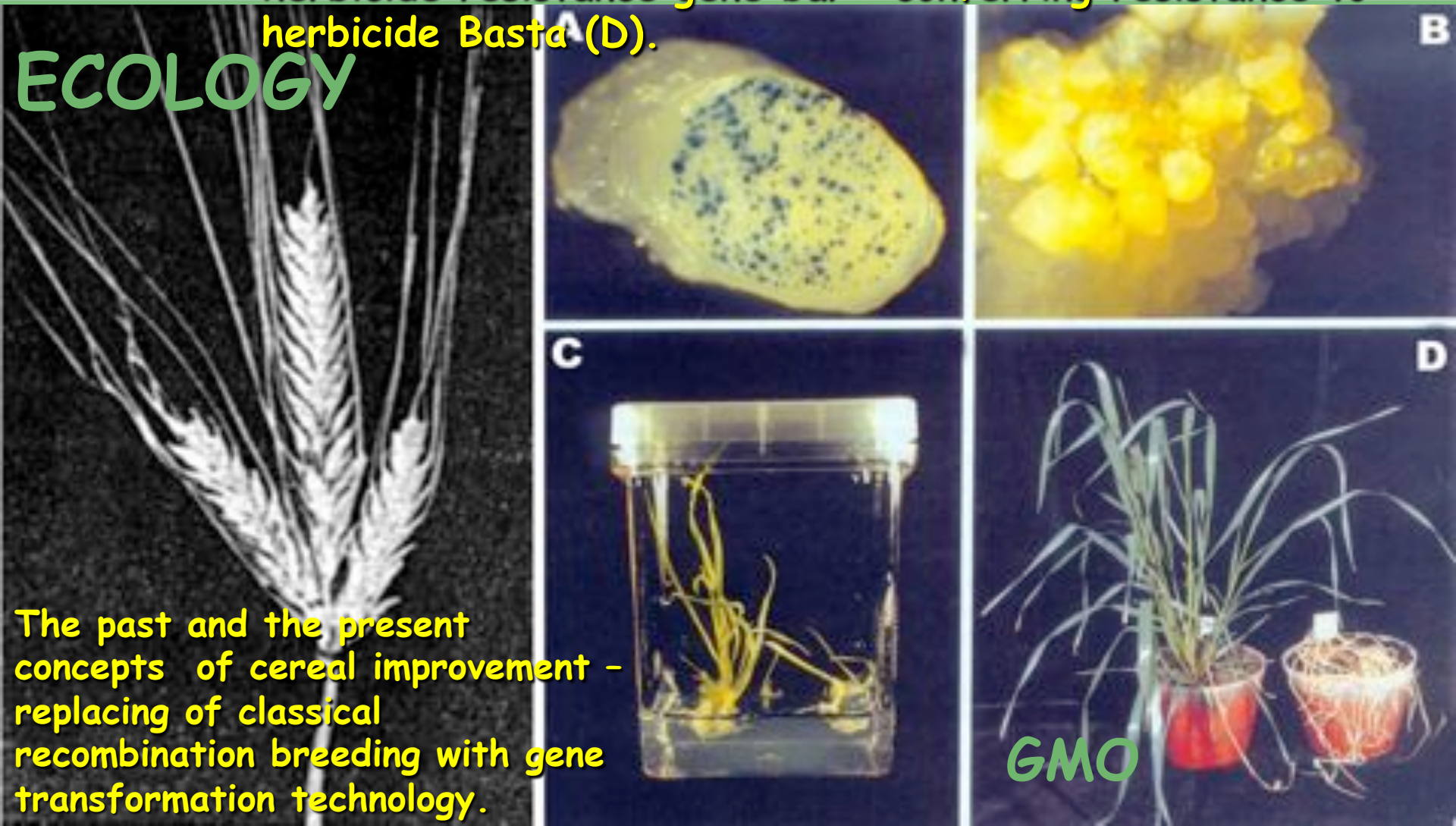


Basic research techniques

- In vitro cultures – somaclones, dihaploids
- Regeneration from protoplsts,
- Molecular markers,
- QTLs.

Classic and transgenic cereal improvement for yield & weed control

Genetic transformation of triticale MAH 1590 with herbicide resistance gene *bar* – conferring resistance to herbicide Basta (D).



The past and the present concepts of cereal improvement – replacing of classical recombination breeding with gene transformation technology.

Examples of IHAR-PIB research on transgenesis:

- histopathological analysis of plant-pathogen interaction and elucidation of oxidative burst role in expression of plant defense against pathogen,
- determine the role and place of GMO, (co-egsistance of clasical and transgenic crop cultivars) in plant production,
- quantitative and qualitative GMO detection in plant products,
- input into the GMO law development and implementation in Poland,
- contribution to the National Biosafety Program of Poland,

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II. Seed science and seed production

Head: Dr L. Boros

Some of objectives of the program:

- determine seed healthiness and other sowing value parameters of seeds from conventional and organic farming,
- study effect of storage on sowing value,
- translation ISTA Rules into Polish and every year edition of amendments, cooperation with ISTA Technical Committees, proficiency tests.
- Membership in the International Seed Testing Association – ISTA,

Kernels of triticale cv. Modus infected by *F. culmorum*

IHAR concentrates on production of certified potato seed free of pathogens, especially quarantine ones

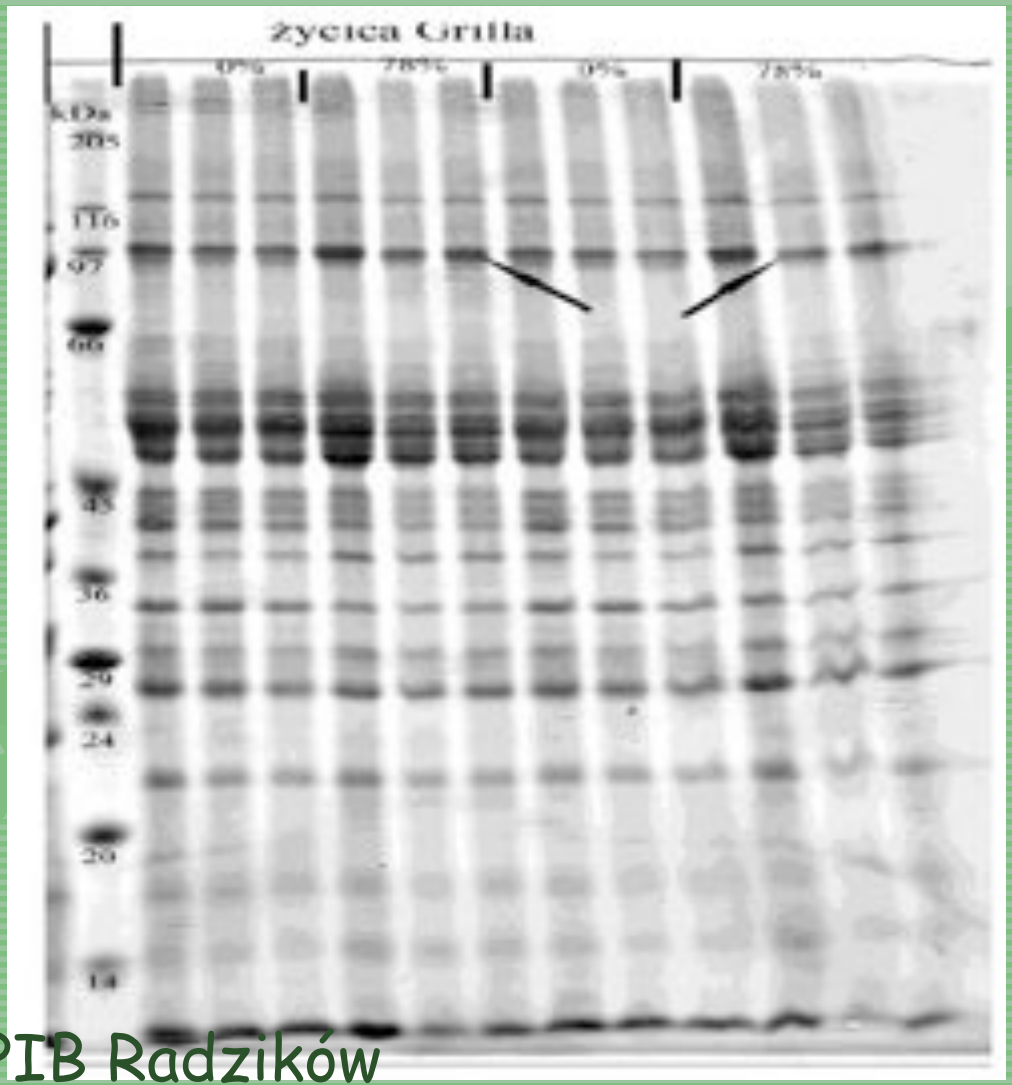
= healthy plants, healthy enviroment, healthy people

- *Synchytrium endobioticum*
- *Ralstonia solanacerum*
- *Clavibacter michiganensis* ssp. *sepedonicus*
- *Globodera pallida*
- *Globodera rostochiensis*

Detection & diagnosis of pests in seeds (here biochemical detection of endophytic fungi *Neothypodium* sp. in seed samples of perennial rygrass Grilla).

Electroforegram of seed proteins:

arrows show a new bar of 97 kDa, specific for seed samples heavily infected (78%), with *Neothypodium*.



Source: B. Wiewióra, IHAR-PIB Radzików

Mapping of R genes and molecular markers to select resistant genotypes to PVY in potato

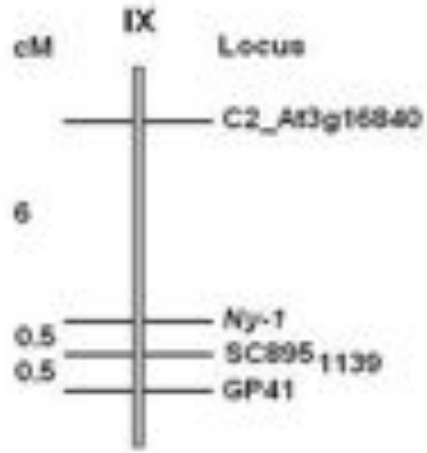
Tubers infected by PVY NTN

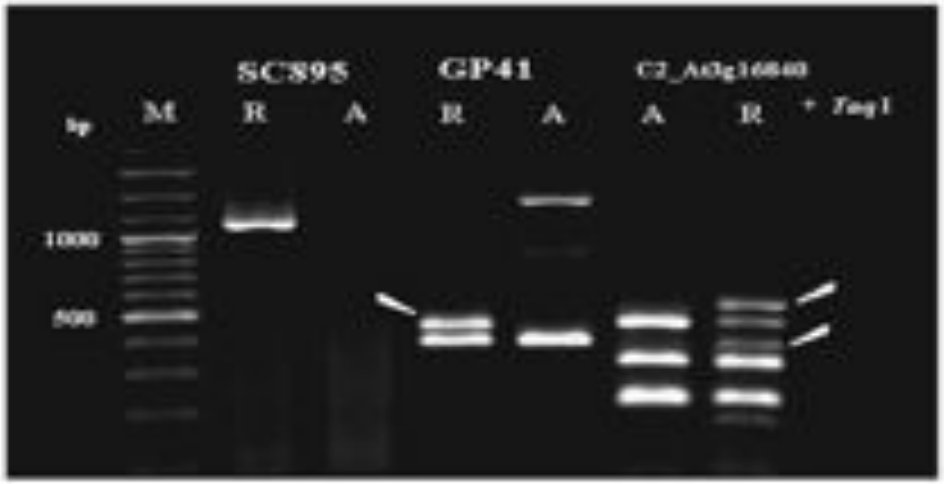
R S

Source: E. Zimnoch-Guzowska
IHAR-PIB Center Młochów

Here, mapping of Ny-1 gene responsible for hypersensitivity reaction to PVY in potato cultivar Rywal

Szajko i wsp. TAG, 2008





R genes to viruses localized on a genetic potato map:

In 1998 – 2010 in Res, Center IHAR-PIB at Młochów there were localized on the map of *Solanum* resistance genes to the most important viruses of potato: PVS, PVY, PVM i PLRV.

For those genes molecular markers were elaborated with PCR what allowed to use genotypic selection (MAS). In total, 7 genes were localized on potato chrmosomes:

Ns (resistance to PVS),

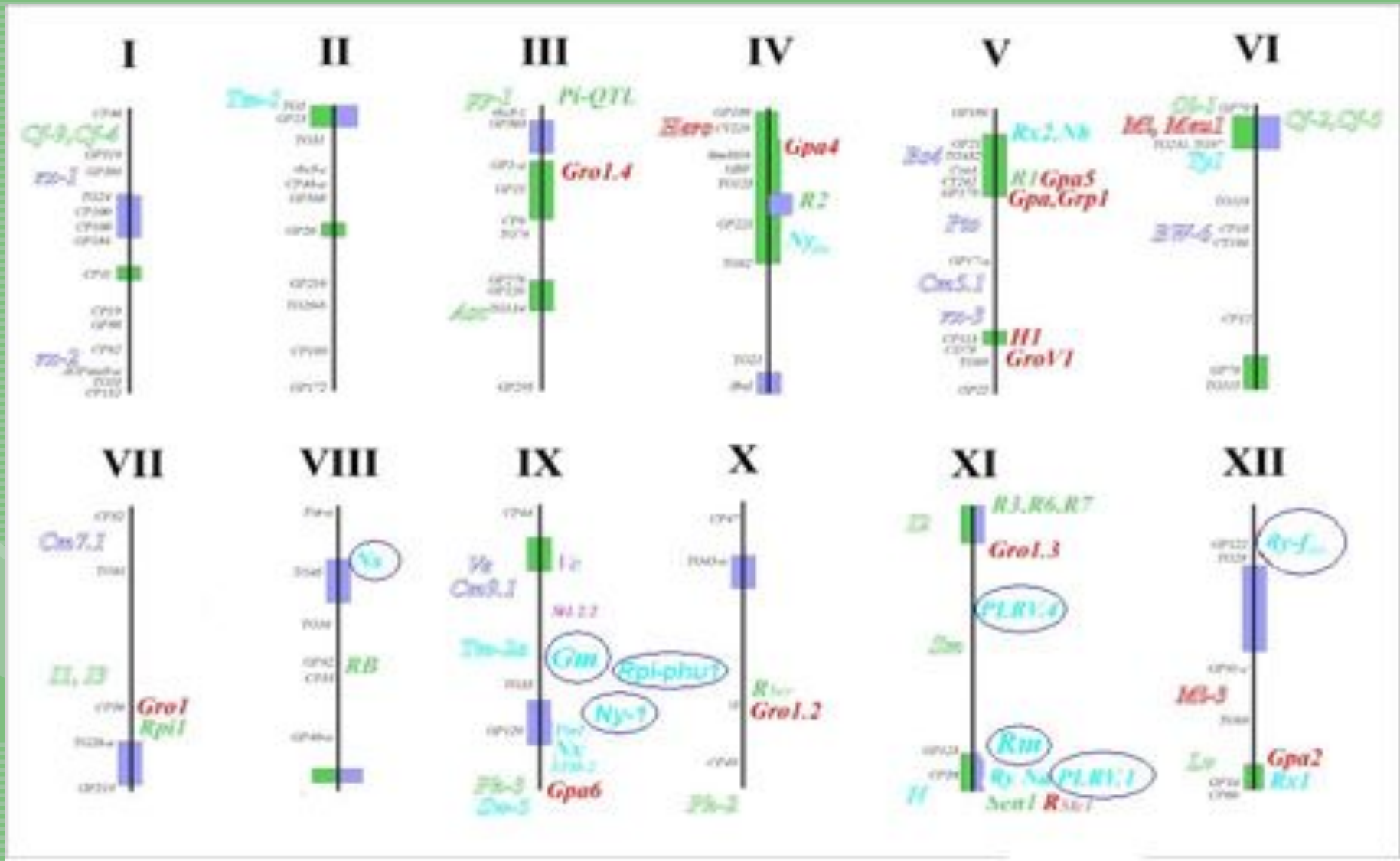
Ry-fsto, Ny-1 (resistance to PVY),

Gm, Rm (resistance to PVM),

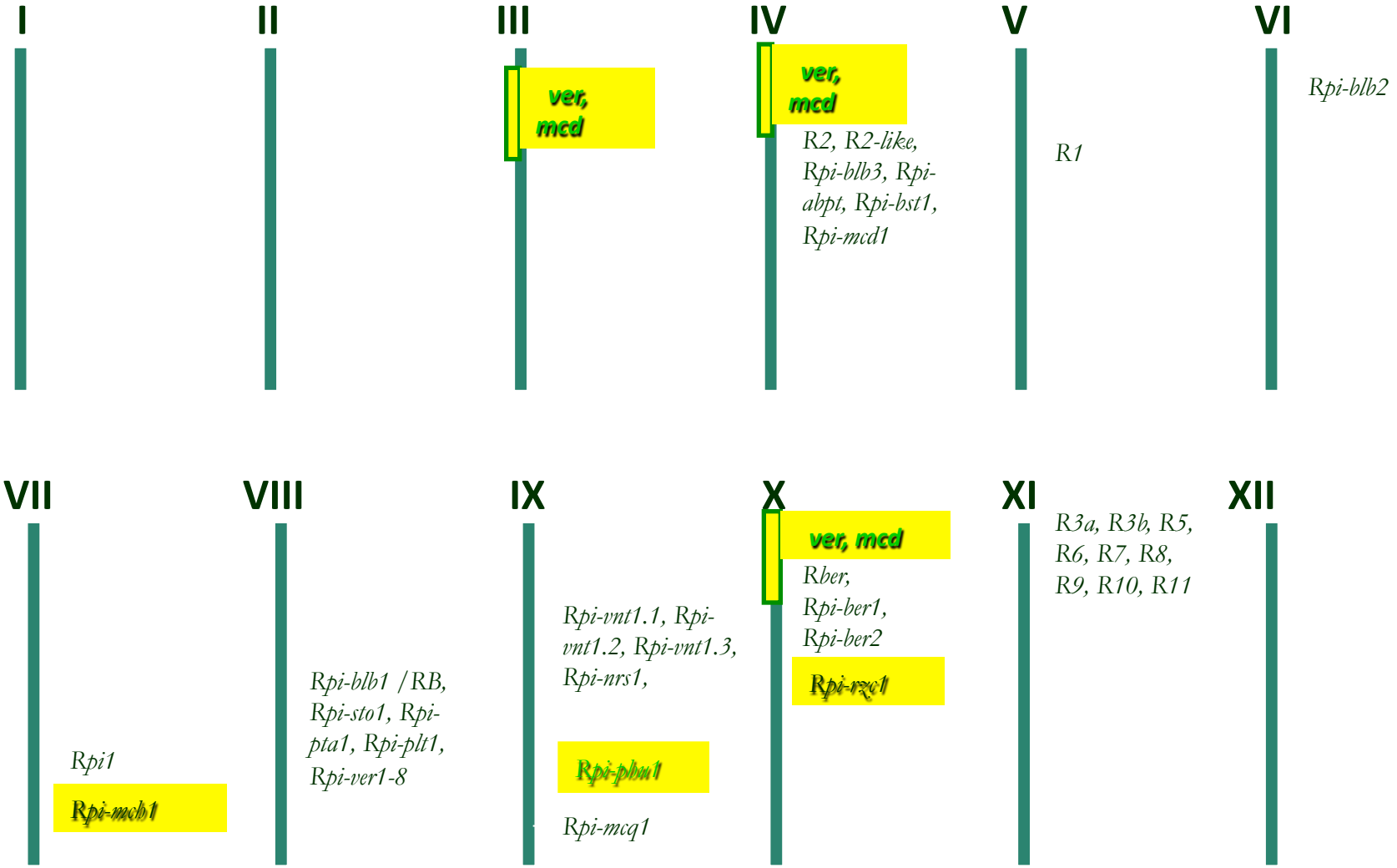
PLRV1 & *PLRV4* (resistance to PLRV).

Source: E. Zimnoch-Guzowska
IHAR-PIB Center Młochów

Potato genome map. R genes to viruses in enircled fields of blue color localized in IHAR-PIB Center Młochów.

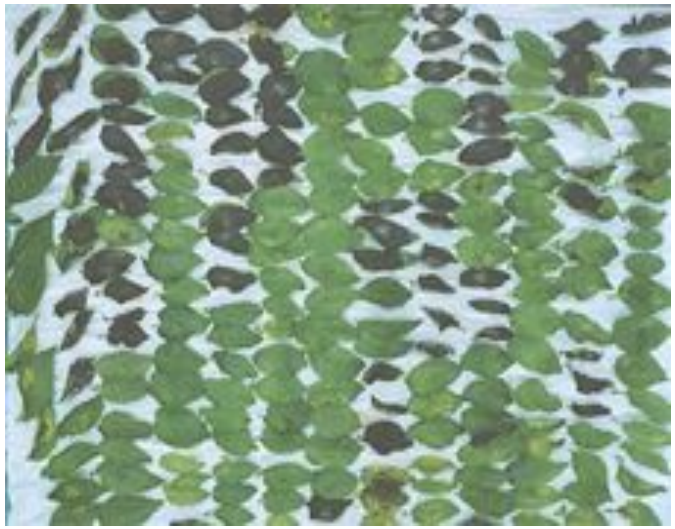


R genes to *P. infestans* on genetic map of potato, yellow color denotes QTL and genes mapped in IHAR-PIB Center Młochów



Origin of genes & QTLs in potato genome conditioning resistance to *P. infestans* in some lines

- gene ***Rpi-phu1*** originating from *S. stenotomum x S. phureja* on IX chromosome,
- gene ***Rpi-mch1*** originating from *S. michoacanum* on VII chromosome. Genes *Rpi-mch1* were mapped with DArT technology, one of the first maps of potato genome with DArT markers.
- gene ***Rpi-rzc1*** originating from *S. ruiz-ceballosii* on chromosome X. (DArT technology),
- **QTL** with resistance to *P. infestans* originating from a hybrid source of *S. microdontum* i *S. verrucosum*.



Source: E. Zimnoch-Guzowska, IHAR-PIB Center Młochów

IHAR-PIB R & D activities

III. Research on plant breeding to identify & broaden genetic base and resources for crop improvement.

Head: Prof. dr. H.J. Czembor

Program priorities

1. testing of plant germplasm in search for sources of resistance to biotic and abiotic stresses,
2. search for agronomic quality traits analysis of plant materials useful for practical breeding,
3. evaluation of uniformity & distictness of breeding materials by conventional and molecular biology techniques,
4. refinement of biotechnology and plant breeding methods for crop improvement.

Testing for resistance of DH lines derived from F1 of winter triticale hybrid Pinokio x Bogo

Detection of QTLs controlling partial resistance to Stagonospora nodorum blotch disease in winter triticale 'Bogo'.

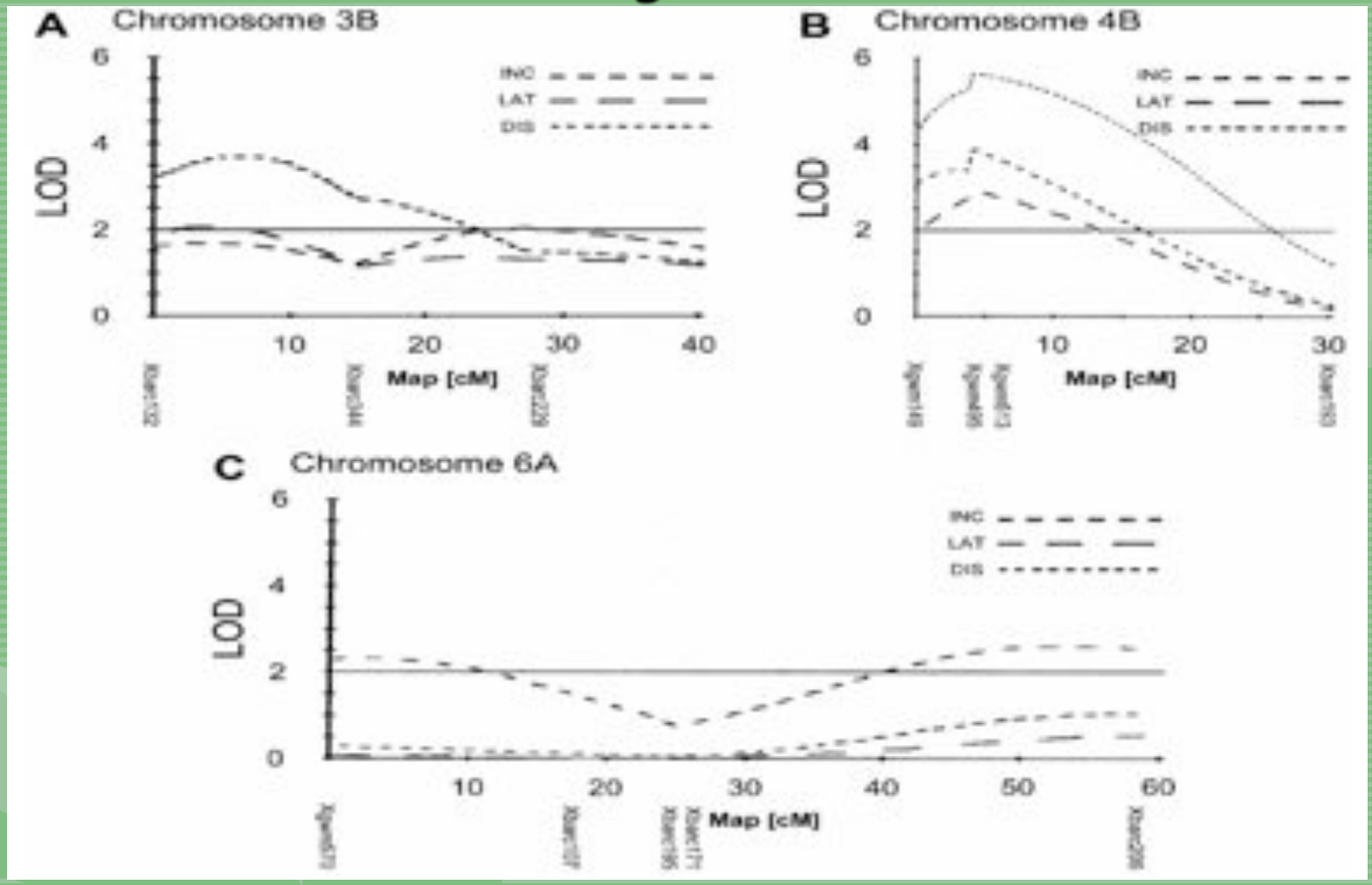


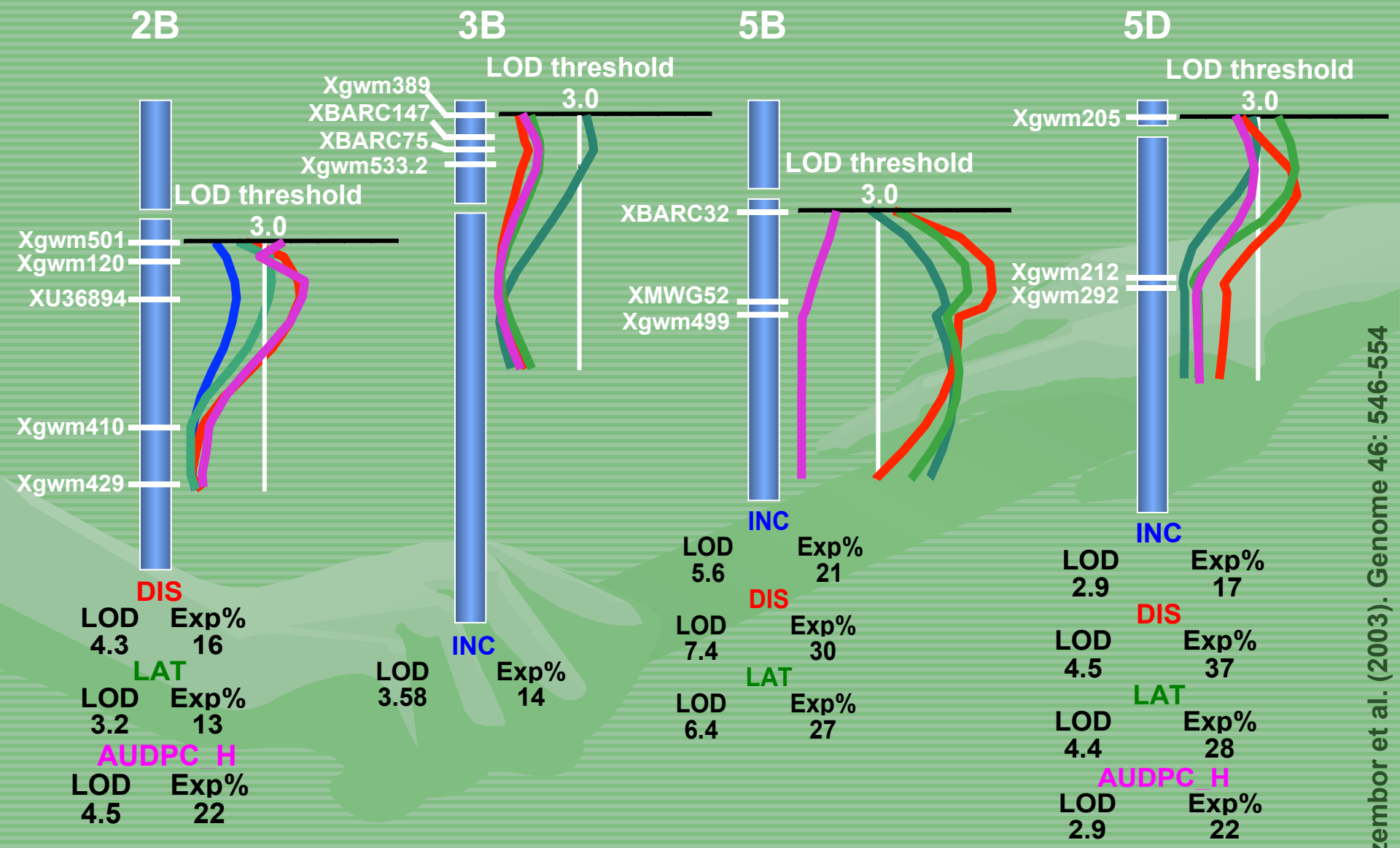
Fig. 1. Logarithm of odds (LOD) scores based on interval mapping of quantitative trait loci (QTLs) for long incubation period (INC), low disease severity (DIS) and long latent period (LAT) on linkage groups corresponding to chromosome 3B (A), 4B (B) and 6A(C).

E. Reszka et al. Plant Pathology Bulletin 16:161-167, 2007.

QTL analysis: population derived from cross LIWILLA (R)×BEGRA (S)

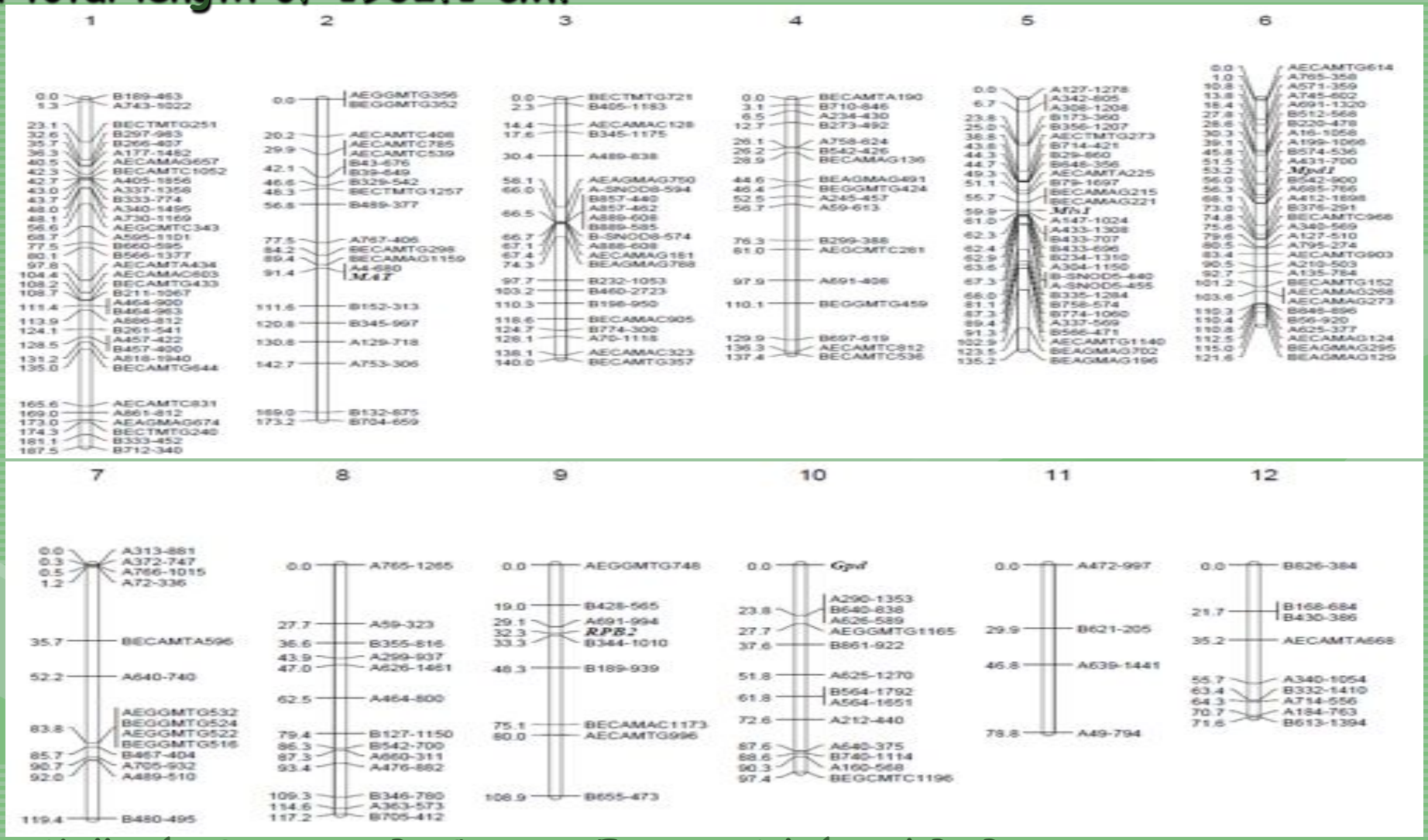
controlled environment, 5th leaf stage, INC, DIS, LAT

field conditions (1 year exp.), AUDPC on heads and leaves



Czembor et al. (2003). Genome 46: 546-554

The genetic linkage map of *Phaeosphaeria nodorum*. Twenty one major linkage groups were assembled with 276 markers and 5 genes covering a total length of 1932.1 cM.



A. Malkus[1], Q. Song, P. Cregan, E. Arseniuk [1] and P. P. Ueng
1. Dep. Plant Pathology, Plant Breeding and Acclimatization Institute, Radzików, Poland. Journal of Phytopathology.

Search for resistance to Fusarium stalk rot in maize

Source: Elżbieta Czembor, IHAR-PIB Radzików