

2nd Symposium on Innovation

Cooperation in Technology and International Transfer of Technology China + 16 CEEC Format

Nitra, Sept 23, 2015

Plant Biotechnology Innovations in Plant Production

(cases from our practice)

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Topics:

1. Assisted plant breeding

- Healthier grains, grains as medicine

2. Plant molecular breeding

3. Gene transfer

- Wheat quality improvement by new proteins
- Cereals producing polyunsaturated fatty acids in grains
- GM plants for agriculture

Plant production & Biotechnology

Plant production - cultivation of plants (and other life forms) for **food, feed, fiber, raw materials, energy** (biofuel), **drugs** and **other** products used to sustain and improve the human life (International Labour Organization)

Biotechnology - the **use** of **living systems** and **organisms** to **develop** or make **products**, or "any technological application that uses biological systems, living organisms or derivatives thereof, to make or modify products or processes for specific use" (UN Convention on Biological Diversity, Art. 2)

1. Assisted Plant Breeding

Biological activity of cereal grains

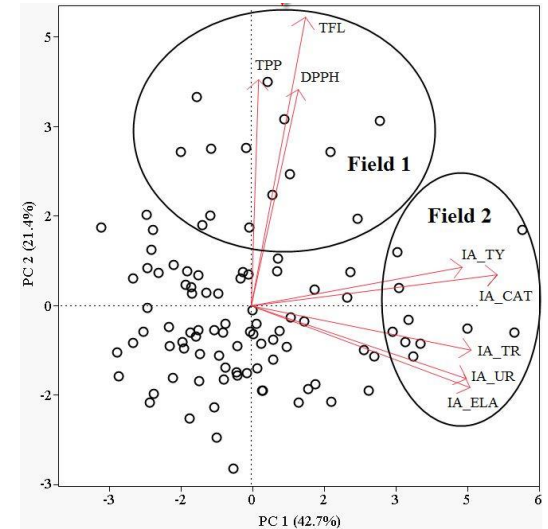
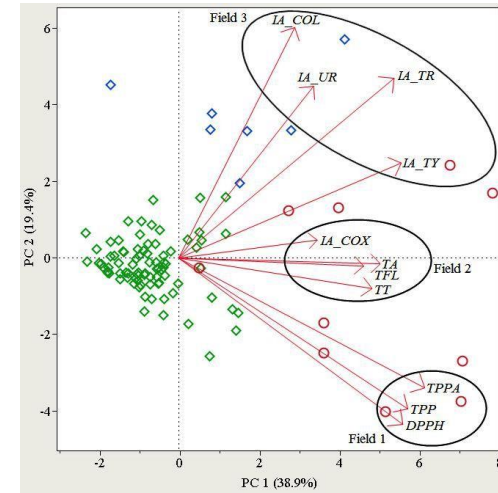
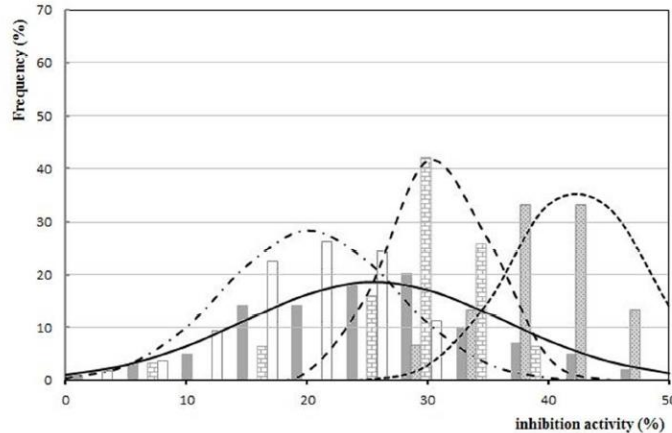
- „**Colored**“ wheat – new compounds in grain – **anthocyanins** - glycosylated cyanidins, delphinidins, malvinidins, pelargonidins, petunidins, and peonidins accumulated in **aleurone** layer or pericarp - **natural compounds** - **purple, blue,** and **red** colored wheat seeds
- Improvement of staple foods and feeds consumed daily by **health-promoting** and **disease-preventing** agents
- Special wheat cv. **PS Kalkulka** (2014) – **purple** grains – functional foods production



Biological activity of cereal grains

- Extracts from seeds - wheat, barley, oat
- Total **polyphenols**
- Total **flavonoids**
- **Antioxidant** activity (DPPH)
- **Inhibitory** activities to **proteases** - TRY, THR, URO, CAT, ELA, COX

Frequency distribution of IA_ELA of oat extracts

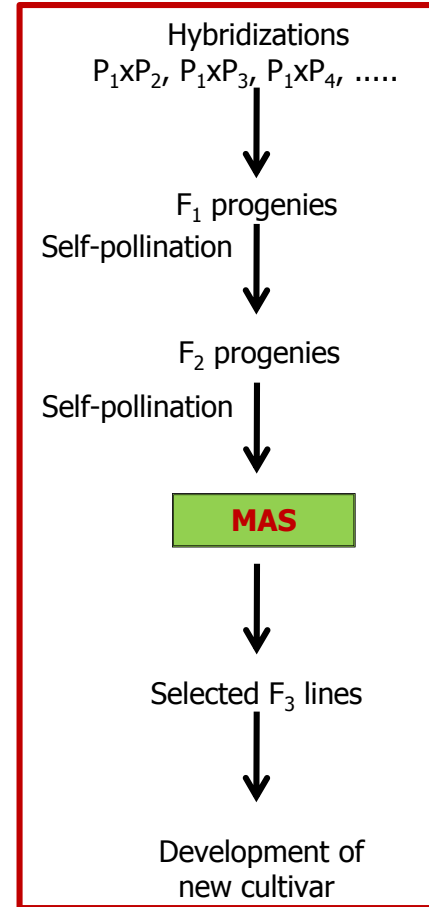


2. Plant Molecular Breeding

Wheat improvement – **Breeding** + **MAS**

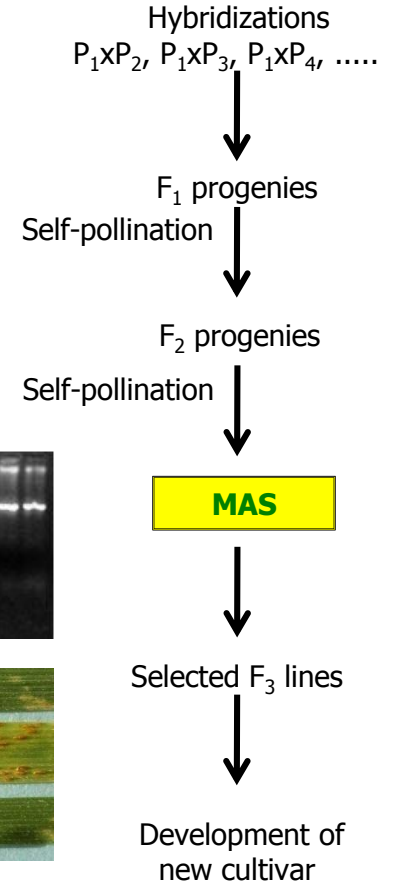
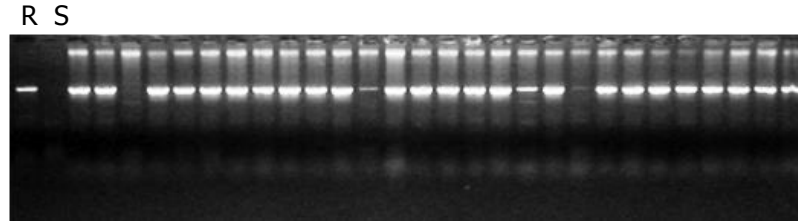
Plant molecular breeding approach:

- **Hybridization** Donor x Acceptor
- **Selection** by **molecular markers**
- Line(s) development, multiplication, testing, registration, marketing



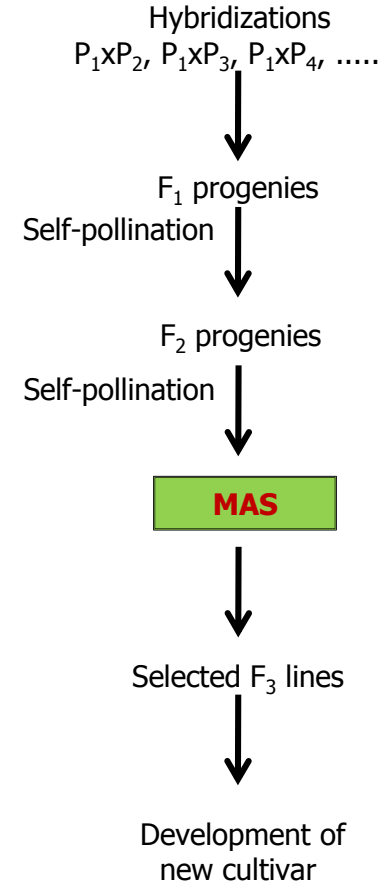
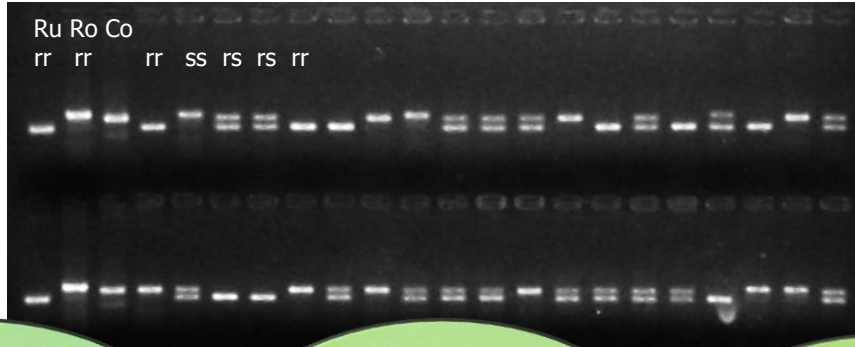
Wheat improvement – **resistance**

- Improvement of **leaf rust resistance**
- Effective **Lr** gene(s) – *Lr19*, *Lr24*, *Lr35*, *Lr19 + Lr24*, ...
- Effective (DNA) marker system - PCR-based



Barley improvement – **resistance**

- Example – **virus resistance** (BaYMV + BaMMV)
- Effective ***rym*** gene(s) – *rym4*, *rym11*, *rym4* + *rym11*
- Effective (DNA) marker system - PCR-based



3. Gene transfer

Wheat quality improvement by new proteins

Wheat improvement – **proteins**

- Wheat **quality** - influenced by seed storage **proteins**
- Gliadins & **Glutenins** - LMW-GS & **HMW-GS**
- HMW-GS - **x-** or **y-type** of subunit - ***Glu-1 loci*** → hexaploid wheat contains theoretically ≤ 6 different HMW-GS
- HMW-GSs contain signal sequence + domain + N- and C- terminal domains consists of amino acids (including **Cys**)
- Cysteine residues - important role in intermolecular **S-S bonds in dough** influencing final **bread-making quality**

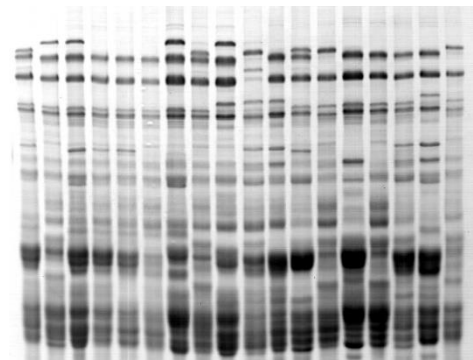
Where are „new and better“ genes & proteins ???

Genetic resources - protein & gene sources

- **Where ?** – national Genebank – maintained wheat **genetic resources** collection contains ~5000 wheat accessions



- **How ?** – extensive **screening** in seed storage **protein patterns**



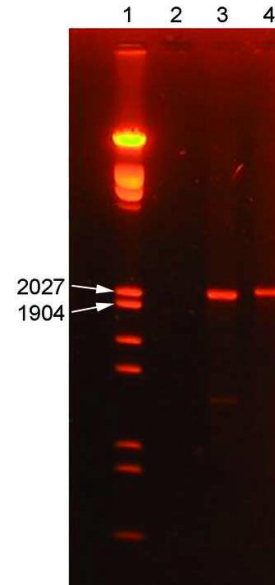
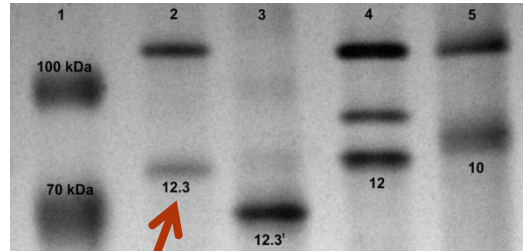
Protein mining in genetic resources

Interest to:

- Identify – **well-known** & highly **frequented** HMW-GS improving quality (1, 2, 2*, 7+8, 7+9, 5+10 ...)
- Identify **low frequented** HMW-GS increasing quality (15+16, 17+18 ...)
- Find **new** HMW-GS with **unknown** effect in **obsolete cultivars** or **landraces** of *T. aestivum* originated from similar environment and agricultural systems
- Look for **new** HMW-GS with **unknown** effect in „**exotic**“ **germplasm** of *T. aestivum* or other *Triticum* species

From protein to gene (story of cv. Noe)

- *T. aestivum* L. cv. **Noe** – French **obsolete cultivar**, genetic background of Russian winter wheat Odyssea, released in 19th century – possess **new** HMW-GS **1Dy12.3**
- **Amplification** with primers derived from 1Dy12 (X03041) and 1Dy10 (X12929)



Cloning
+
sequencing

Protein and gene characterization (story of cv. Noe)

- **1Dy12.3** – different **amino acid** composition

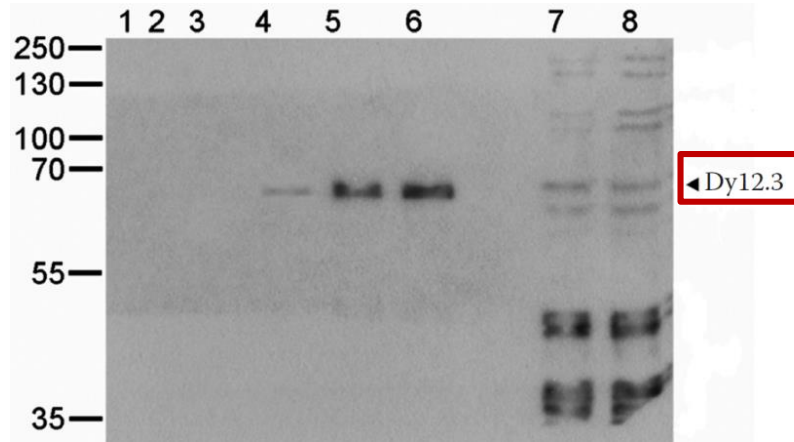
Table 3. Comparison of essential amino acid content in selected HMW-GS 1Dy subunits of genus *Triticum* L. and *Ae. tauschii*

Essential amino acids	Subunits							
	1Dy12.3	1Dy10	1Dy12	1Dy10.1	1D ^y 10	1Dy12 ^t	1Dy12.1 ^t	1Dy13 ^t
Phe	3	3	3	3	3	3	3	3
His	12	13	13	13	14	14	13	13
Ile	7	5	8	8	7	6	6	5
Lys	9	8	9	8	7	8	9	8
Leu	28	28	29	27	28	29	29	29
Met	6	4	5	4	4	4	4	4
Thr	25	26	25	26	27	26	26	27
Val	19	20	19	19	19	18	18	18
Trp	6	6	6	6	7	6	6	5



Heterologous expression of 1Dy12.3 (story of cv. Noe)

- Western blott analyses of cell lysates of *E. coli* transformed with 1Dy12.3



3. Gene transfer

Cereals producing polyunsaturated fatty acids in
grains

Polyunsaturated fatty acids (PUFAs)

- **Unique** structural and functional **characteristics** of PUFAs:
 - Regulation of architecture, dynamics, phase transition, **permeability of membranes** – modulating behavior of membrane-bound proteins
 - **Controlling** of certain **genes expression**, affecting processes including FA biosynthesis and cholesterol transport
 - **Precursors** of many **metabolites** (prostaglandins, leukotrienes, hydroxy-fatty acids) regulating critical biological functions
 - PUFAs are **required** in **every organ** in body to function normally
 - **Insufficient consumption** of PUFAs leads to **abnormalities** in skin, diabetes, cardiovascular, endocrine, nervous, immune, inflammatory, respiratory, reproductive systems, etc.
 - **Mammals** are not able to synthesize **PUFAs** → must be **supplied** in diet

PUFAs of interest

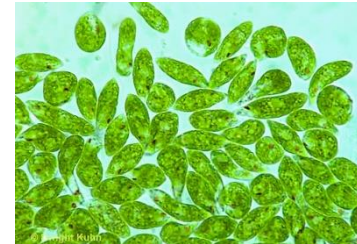
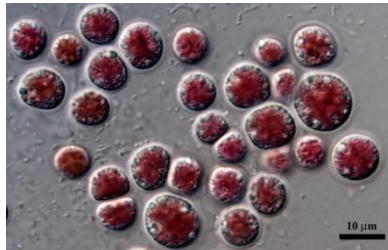
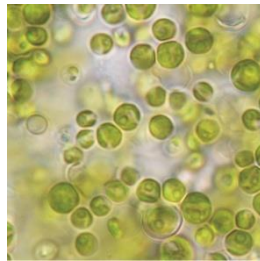
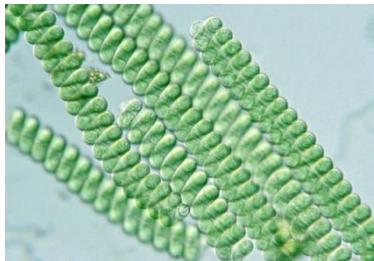
- PUFAs of interests – **γ-linolenic acid** (18:3 n-6; GLA), dihomo-γ-linolenic acid (20:3 n-6; DGLA), arachidonic acid (20:4 n-6; AA), eicosapentaenoic acid (20:5 n-3; EPA), docosapentaenoic acid (22:5 n-3; DPA), docosahexaenoic acid (22:6 n-3; DHA)
- PUFAs are **insufficient** in **natural sources** of food and feed
- Strategies for food and feed improvement by PUFAs:
 - ✓ **enrichment** by PUFAs produced elsewhere (external)
 - ✓ **production** by own (internal)
- **Cereal** grains are **low** in fatty acids content
- **Linoleic acid** – major fatty acid of n-6 family in grains, **α-linolenic acid** (n-3 family) in very small quantities

Sources of PUFAs

- Beneficial sources of PUFAs – **fishes** (tuna, herring, menhaden, sardine, salmon) or **shellfishes** (blue crab, oyster, lobster, mussels) – oils (C20, C22, n-3) and fatty acids – EPA, DPA, DHA

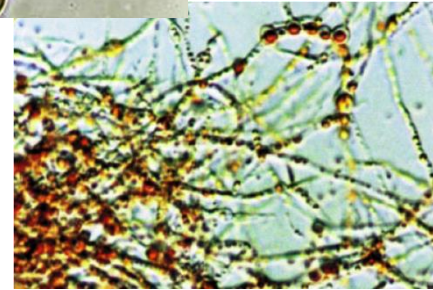
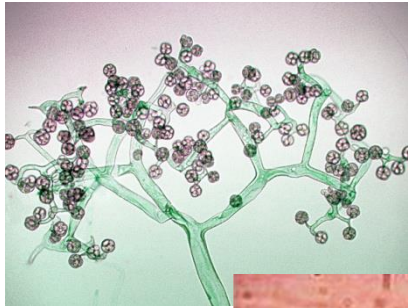


- Alternative sources** – marine bacteria, heterotrophic and phototrophic microalgae (*Spirulina platensis*, *Chlorella vulgaris*, *Porphyridium cruentum*, *Sargassum salicifolium*, *Euglena gracilis*), mosses



Sources of PUFAs

- **Alternative sources – oleaginous fungi** – fungi *Zygomycetes* (*Thamnidium elegans*, *Pythium irregulare*, *Rhizopus arrhizus*, *Cunninghamella echinulata*, *Mucor circinelloides*, *Mortierella alpina*)
- Particularly active in synthesis of PUFAs – donors of **genes** involved in PUFAs biosynthesis



Plant sources of PUFAs

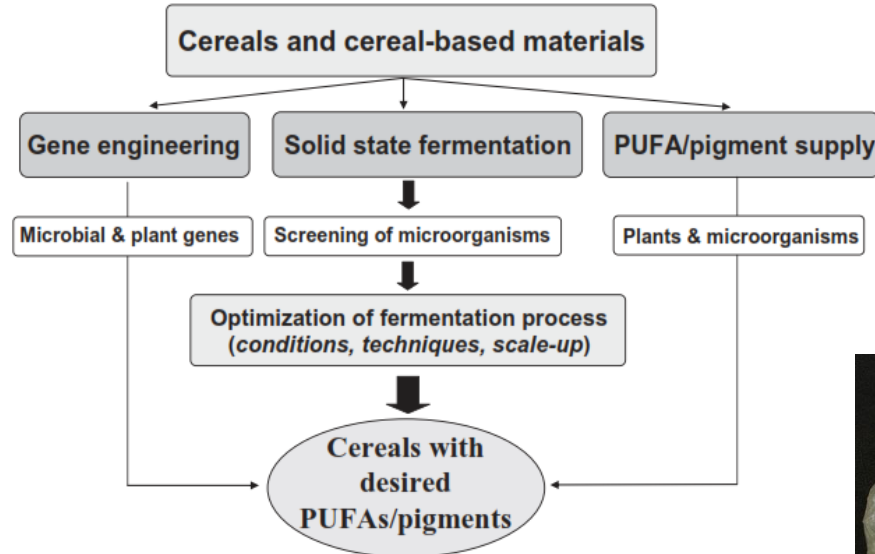
- Main sources of C18 PUFAs – seeds with dominant LA (18:2, n-6) and ALA (18:3, n-3) but occurrence of significant levels of essential **GLA in plants is rare**
- Most commercially important sources of GLA – seeds of **evening primrose** (8–10%), **borage seeds** (24–25%), **black currant seeds** (16–17%)



- PUFAs **above C18 cannot** be synthesized **by higher plants** in any significant amounts owing to a **lack** of requisite **enzymes**

PUFAs in cereals ?

- Challenge for enrichment of cereals with PUFAs:
 - Solid state fermentations** – oleaginous fungi (*Zygomycetes*, *Thamnidium* sp., *Cunninghamella* sp., *Mucor* sp., *Mortierella* sp.) on crop residues
 - Genetic engineering** of plants → „producers“ of FA



Gene transfer & PUFAs production in plants

- Some plant species were modified for GLA production:

Transformed Plant	Source of D6D gene	Content of GLA (% of FA)	Authors, year
Tobacco (<i>Nicotiniana tabacum</i>)	<i>Cyanobacterium</i>	~1,2 %	Reddy, Thomas, 1996
Tobacco (<i>Nicotiniana tabacum</i>)	Borage (<i>Borago officinalis</i>)	~13 %	Sayanova et al., 1997
Canola (<i>Brassica napus</i> L.)	<i>Mortierella alpina</i>	43 %	Liu et al., 2001
Mustard greens (<i>Brassica juncea</i>)	<i>Pythium irregulare</i>	25-40 %	Hong et al., 2002
Soybean (<i>Glycine max</i>)	Borage (<i>Borago officinalis</i>)	31 %	Sato et al., 2004
Tobacco (<i>Nicotiniana tabacum</i>)	<i>Phaeodactylum tricornutum</i>	29,3 %	Abbadi et al., 2004
Linseed (<i>Linum usitatissimum</i>)	<i>Phaeodactylum tricornutum</i>	16,8 %	Abbadi et al., 2004
Mustard greens (<i>Brassica juncea</i>)	<i>Pythium irregulare</i>	27-29 %	Wu et al., 2005
Safflower (<i>Carthamus tinctorius</i>)	<i>Saprolegia diclina</i>	70 %	Nykiforuk et al., 2012
Safflower (<i>Carthamus tinctorius</i>)	<i>Mortierella alpina</i>	50 %	Nykiforuk et al., 2012

Barley improvement with PUFAs

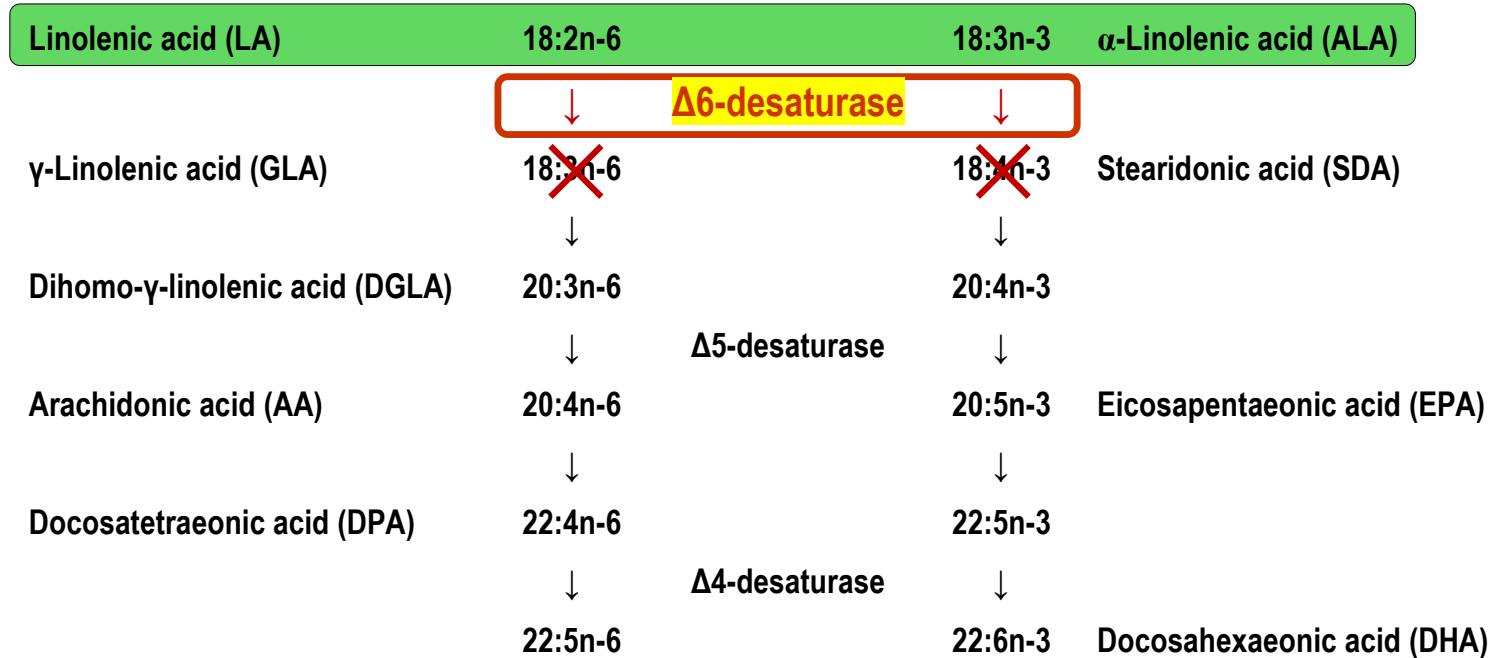
- Barley (*Hordeum vulgare* L.) – **absence** of n-3 and n-6 PUFAs
- **Cereals** do **not produce** essential **PUFAs** but produce metabolites that are substrates for enzymes catalyzing formation of n-6 PUFAs – **Δ -6-desaturase** - catalyses conversion of LA (C18:2, n-6) to GLA (C18:3, n-6)
- Changes in composition of fatty acids in cereal grains are **not feasible** by **conventional breeding**

How to produce GLA in barley ???

Barley improvement with PUFAs

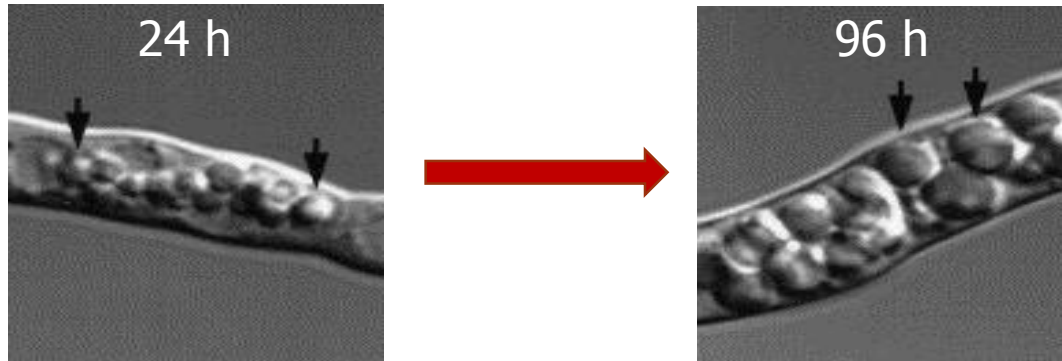
- Δ -6-desaturase** – catalyses conversion of LA (C18:2, n-6) to GLA (C18:3, n-6)

Cereals
terminate
 fatty acid
synthesis
 at this level
 due to
absence of
D6D



Barley improvement with PUFAs

- **Source** of **Δ -6-desaturase gene** for genetic transformation of barley – oleaginous fungus *Thamnidium elegans* CC1456 producing:
 - **20%** of **fats** in dry mass
 - **15-30%** of **GLA**



Barley improvement with PUFAs

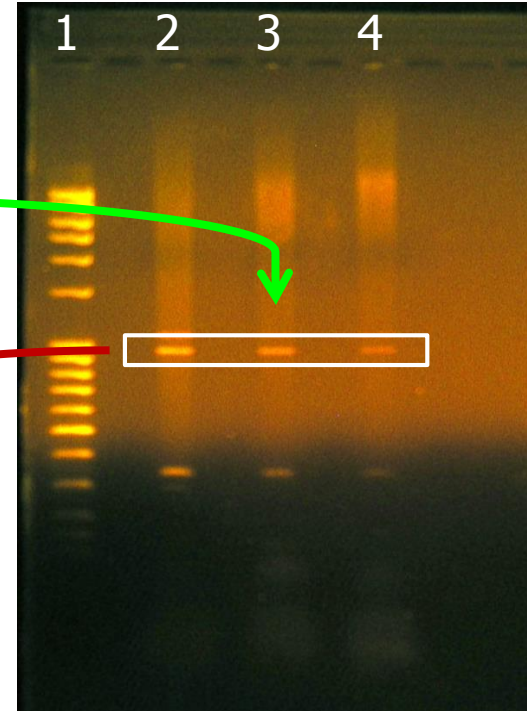
- **D6D** gene isolation from *Thamnidium elegans* CC1456:
 - RNA isolation and cDNA synthesis
 - PCR – design of degenerated primers for **D6D** cDNA **amplification** by: primers 5'-GAYCAYCCYGGWGGWCT-3' and 5'-ACRGGCATWCCGTTTGTGTT-3':

Th.elegans 941161	MSTLDRQSI	FTIKELES	ISORIHGDDE	EAMKFIIDK	MVYDVFTEFIE	DHPGGAQ	LL	THVGKSDV	FHAMHESAY	77
Rh. stolonifer 795076	MSTLDRQSI	FTIKELES	ISORIHGDDE	EAMKFIIDK	KVYDVFTEFIE	DHPGGAQ	LL	THVGKSDV	FHAMHESAY	77
Rh.oryzae 583316	MSTSDRQSV	FTLKELEL	INOKHRDGDK	SAMKFIIDR	KVYDVFTEFIE	DHPGGAQ	LL	THVGKSDV	FHAMHESAY	77
M.circinelloides 052086	MSDVGATVP	HFYTRAEALD	IHDVLDKPK	EARKLIVVEN	KVYDVFTEFIE	DHPGGER	LL	TQERDATDV	FHEHHPESAY	80
Th.elegans 941161	EVLNMYFVGD	VQ-----ETV	VTEKSSSAQF	AVEMRQLRDQ	LKKEGYFHSS	KLFYAYKVL	LS	TLAICIAGLS	LLYAYGVLPL	152
Rh. stolonifer 795076	EVLNMYFVGD	VQ-----ETV	VTEKSSSAQF	AVEMRQLRDQ	LKKEGYFHSS	KLFYAYKVL	LS	TLAICIAGLS	LLYAYGRTST	152
Rh.oryzae 583316	EILNMYFVGD	VK-----DAH	VKE--TPSAQF	ASEMRQLRDQ	LKKEGYFHSS	KAYVYKVL	LS	TLALCAAGLT	LLYAYGHTST	151
M.circinelloides 052086	ELLANCYVGD	CEPKLRIDST	DKKALNSAAF	AQEIRDLRDK	LEKQGYFDAS	TGFVYKVL	ST	TLLVCIVGLA	ILKAWGREST	160
Th.elegans 941161	WLSHLLLL	VSFGNVVGW	LTSDITNAS	--KTAGTMTF	LVVFLGNFCQ	GFSLSWWKNK	DK	HNVHASTNV	HGQDPDIDTA	230
Rh. stolonifer 795076	LAVVASAIT	VGIFWQQCGW	LAHDFGHHQ	CFEDRTWNDV	LVVFLGNFCQ	GFSLSWWKNK	NK	HNTHASTNV	HGQDPDIDTA	230
Rh.oryzae 583316	LAVVASAIT	VGIFWQQCGW	LAHDFGHHQ	CFEDRSWNDV	LVVFLGNFCQ	GFSLSWWKNK	NK	HNTHASTNV	HGQDPDIDTA	229
M.circinelloides 052086	LAVFIAASL	VGLFWQQCGW	LAHDFYAHYQ	VIKDPNVNLL	FLVTFGNLVO	GFSLSWWKNK	NK	HNTHASTNV	SGEDPDIDTA	238
Th.elegans 941161	PVLLWDEYAS	AAYYASLDQE	PTMVSRLAE	QVLPHQTRYF	FFILAFARLS	WALQSLYSF	YF	KKESINKSRQ	LNLFERVCLIV	310
Rh. stolonifer 795076	PVLLWDEYAS	AAYYASLDQE	PTMVSRLAE	QVLPHQTRYF	FFILAFARLS	WALQSLYSF	YF	KKESINKSRQ	LNLFERVCLIV	310
Rh.oryzae 583316	PVLLWDEYAS	AAYYASLDQE	PTMVSRLAE	SVLPHQTRYF	FFVLFARLS	WAIQSLYSF	YF	KOGAINKSHQ	LNLFERFCLIV	309
M.circinelloides 052086	PILLWDEFAY	ANFYGSLKDN	ASGDFRFAE	HILPYQTRYF	FFVLFARLS	WAIQSLYSF	YF	KNETLNKSKL	LSWCEFLIV	318
Th.elegans 941161	GHWALFAFCI	YSWCNRYVHM	VLFFLVSQAT	TGYTLALVFA	LNHNGMPVIT	EKAESMEFF	YF	EIQVITGRDV	TLSPLGDWFM	390
Rh. stolonifer 795076	GHWALFAFCI	YSWCNRYVHM	VLFFLVSQAT	TGYTLALVFA	LNHNGMPVIT	EKAESMEFF	YF	EIQVITGRDV	TLSPLGDWFM	390
Rh.oryzae 583316	SHWTLRTYCT	LWVCNRYVHM	VLFFLVSQAT	TGYTLALVFA	LNHNGMPVIT	EKAESMEFF	YF	EIQVITGRDV	TLSPLGDWFM	389
M.circinelloides 052086	VHWVFRTYCT	IAWISIRNI	AMFFVVSQIT	TGYTLALVFA	MNHNGMPVYS	PEEANTHEF	YF	ELDCITGRDV	NCTVFGDWLM	398
Th.elegans 941161	GGLNYQIEHH	VFFNMPRHNL	PTVMPNVKSL	CQKYDINYHD	TGFLKGTLEV	LQTLDITSKL	YF	SLQLSKKSF	459	
Rh. stolonifer 795076	GGLNYQIEHH	VFFNMPRHNL	PTVKPMVKSL	CQKYDINYHD	TGFLKGTLEV	LQTLDITSKL	YF	SLQLSKKSF	459	
Rh.oryzae 583316	GGLNYQIEHH	VFFNMPRHNL	PKVKPMVKSL	CCKYDINYHD	TGFLKGTLEV	LKTLDITSKL	YF	SLQLSKKSF	458	
M.circinelloides 052086	GGLNYQIEHH	LFPEMPRHNL	SKVKSMVKPI	AQKNIPYHD	ITVIGSTIEV	LQTLDFVQKI	YF	SQKFSKML	467	

Barley improvement with PUFAs

- Amplification of D6D gene from *T. elegans* cDNA:
 - 1 – 100 bp ladder
 - 2-4 – fragment from PCR cca 930 bp

- **Cloning** and **sequencing**



Barley improvement with PUFAs

- ***Thamnidium elegans***
 - sequence of **D6D cDNA** – Genbank accession **HM856138**:

Thamnidium elegans strain CCF 1456 delta-6 desaturase mRNA, partial cds

GenBank: HM856138.1

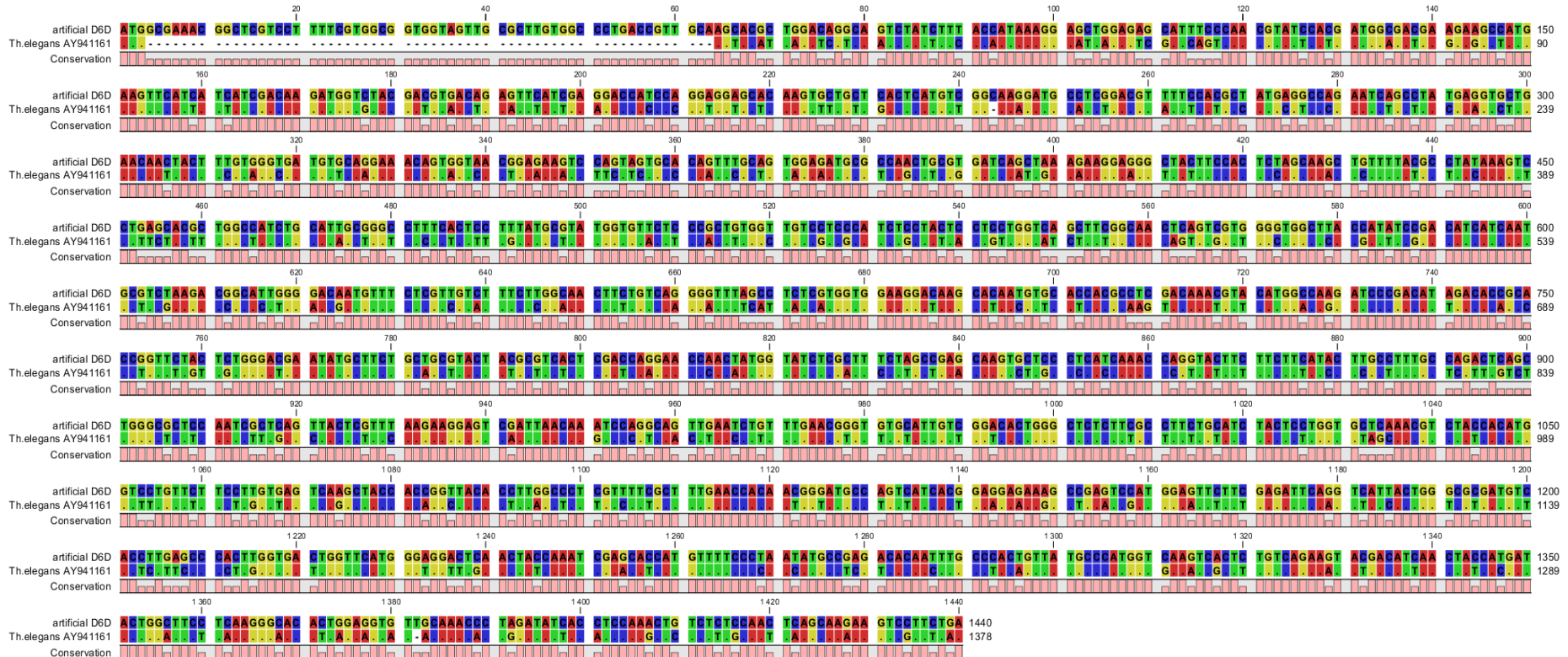
[FASTA](#) [Graphics](#)

[Go to:](#)

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LOCUS      HM856138                932 bp    mRNA    linear   PLN 09-OCT-2010
DEFINITION Thamnidium elegans strain CCF 1456 delta-6 desaturase mRNA, partial
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ACCESSION  HM856138
VERSION   HM856138.1  GI:308096429
KEYWORDS  .
SOURCE    Thamnidium elegans
            ORGANISM  Thamnidium elegans
            Eukaryota; Fungi; Fungi incertae sedis; Early diverging fungal
            lineages; Mucoromycotina; Mucorales; Mucorineae; Mucoraceae;
            Thamnidium.
REFERENCE  1 (bases 1 to 932)
            AUTHORS  Mihalik,D. and Klempova,T.
            TITLE    Partial cDNA of delta-6-desaturase from Thamnidium elegans CCF 1456
            JOURNAL  Unpublished
REFERENCE  2 (bases 1 to 932)
            AUTHORS  Mihalik,D. and Klempova,T.
            TITLE    Direct Submission
            JOURNAL  Submitted (21-JUN-2010) Dept. of Plant Biotechnology, Research
            Centre of Plant Production, Bratislavská Cesta 122, Piestany,
            Piestany 92168, Slovakia
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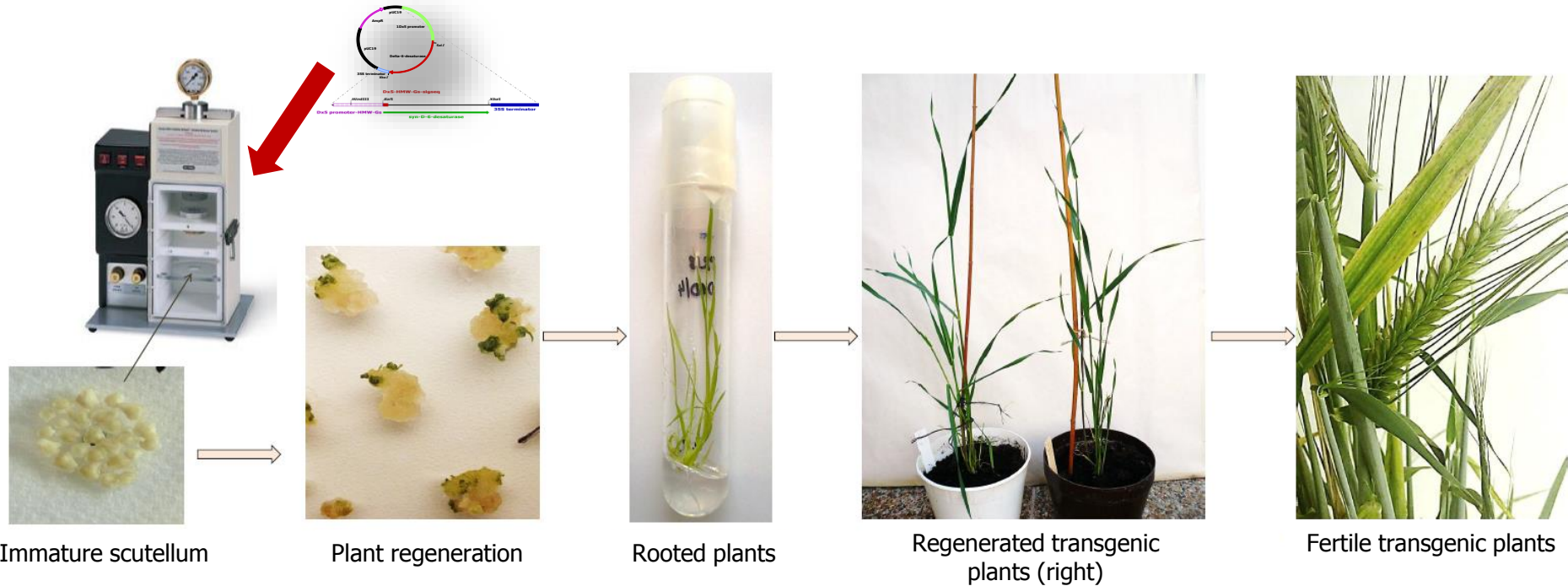
Barley improvement with PUFAs

Synthetic biology approach – artificial **gene synthesis** of **gene** – based on *T. elegans* (AY941161) sequence :



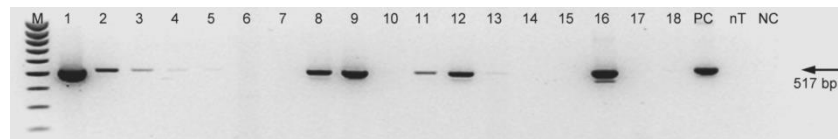
Barley improvement with PUFAs

- **D6D gene transfer** to barley:

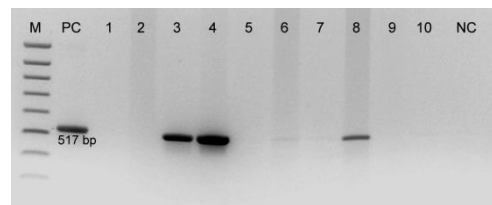


Barley nutritional quality **improvement**

- Presence and **transcription** of $\Delta 6D$ transgene in T_0 barleys
- **Expression** of GLA and SDA in **mature** barley **seeds**

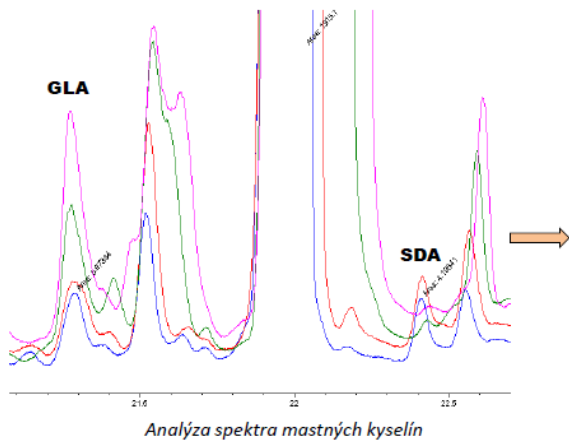


RNA

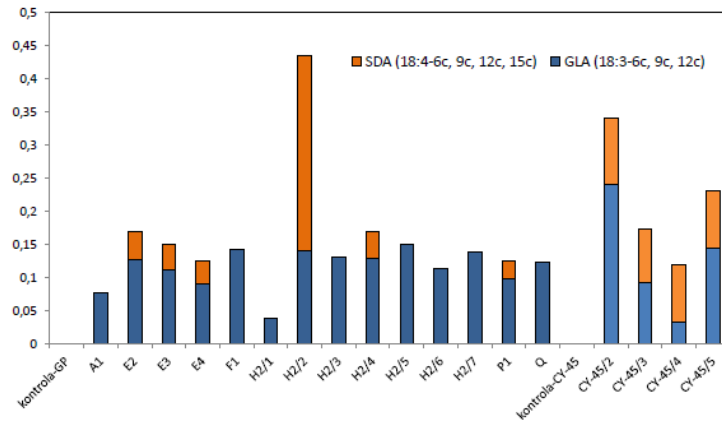


DNA

Fatty acids



Obsah polynenasátených mastných kyselín GLA a SDA v transgenných rastlinách jačmeňa siateho, genotyp Golden Promise (A1 – Q) a pšenice letnej, genotyp CY-45.

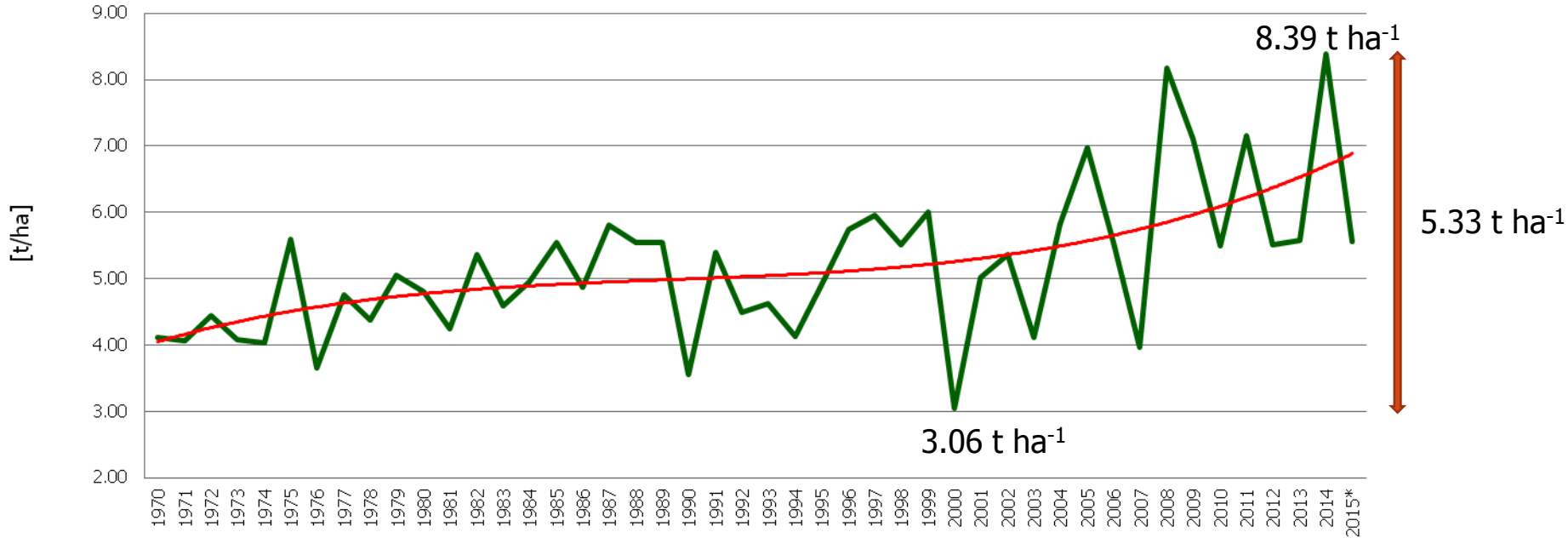


3. Gene transfer

GM plants for agriculture

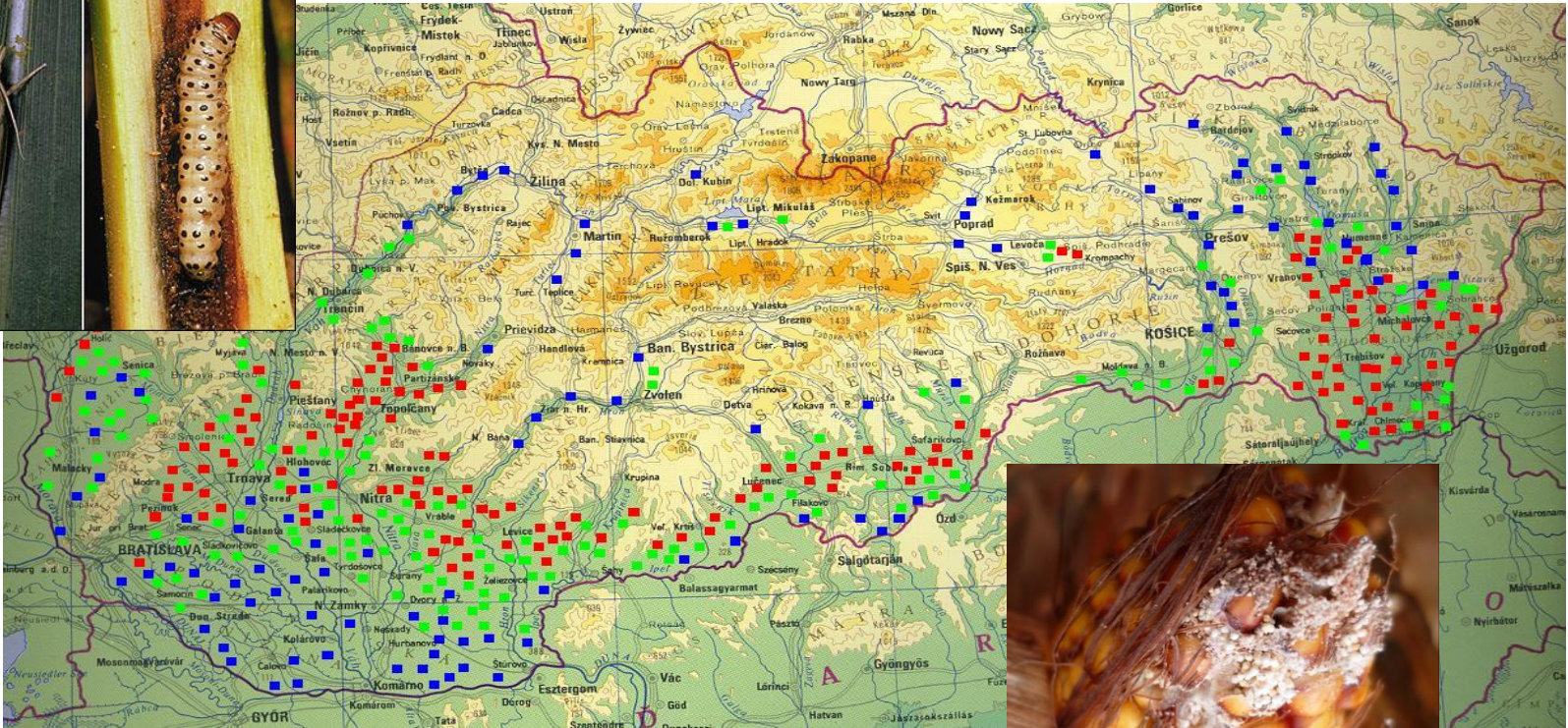
Long-term **trend** in **maize production** in Slovakia

- Average yield of grain maize in Slovakia 1970-2015*:



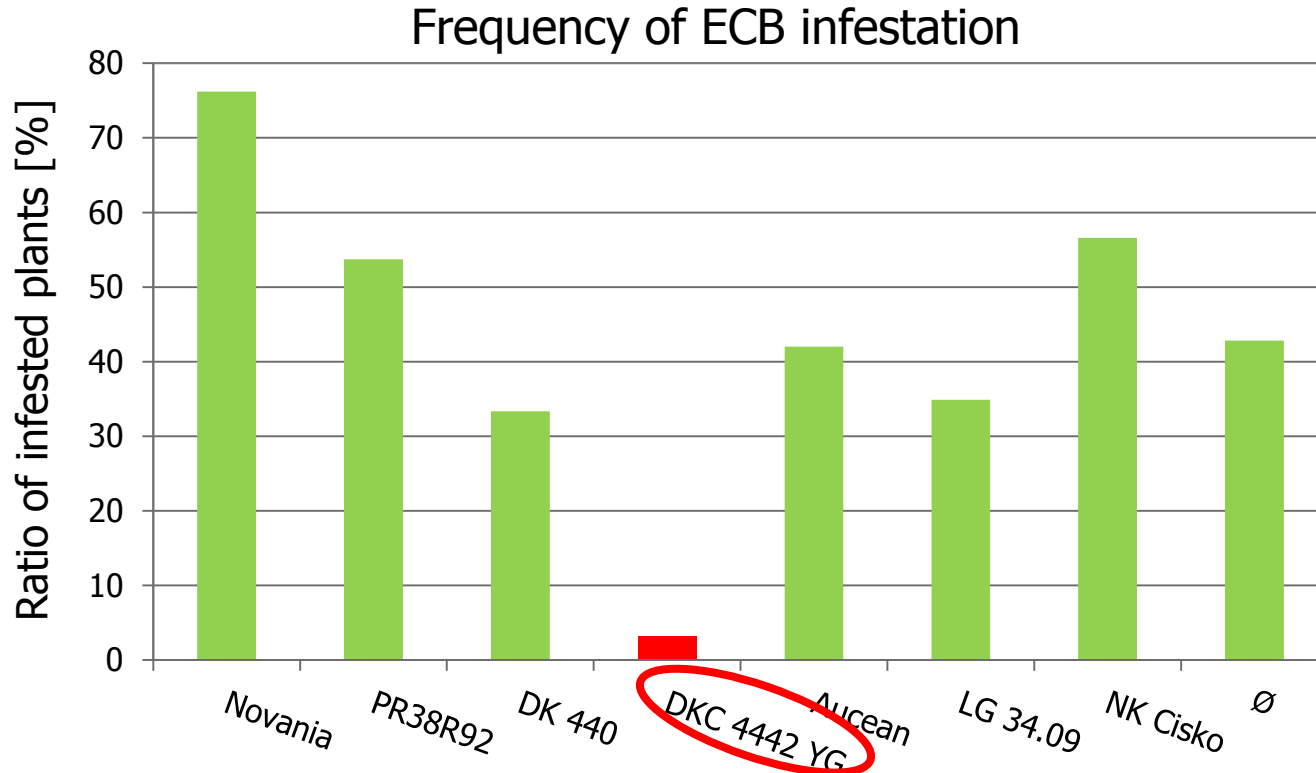
- Average yield (2000-2015): **5.80 t ha⁻¹**

Potention of ECB resistant GM maize in Slovakia

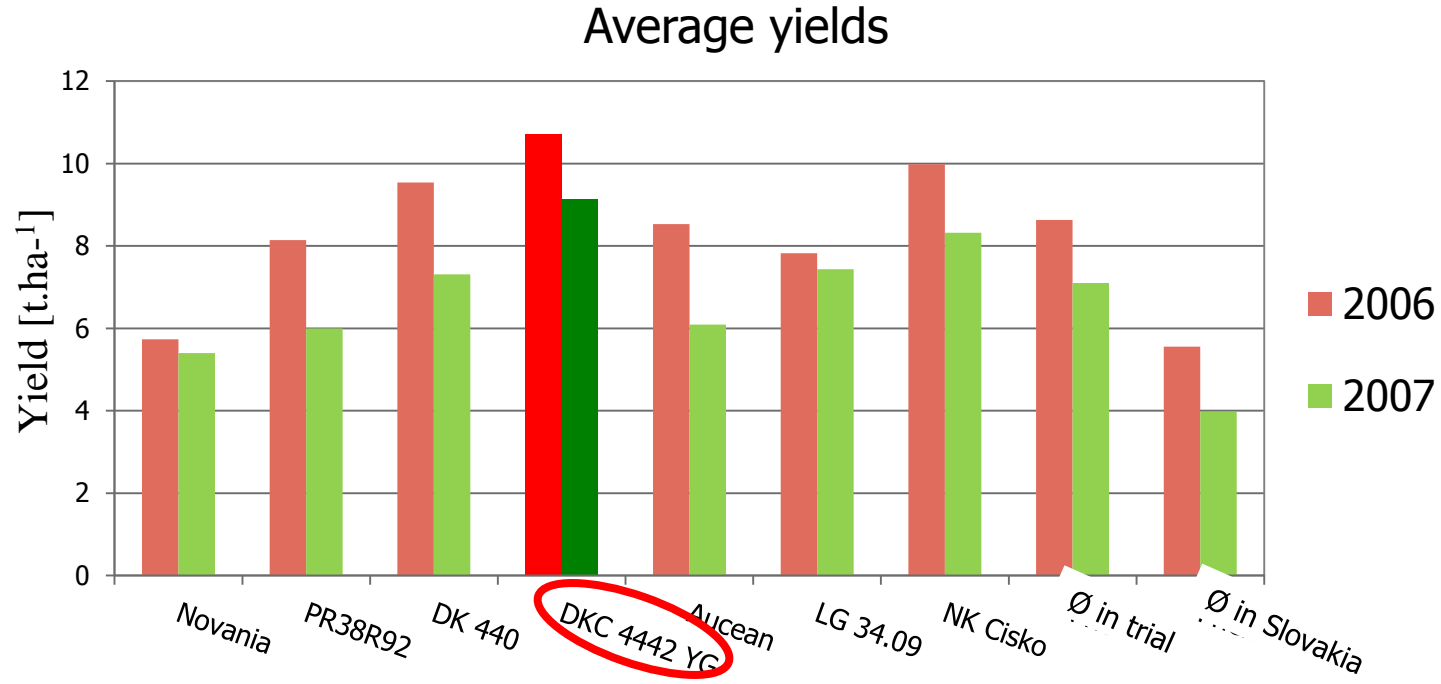


Maize plants damaged by ECB in Slovakia 1985-2006 (blue: 0-32 % green: 33-66 % red: 67-100 %)

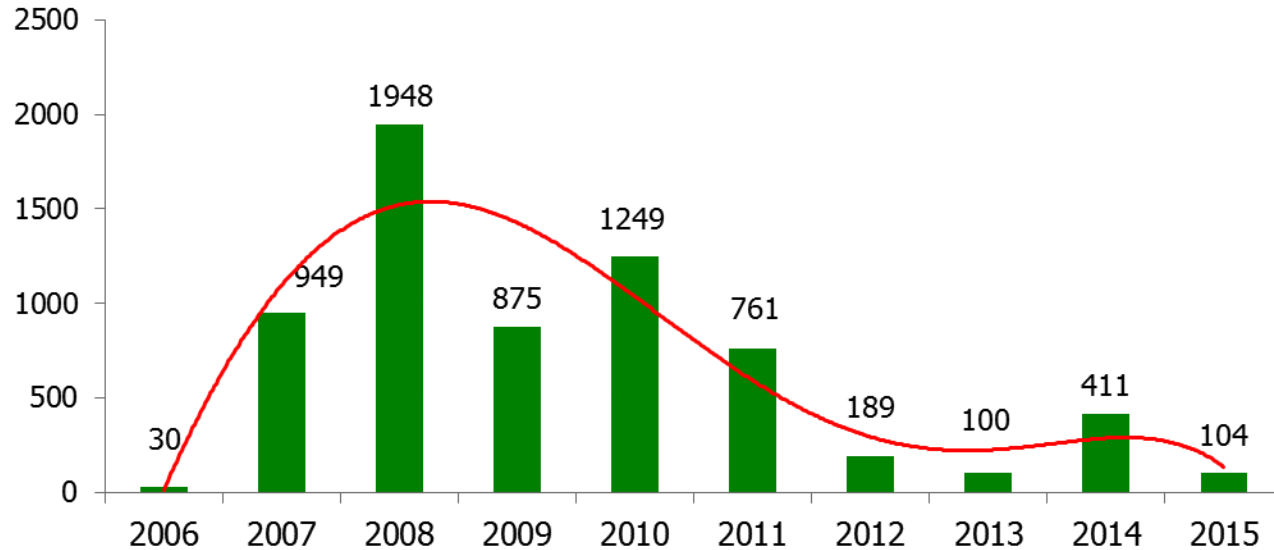
Resistance of ECB resistant MON 810 to in Slovakia



Benefit of **ECB resistant** MON 810 to in Slovakia in climatically different years (2006, 2007)



Story of MON 810 in Slovakia (2006-2015)



- Average (2008-2012) maize production: 1.15 mil tons
- **Overproduction** by $\approx 45\%$
- **Starch processing** (Amylum) – 350 000 tones (700 000 tones)
- **Bioethanol production** (Enviral) – 300 000 tones



Expected economical benefit of MON 810 growing in Slovakia

	E	F	D	CZ	P	PL	SK
Ø yield Bt vs. conventional maize (%)	+1-15 %	+5-24 %	+14-15 %	+9-10 %	+12 %	?	+10-14%
Ø impact on profitability (%)	+12	+16-21 %	+12-14 %	+15	+22	?	+8-18%
Impact on content of mycotoxins	Signif. decreas.	Signif. decreas.	Signif. decreas.	Signif. decreas.	?	Signif. decreas.	?

(Brookes, G.: The benefits of adopting genetically modified, insect resistant (Bt) maize in the European Union (EU): first results from 1998-2006 plantings)

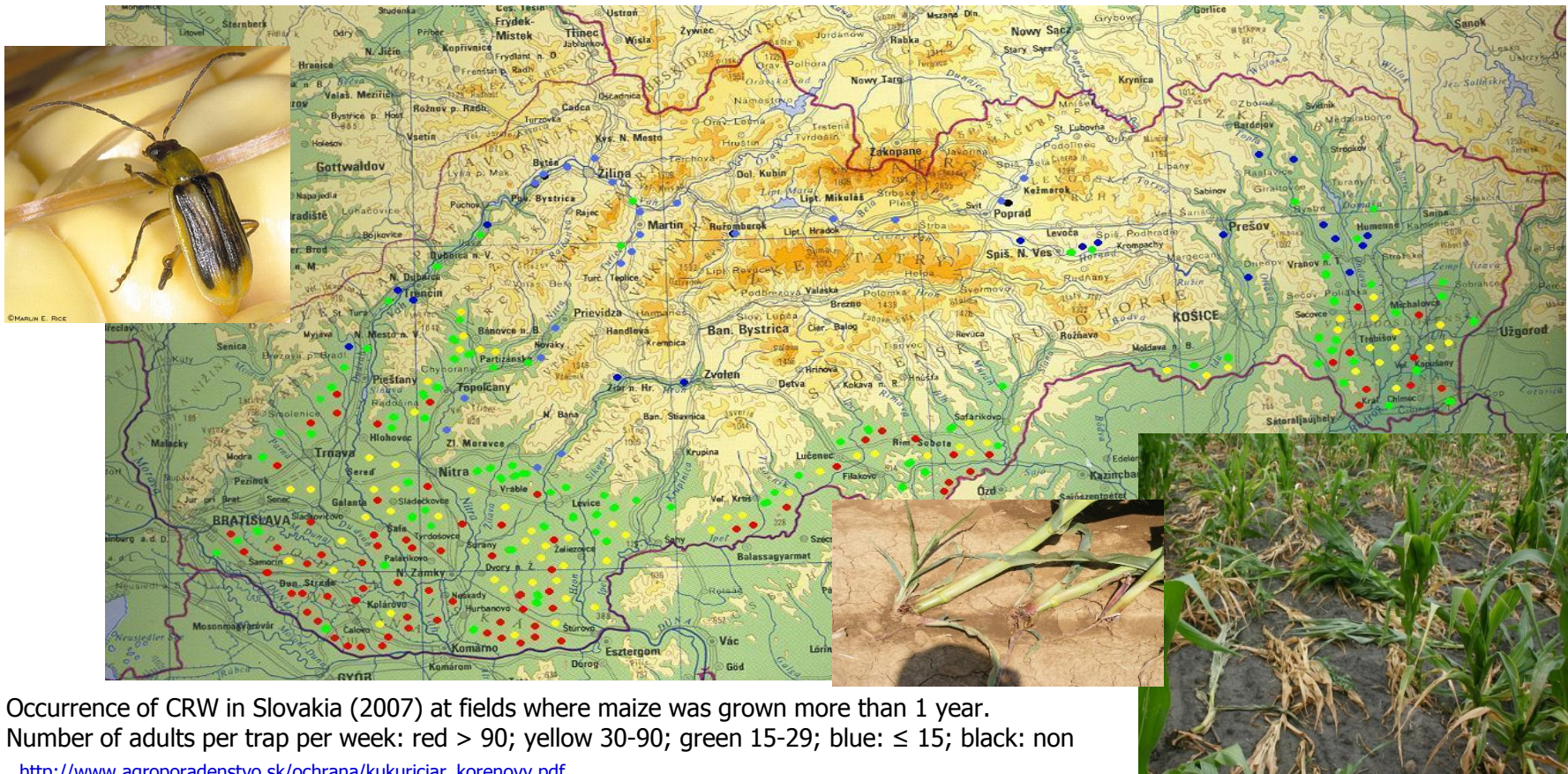
Observed economical benefit of MON 810 growing in Slovakia

Locality	Yield of control* [t/ha]	Yield of YieldGard® [t/ha]	Yield increasing [t/ha]	Yield increasing [%]	Income increasing [€/ha]
1	5,13	6,37	1,34	+24	+119.50
2	9,13	10,47	1,24	+14	+132.78
3	10,31	11,34	1,03	+10	+89.62

Mean: +16 % +113.97 €/ha

*control = isogenic hybrid without insecticide resistance

Potention of CRW resistant GM maize in Slovakia



Occurrence of CRW in Slovakia (2007) at fields where maize was grown more than 1 year.
Number of adults per trap per week: red > 90; yellow 30-90; green 15-29; blue: ≤ 15; black: non

http://www.agroporadenstvo.sk/ochrana/kukuriciar_korenovy.pdf

GM sugar-beet H7-1 in field trials in Slovakia



GM sugar-beet H7-1 in field trials in Slovakia

Conventional sugar-beet			
Herbicide	Application l/ha kg/ha %	Cost per l, kg (€)	Cost per ha (€)
T1 Goltix Top (l)	1.3	42.00	54.60
Kontakttwin (l)	1.8	22.63	40.73
T2 Mix double FL 2 (l)	1.0	32.08	32.08
Safari 50 WG (kg)	0.03	1386.32	41.59
0,05% Trend 90 (l)	0.1	9.60	0.96
Agil 100 EC (l)	0.5	44.16	22.08
T3 Betanal Expert (l)	1.0	51.50	51.50
Goltix Top (l)	0.5	42.00	21.00
Garland Forte (l)	0.8	44.19	35.35
Cost			299.90 €

Glyphosate resistant GM sugar-beet			
Herbicide	Application l/ha kg/ha %	Cost per l, kg (€)	Cost per ha (€)
Roundup Rapid (l)	2.4	11.58	27.79
Roundup Rapid (l)	2.4	11.58	27.79
Roundup Rapid (l)	2.4	11.58	27.79
Cost			83.37 €

Diference between conventional and GM sugar-beet (€/ha)

-216.52 €

Conclusions:

We are able to provide know-how for reciprocally profitable co-operation in topics:

- Breeding of new plant cultivars possessing novel and very specific traits
- Gene transfer technology for introduction of new traits into main cereals
- Long-term experiences in field testing of GM crops
- DNA profiling assays of plant genomes
- Development of protein and DNA-based diagnostic assays of plant pathogens