SUSVAR Winter Wheat Ringtest 2006-2008 over 36 environments in four countries :

Analysis of Genotype by Environment Interaction and Consequences for Direct and Indirect Selection Strategies

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„Low Input Research“

Participants in COST Action 860 – SUSVAR
(Sustainable low-input cereal production: required varietal characteristics and crop diversity)
decided to do a small ringtest – without project

Ideas behind:

* Exchange material for crosses – gain knowledge about it
* Compare Selection on Organic, Low Input and Conventional Environments
* Find broadly adapted stable genotypes for organic farming
* Learn more about broad or local adaptation
* Learn more about favourable selection traits for organic agriculture

COST 860 - SUSVAR Winter bread wheat ringtest 2006 – 2008 ● Trial sites

Trial sites 2006 - 2008

AUSTRIA			
Environment	**Location**	**ENV_ID**	**synthetic N**
AT_HI06	Probstdorf	1	130
AT_HI07	Probstdorf	2	130
AT_HI08	Probstdorf	3	130
AT_ORG06	Dörfles	4	0
AT_ORG07	Dörfles	5	0
AT_ORG08	Dörfles	6	0

SWITZERLAND			
Environment	**Location**	**ENV_ID**	**synth.N**
CH_HI06	Changins	7	180
CH_HI07	Changins	8	170
CH_LI06	Changins	9	100
CH_LI07	Changins	10	90
CH_NI06	Changins	11	0
CH_NI07	Changins	12	0

FRANCE			
Environment	**Location**	**ENV_ID**	**synth.N**
FR1_LI06	Rennes	14	40
FR1_LI08	Rennes	15	40
FR1_ORG06	Rennes	16	0
FR1_ORG07	Rennes	17	0
FR1_ORG08	Rennes	18	0
FR2_LI06	Le Moulon	19	100
FR2_LI07	Le Moulon	20	100
FR2_ORG06	Le Moulon	21	0
FR2_ORG07	Le Moulon	22	0
FR3_LI06	Lusignan	23	90
FR3_LI07	Lusignan	24	150
FR3_ORG06	Lusignan	25	0
FR3_ORG07	Lusignan	26	0

ROMANIA			
Environment	**Location**	**ENV_ID**	**synth.N**
RO_HI06	Fundulea	27	100
RO_HIIrr07	Fundulea	28	100
RO_HI07	Fundulea	29	100
RO_HI08	Fundulea	30	100
RO_LI06	Fundulea	31	0
RO_LIIrr07	Fundulea	32	0
RO_LI07	Fundulea	33	0
RO_LI08	Fundulea	34	0
RO_ORG06	Fundulea	35	0
RO_ORG07	Fundulea	36	0
RO_ORG08	Fundulea	37	0

ORG	NI - Zero org N	LI < 100kg N	HI > 100kg N
NO		**NS**	

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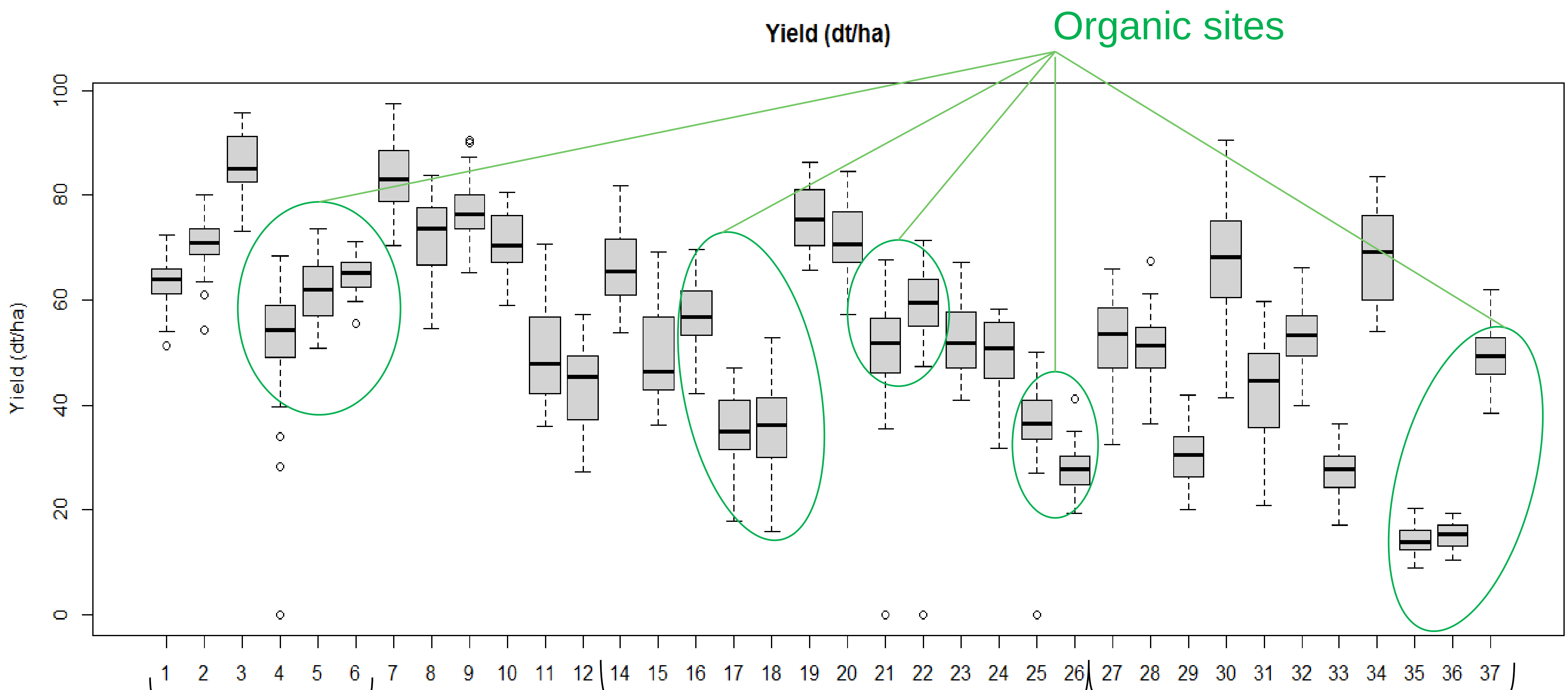
Genotypes COST 860 - SUSVAR ring test 2006 - 2008

	Genotype	origin: 3xAT, 3xCH, 2xDE, 3xFR, 3xRO
AR	ARDEAL	RO
AU	AUROLUS	AT
BI	BITOP	AT
CF	CF99102 = SKERZZO	FR
CO	CORNELIUS	AT
DI	DI9714	FR
FO	FORMAT	DE
JU	JUNONA	RO
JU	JUPITER	RO
NA	NATURASTAR	DE
RE	RENAN	FR
SI	SIALA	CH
TI	TITLIS	CH
ZI	ZINAL	CH

Yield dt/ha COST 860 - SUSVAR ring test 2006 - 2008



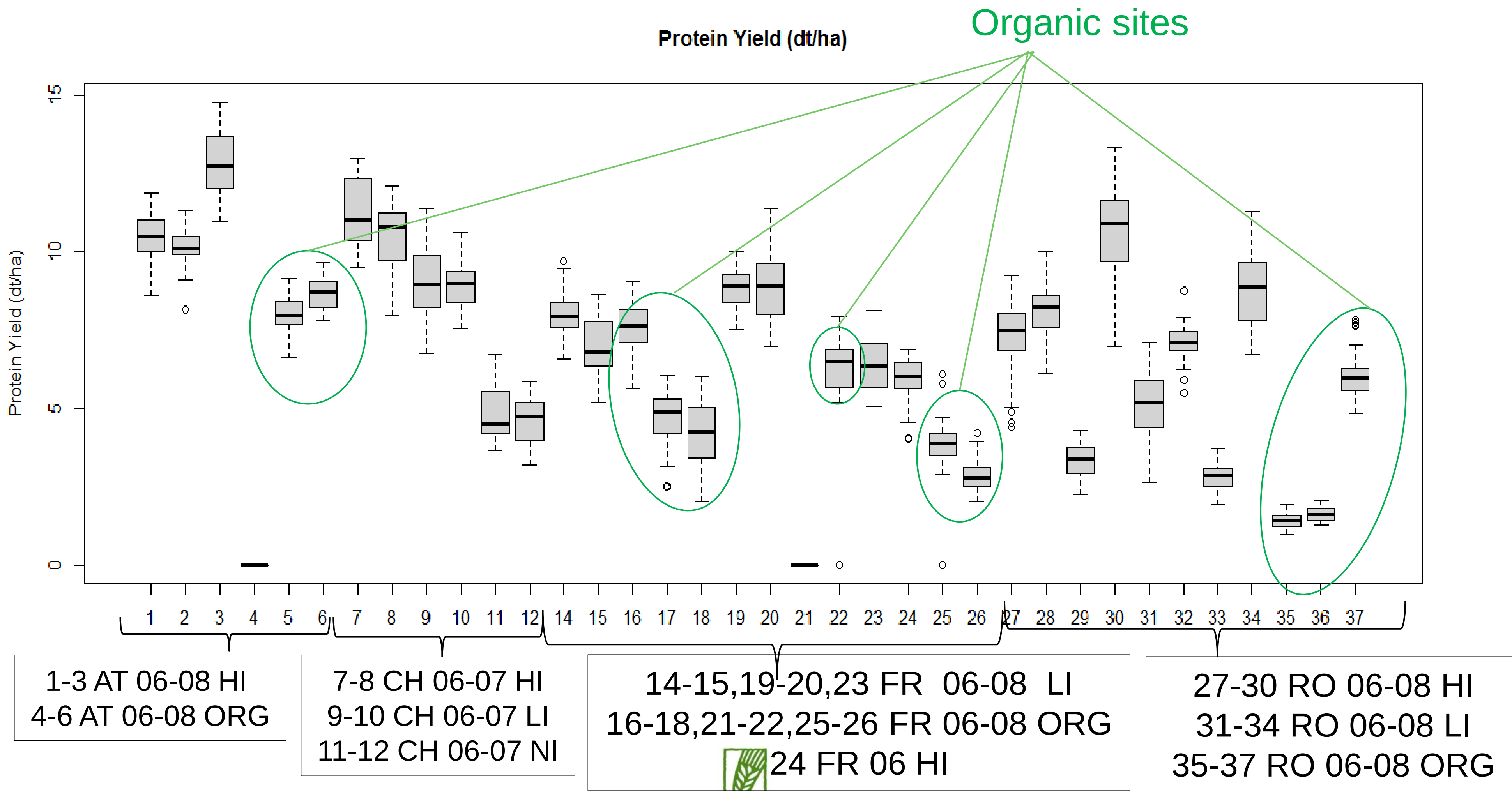
1-3 AT 06-08 HI
4-6 AT 06-08 ORG

7-8 CH 06-07 HI
9-10 CH 06-07 LI
11-12 CH 06-07 NI

14-15,19-20,23 FR 06-08 LI
16-18,21-22,25-26 FR 06-08 ORG
24 FR 06 HI

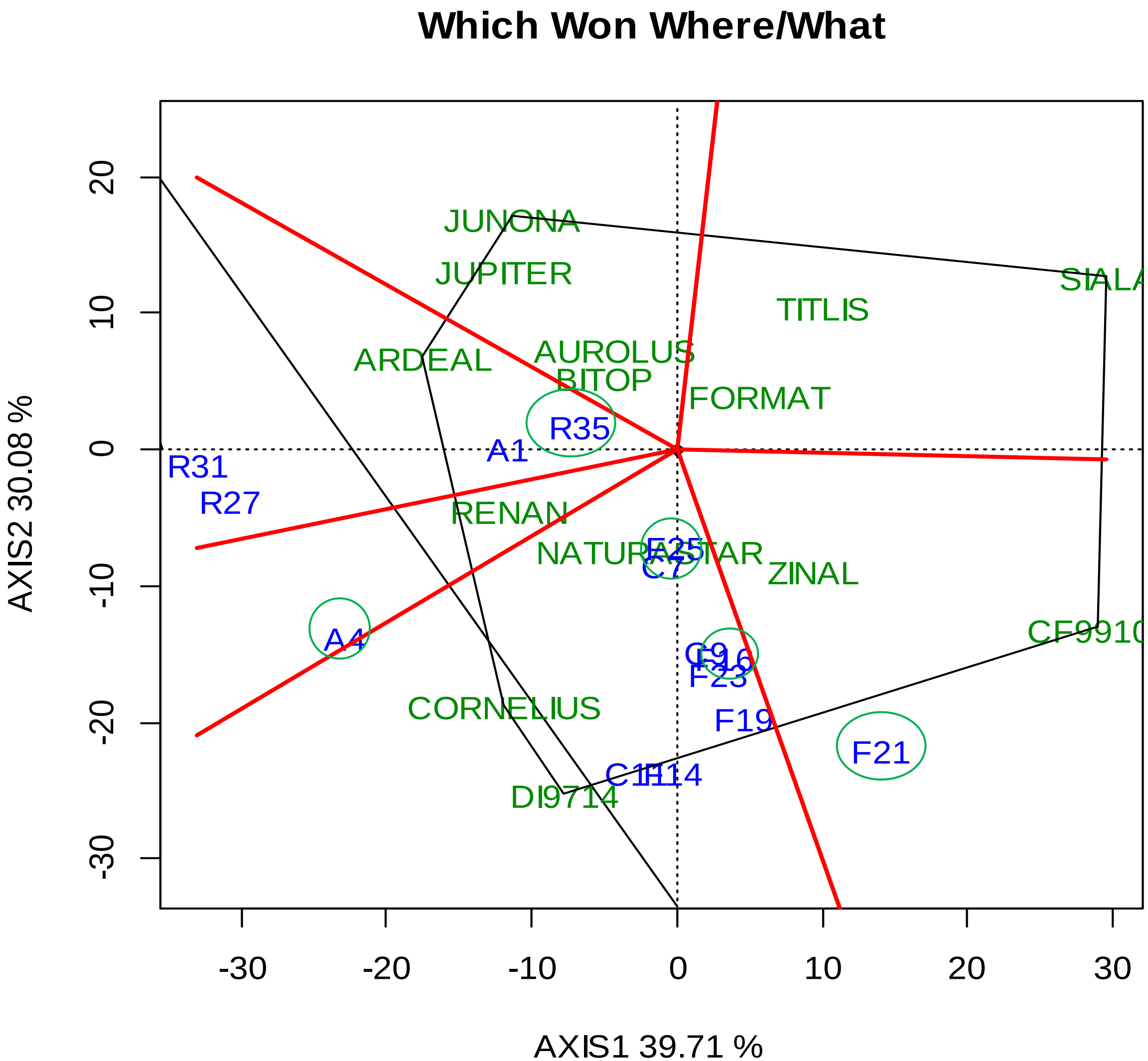
27-30 RO 06-08 HI
31-34 RO 06-08 LI
35-37 RO 06-08 ORG

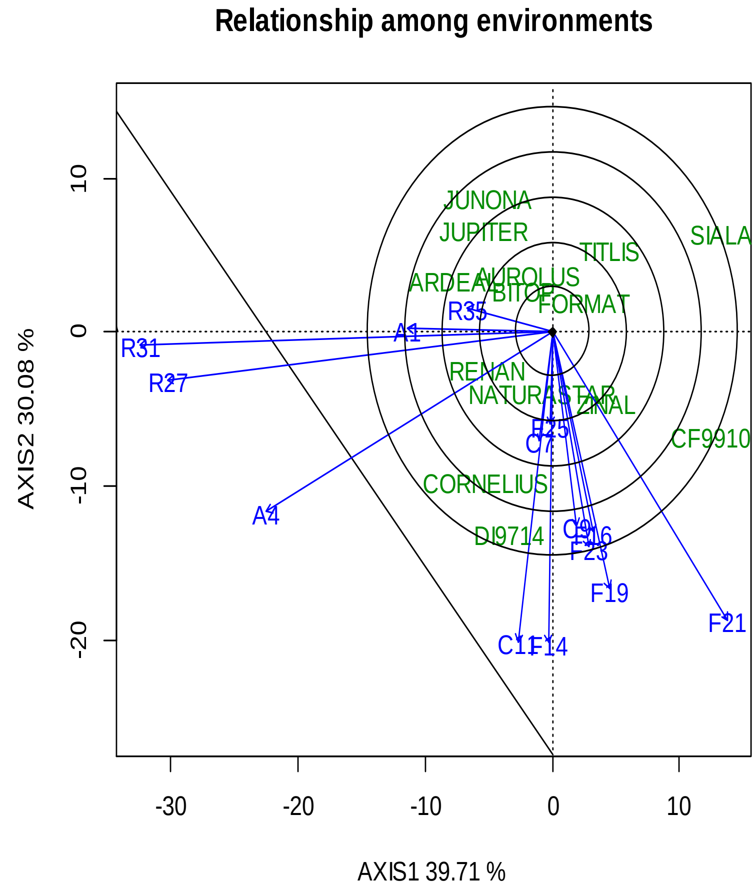
Genotypes COST 860 - SUSVAR ring test 2006 - 2008



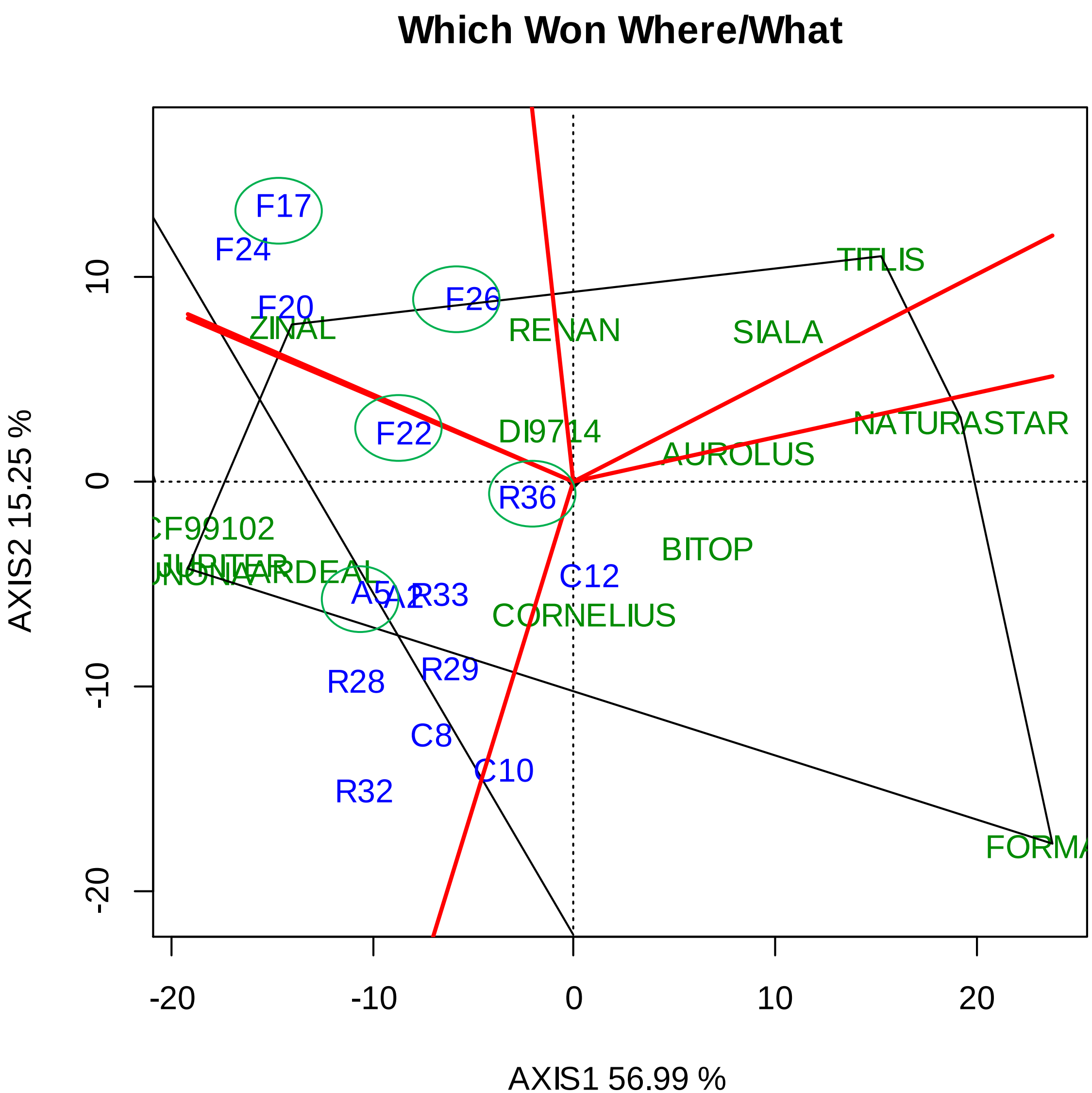
Environment - ID

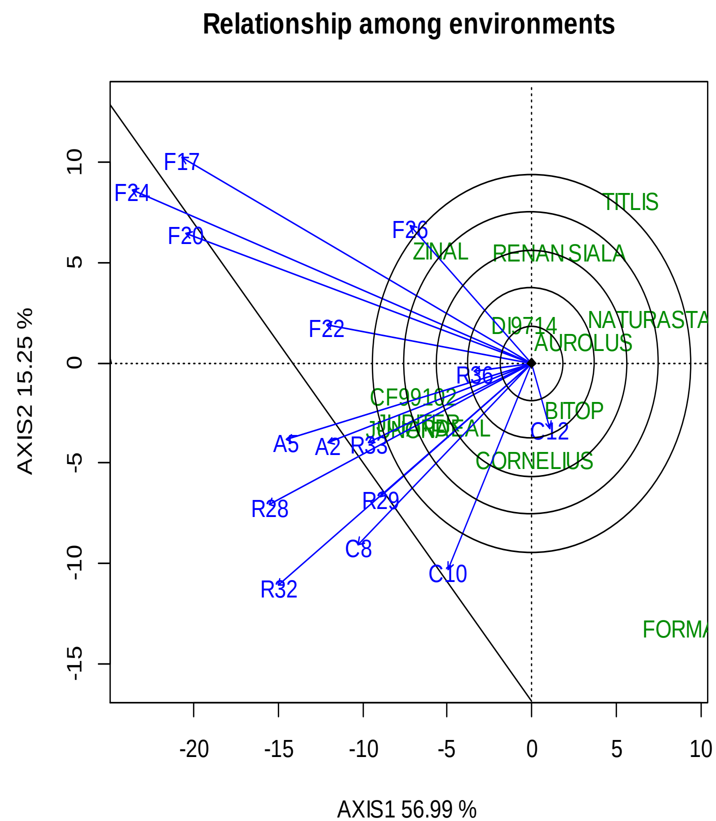
Trial sites – Genotypes 2006



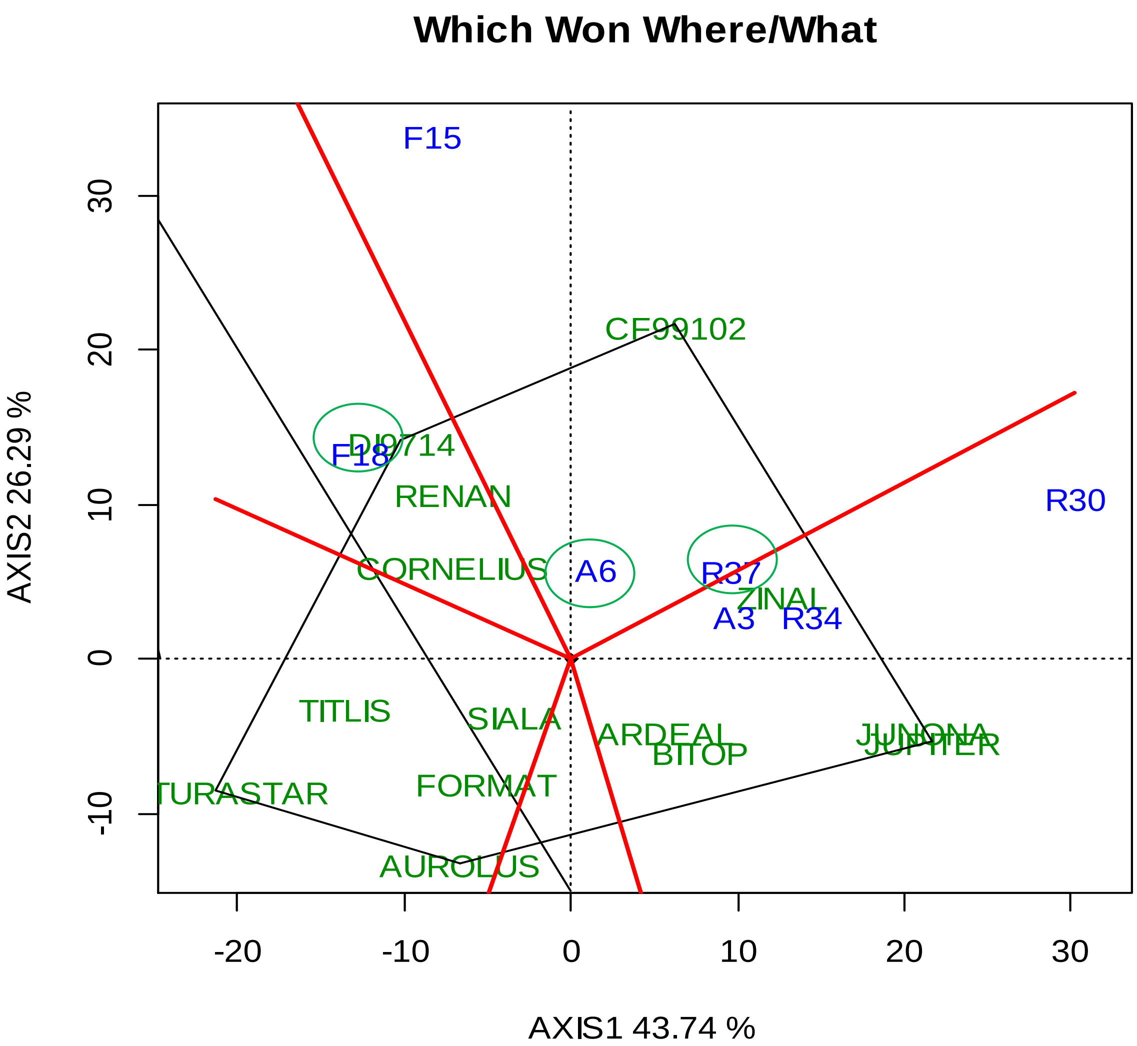


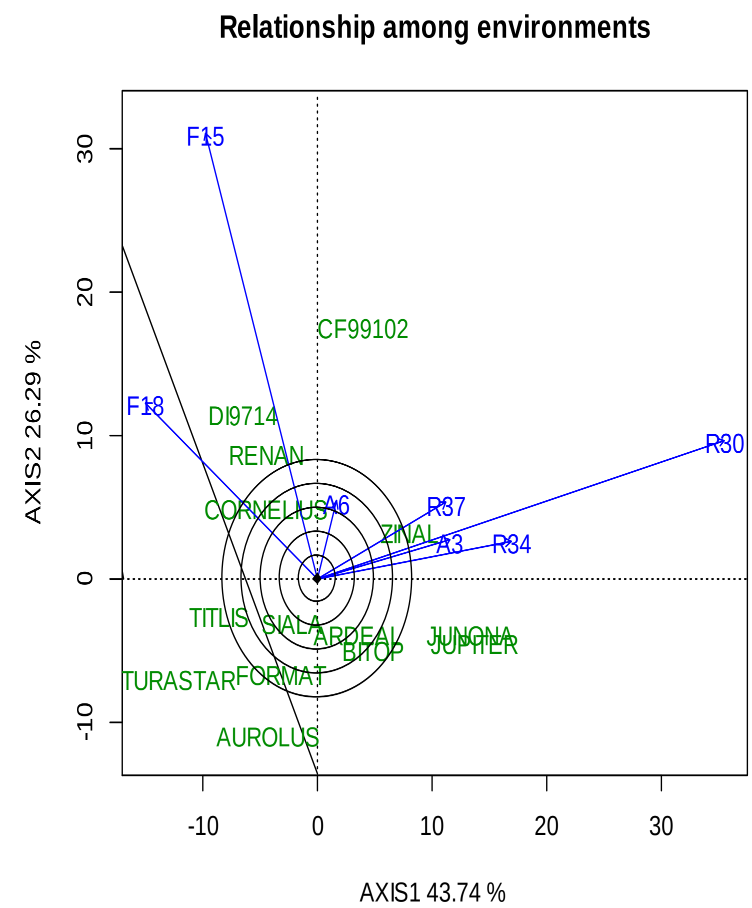
GGE Biplots for Trial sites – Genotypes 2007





Trial sites – Genotypes 2008





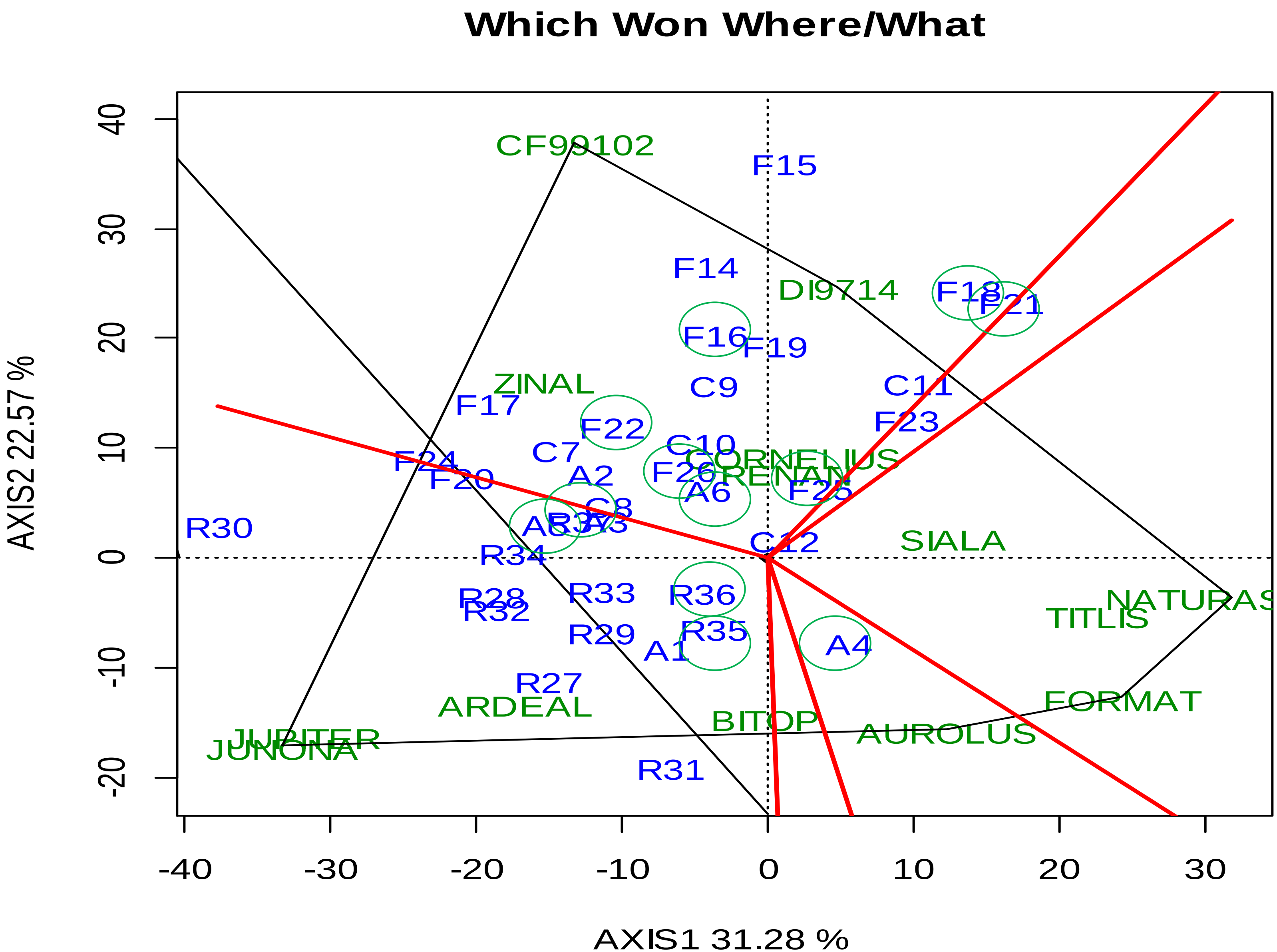
36 Environments 1420 – 8666 kg/ha organic – low input – untreated „high input“

- Countries make more difference

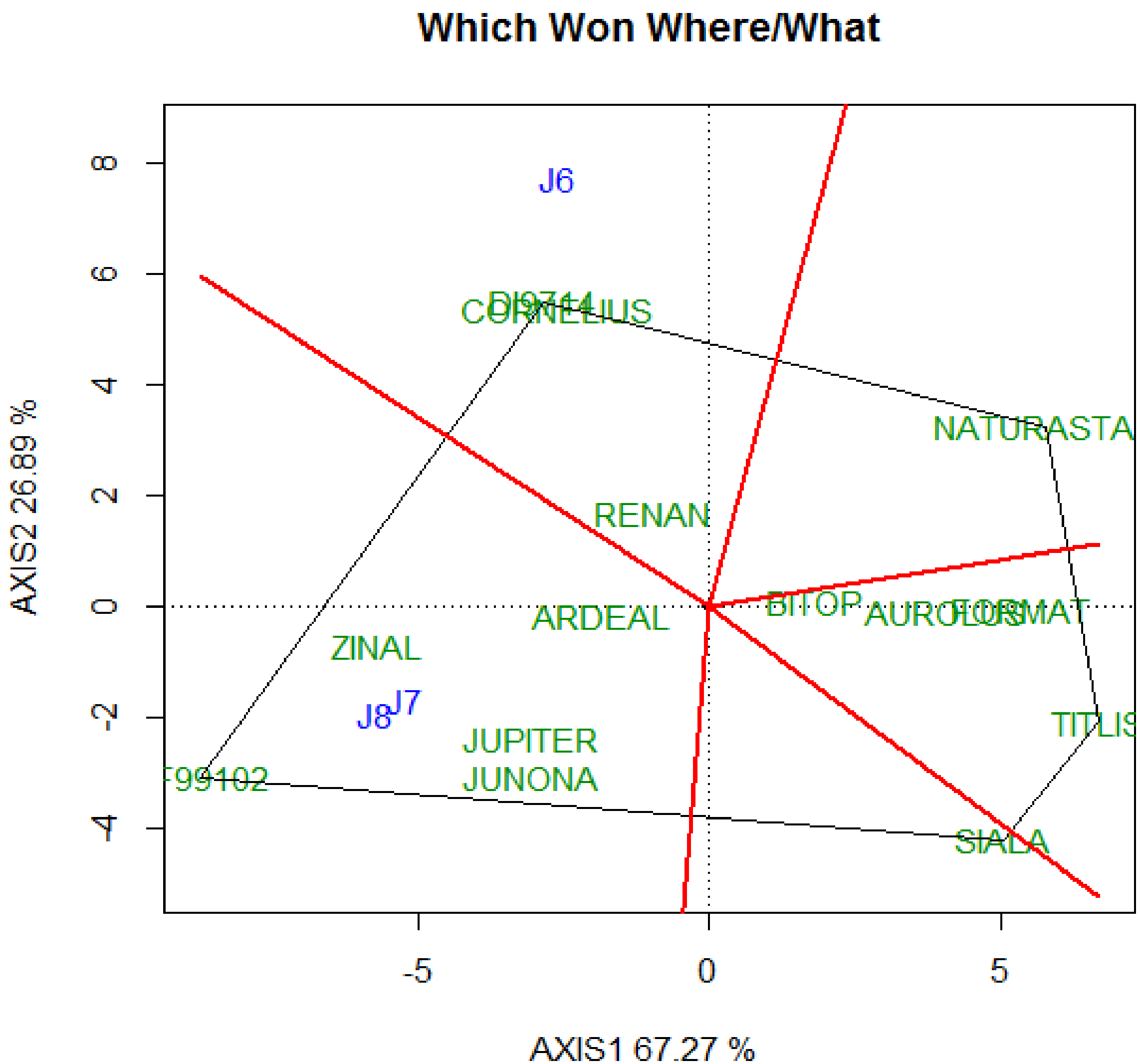
  than the systems organic or conventional
- Romania and Austrian results go together

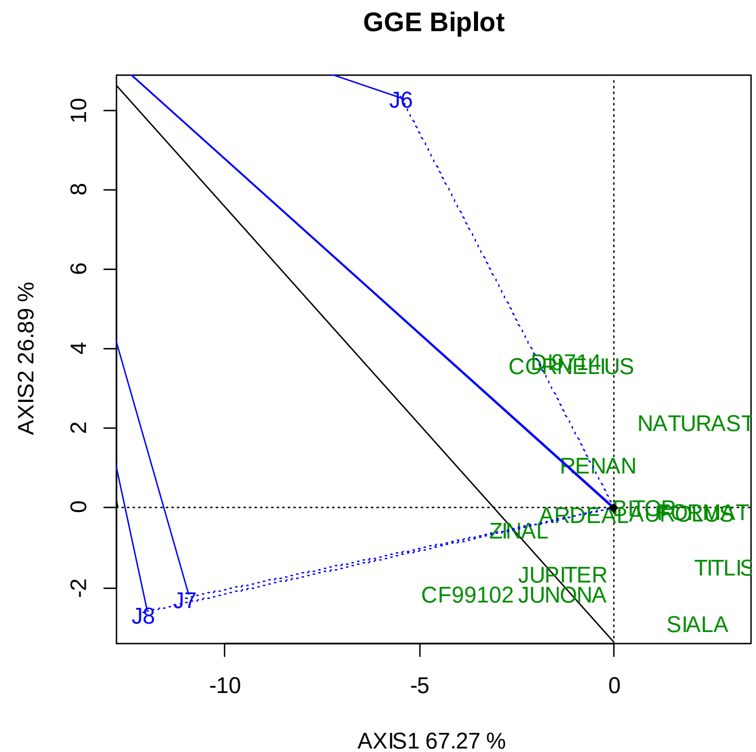
  → 1 „Mega-Environment“
- France is different
- Switzerland – 2006 with France, 2007 with AT+RO

Trial sites – Genotypes 2006-2008

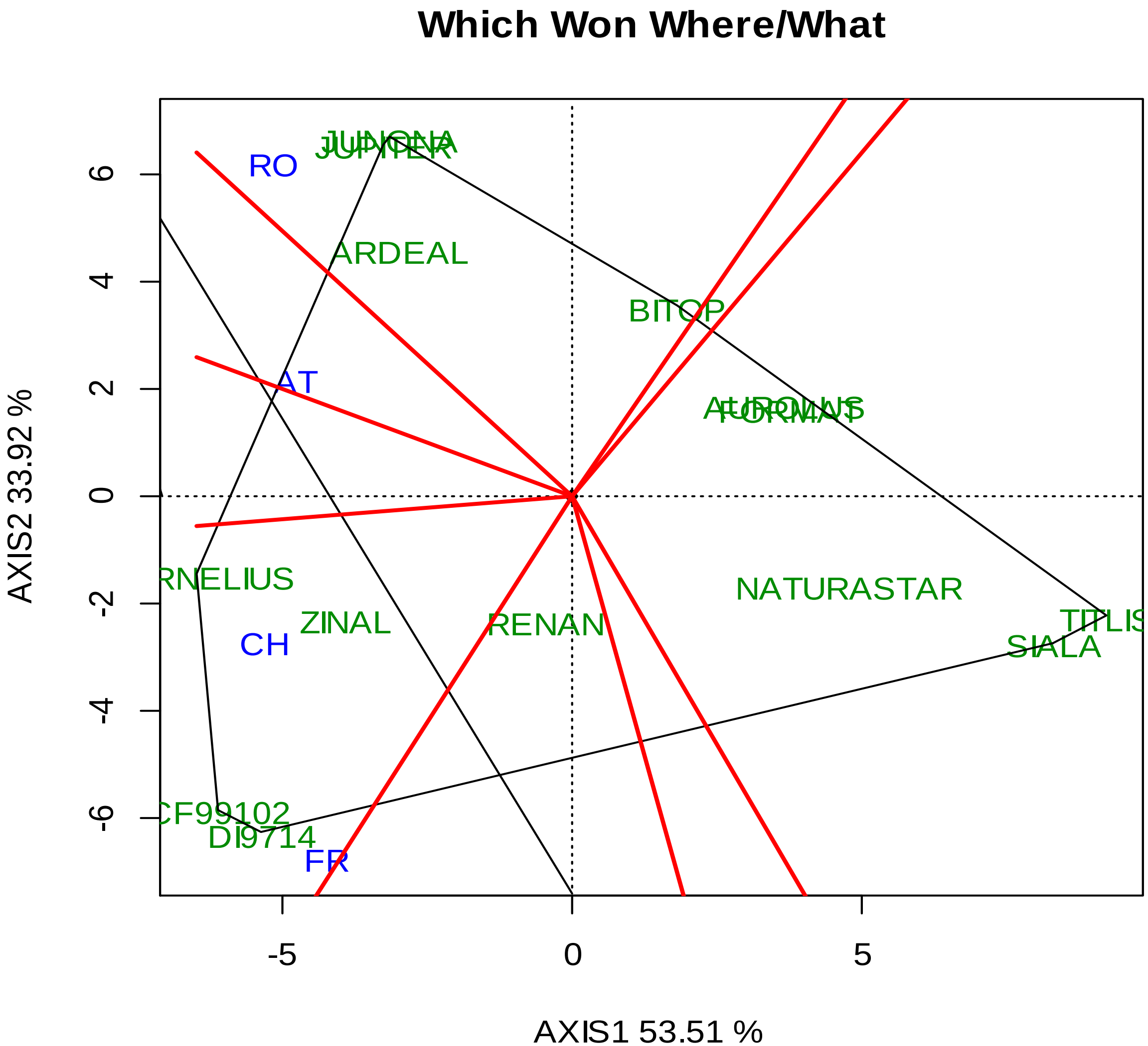


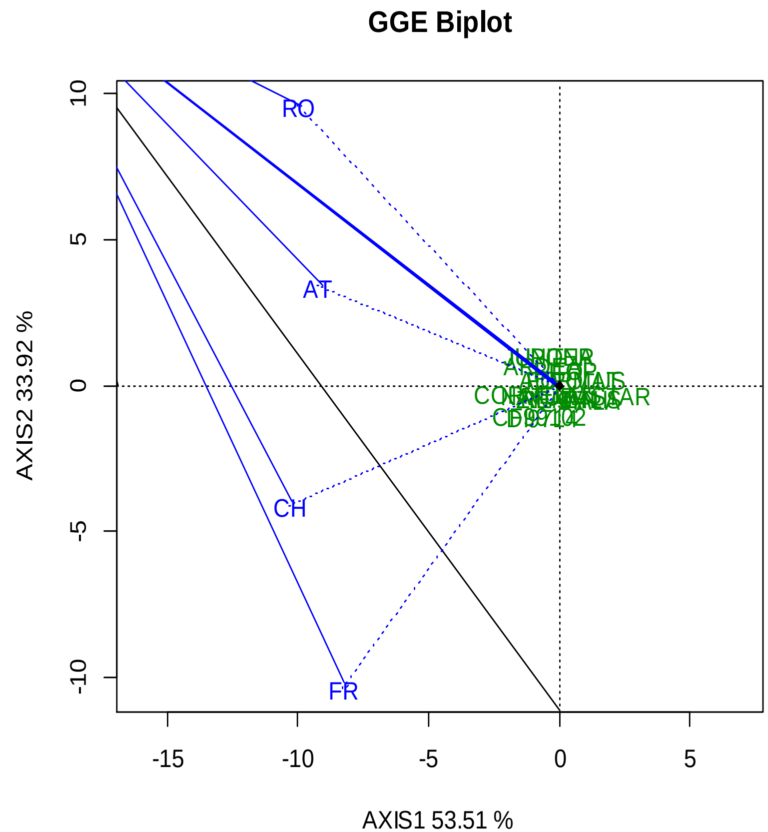
Varieties and Years 2006 - 2008





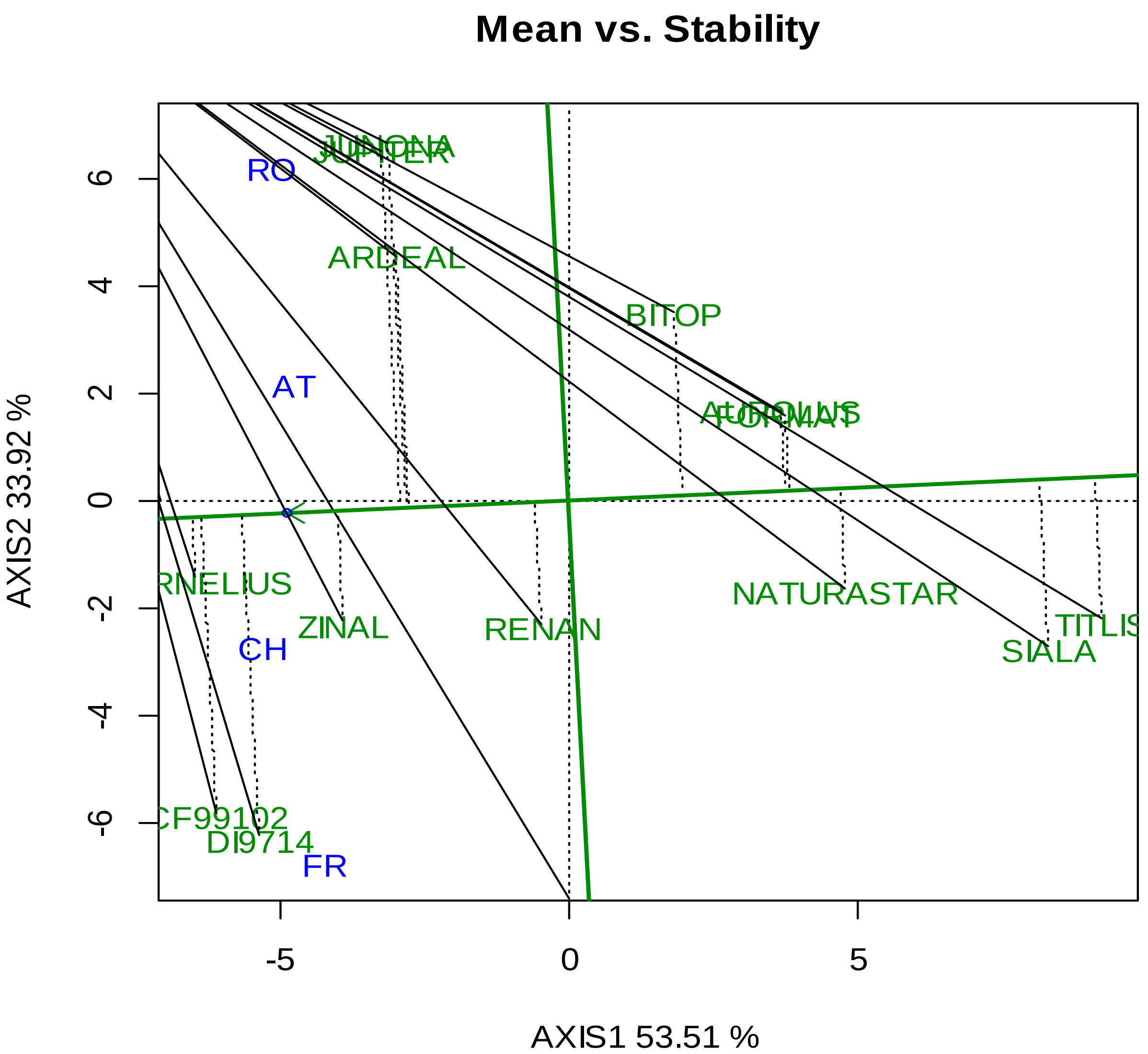
Genotypes and Countries 2006 - 2008





left: row metric=genotypes; right: column metric=countries

Yield stability - Genotypes 2006 - 2008



Traits COST 860 – SUSVAR - Ringtest 2006 - 2008

	CODE	n	Explanation	Scoring information
YL	**DTHA**	**36**	**Yield**	**dt/ha**
PR	**PROT %**	**34**	**Protein content DM**	**%**
PY	**P_DTHA**	**34**	**Protein yield**	**dt/ha**
HL	HLG	33	Hectolitre weight	kg
TK	TKG	14	Thousand kernel weight	g
NW	NWNT	10	Stand after winter	1 (good) - 9
DT	DTAE orig	30	Heading date	Days from May 1st
WH1	WHO 1	7	Plant height	Plant height EC31-32
WH	WHO	33	Plant height	Plant height final cm
LA	LAG	24	Lodging susceptibility	1-9 (susceptible)
RE	REIFE	3	Ripening	1 (early) - 9
ME	MEHL	16	Powdery mildew	1-9 (susceptible)
GR	GROST	12	Yellow rust	1-9 (susceptible)
BR	BROST	19	Leaf rust	1-9 (susceptible)
SE	SEPB	13	Leaf Septoria (nodorum)	1-9 (susceptible)
B32	BBED_32	12	Soil coverage at EC 32	%
	BBED_49	6	Soil coverage at EC 49	%
	BBED_55	6	Soil coverage at EC 55	%
	BBED _71	3	Soil coverage at EC 71	%
	BBED _75	3	Soil coverage at EC 75	%

	CODE	n	Explanation	Scoring information
VA	**VIGOR**	**4**	**Early vigor**	**1-9(low vigor))**
	WUFO_29	**2**	**Plant growth habit**	**1-9(totally prostrate)**
BL32	**BLHA_32-35**	**10**	**Leaf inclination**	**1-9(flag leaf curved)**
	BLAHA_37	3	Leaf inclination	1-9(flag leaf totally curved)
	BLAHA_49	4	Leaf inclination	1-9(flag leaf totally curved)
	BLAHA_72	3	Leaf inclination	1-9(flag leaf totally curved)
	BETF	4	Tillering	Number of tillers per plant
ÄH	ÄHNR	11	Heads per m2	number
	FUS	4	Fusarium head blight	1-9(susceptible)
	DICHTE_26	4	Plant density	1-9(very dense stand)
	VERUNKRAUT	5	Weed in the plot	1-9(strong weed)
	LAI 45	**4**	**Leaf Area Index**	**Leaf Area Index**
	FARBE	6	Plant Colour	1=green, 5=yellow

Traits in GGE- Biplots: yellow: n>7; n for N and N0 > 3

traits with only 1 score/location combination are not shown

33 traits shown

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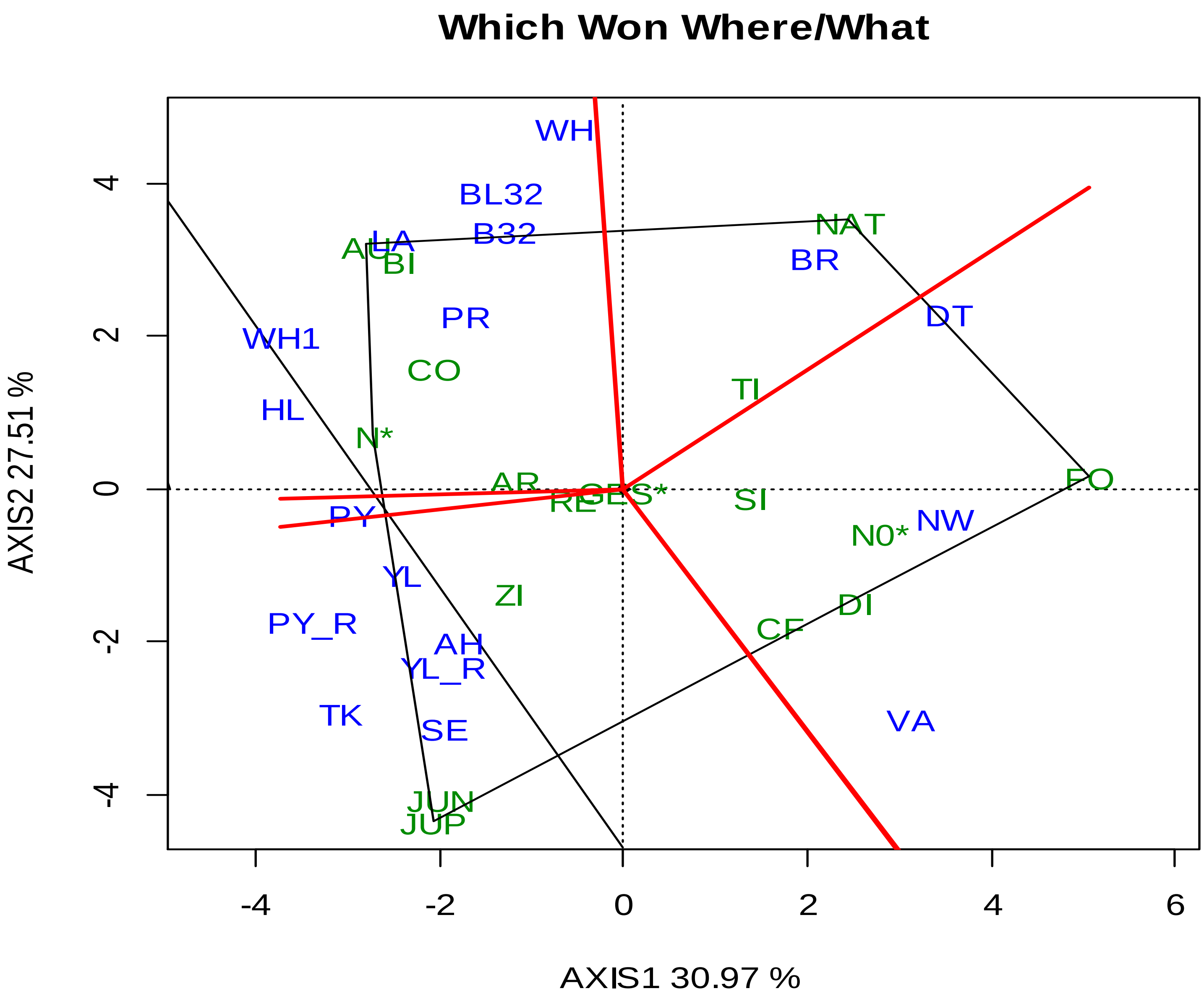
Genotypes and Traits 2006 - 2008



Ringtest 2006 – 2008: Phenotypic Correlations – heading date, plant height, resistance traits -YLD

n= 14 genotypes

	Grain Yield			Protein Content			Protein Yield		
	DTHA_N	DTHA_N0	DTHA_Ges	PROT%_N	PROT%_N0	PROT%_Ges	P_DTHA_N	P_DTHA_N0	P_DTHA_Ges
DTAE_N	-0,49	-0,37	-0,46	0,03	0,22	0,11	-0,81	-0,66	-0,79
DTAE_N0	-0,54	-0,42	-0,52	0,07	0,28	0,16	-0,84	-0,69	-0,82
DTAE_Ges	-0,51	-0,39	-0,49	0,05	0,25	0,13	-0,83	-0,68	-0,80
WHO_N	-0,60	-0,06	-0,40	0,52	0,38	0,48	-0,44	-0,02	-0,29
WHO_N0	-0,65	-0,12	-0,46	0,61	0,46	0,57	-0,44	-0,02	-0,28
WHO_Ges	-0,63	-0,09	-0,43	0,56	0,41	0,52	-0,44	-0,02	-0,28
BROST_N	-0,52	-0,46	-0,52	0,18	0,36	0,26	-0,67	-0,64	-0,69
BROST_N0	-0,55	-0,52	-0,57	0,25	0,47	0,34	-0,65	-0,63	-0,67
BROST_Ges	-0,54	-0,50	-0,55	0,22	0,42	0,31	-0,67	-0,64	-0,69
MEHL_N	-0,07	0,18	0,03	0,03	0,16	0,08	-0,12	0,17	0,00
MEHL_N0	-0,16	0,01	-0,10	0,02	0,18	0,08	-0,29	-0,09	-0,22
MEHL_Ges	-0,11	0,09	-0,03	0,02	0,18	0,09	-0,21	0,04	-0,11
GROST_N	0,10	0,19	0,14	0,00	-0,16	-0,07	0,18	0,20	0,20
GROST_N0	-0,08	0,06	-0,03	0,24	0,01	0,16	0,16	0,18	0,18
GROST_Ges	0,02	0,14	0,07	0,10	-0,09	0,03	0,18	0,20	0,20
FUS_N	0,62	0,36	0,54	-0,29	-0,46	-0,36	0,74	0,38	0,62
FUS_N0	0,52	0,42	0,51	-0,44	-0,52	-0,49	0,40	0,21	0,34
FUS_Ges	0,63	0,41	0,57	-0,37	-0,52	-0,44	0,67	0,35	0,56

Ringtest 2006 – 2008: Phenotypic Correlations –“organic traits“ -YLD

n= 14 genotypes

	Grain Yield			Protein Content			Protein Yield		
	DTHA_N	DTHA_N0	DTHA_Ges	PROT%_N	PROT%_N0	PROT%_Ges	P_DTHA_N	P_DTHA_N0	P_DTHA_Ges
BED49_N	0,26	0,53	0,39	-0,15	-0,20	-0,18	0,29	0,51	0,40
BED49_N0	0,17	0,51	0,32	-0,05	-0,16	-0,10	0,23	0,53	0,37
BED49_Ges	0,24	0,54	0,38	-0,12	-0,19	-0,15	0,27	0,53	0,40
BED71_N	0,50	0,63	0,58	-0,30	-0,34	-0,32	0,53	0,62	0,59
BED71_N0	0,39	0,49	0,46	-0,13	-0,20	-0,16	0,53	0,60	0,59
BED71_Ges	0,48	0,60	0,56	-0,26	-0,31	-0,29	0,54	0,62	0,60
WUFO_N	-0,36	-0,12	-0,28	-0,01	0,20	0,07	-0,62	-0,40	-0,56
WUFO_N0	-0,23	0,10	-0,10	-0,03	0,07	0,01	-0,44	-0,15	-0,34
WUFO_Ges	-0,29	0,00	-0,18	-0,02	0,13	0,04	-0,53	-0,26	-0,44
BLH49_N	0,41	0,58	0,50	-0,30	-0,38	-0,34	0,38	0,59	0,49
BLH49_N0	0,46	0,62	0,55	-0,31	-0,37	-0,34	0,45	0,62	0,54
BLH49_Ges	0,44	0,61	0,53	-0,31	-0,38	-0,35	0,42	0,61	0,52
BLH72_N	-0,03	0,39	0,15	-0,08	-0,04	-0,07	-0,21	0,24	-0,03
BLH72_N0	0,19	0,47	0,32	-0,10	-0,06	-0,08	0,13	0,36	0,23
BLH72_Ges	0,05	0,44	0,21	-0,09	-0,05	-0,08	-0,11	0,29	0,06

BED (EC stage) = soil coverage;
WUFO= plant growht habit

BLH (EC) = leaf inclinatiion;

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2006 – 2008 – high correlations among „traits for organic“

	BETF_N	BETF_N0	BETF_Ges	WHO_N	WHO_N0	WHO_Ges	LAI_N	LAI_N0	LAI_Ges
BED32_N	0,61	0,62	0,63	0,51	0,49	0,50	0,43	0,75	0,64
BED32_N0	0,81	0,88	0,87	0,60	0,58	0,59	0,62	0,90	0,82
BED32_Ges	0,80	0,86	0,85	0,60	0,58	0,59	0,60	0,90	0,81
BED49_N	0,57	0,73	0,68	0,31	0,28	0,30	0,63	0,65	0,70
BED49_N0	0,53	0,69	0,64	0,38	0,38	0,38	0,68	0,74	0,77
BED49_Ges	0,57	0,74	0,69	0,35	0,32	0,34	0,67	0,70	0,75
BED55_N	0,69	0,67	0,69	0,53	0,46	0,50	0,05	0,54	0,31
BED55_N0	0,62	0,77	0,73	0,45	0,46	0,45	0,70	0,75	0,80
BED55_Ges	0,69	0,82	0,79	0,50	0,50	0,50	0,64	0,78	0,78
BED71_N	0,40	0,54	0,50	-0,07	-0,08	-0,07	0,39	0,45	0,46
BED71_N0	0,34	0,52	0,47	-0,09	-0,08	-0,09	0,45	0,41	0,48
BED71_Ges	0,39	0,55	0,50	-0,07	-0,08	-0,08	0,41	0,44	0,47
BED75_N	0,56	0,61	0,60	0,34	0,31	0,33	0,65	0,51	0,64
BED75_N0	0,52	0,56	0,55	0,34	0,34	0,34	0,80	0,68	0,82
BED75_Ges	0,58	0,63	0,63	0,37	0,35	0,36	0,78	0,64	0,79
WUFO_N	0,81	0,69	0,75	0,49	0,48	0,49	0,33	0,72	0,56
WUFO_N0	0,88	0,83	0,86	0,60	0,57	0,59	0,39	0,83	0,66
WUFO_Ges	0,87	0,79	0,83	0,56	0,54	0,56	0,37	0,80	0,63

cont.	BETF_N	BETF_N0	BETF_Ges	WHO_N	WHO_N0	WHO_Ges	LAI_N	LAI_N0	LAI_Ges
BLH32_N	0,63	0,77	0,73	0,70	0,70	0,70	0,52	0,69	0,65
BLH32_N0	0,82	0,87	0,87	0,63	0,61	0,62	0,48	0,83	0,71
BLH32_Ges	0,76	0,85	0,83	0,68	0,67	0,68	0,51	0,79	0,70
BLH37_N	0,75	0,79	0,79	0,65	0,63	0,65	0,69	0,82	0,82
BLH37_N0	0,76	0,81	0,80	0,77	0,76	0,77	0,62	0,88	0,81
BLH37_Ges	0,77	0,82	0,81	0,71	0,69	0,70	0,68	0,86	0,84
BLH49_N	0,25	0,41	0,36	0,00	-0,03	-0,01	0,29	0,36	0,36
BLH49_N0	0,32	0,47	0,42	0,02	0,00	0,01	0,44	0,48	0,51
BLH49_Ges	0,28	0,44	0,39	0,01	-0,01	0,00	0,36	0,42	0,43
BLH72_N	0,47	0,44	0,46	0,41	0,37	0,39	0,32	0,59	0,49
BLH72_N0	0,47	0,44	0,46	0,29	0,28	0,29	0,58	0,67	0,68
BLH72_Ges	0,50	0,47	0,48	0,39	0,36	0,38	0,43	0,65	0,59
BETF_N	1,00	0,93	0,97	0,58	0,54	0,56	0,55	0,87	0,77
BETF_N0	0,93	1,00	0,99	0,66	0,64	0,65	0,55	0,90	0,78
BETF_Ges	0,97	0,99	1,00	0,64	0,61	0,63	0,56	0,90	0,79
LAI_N	0,55	0,55	0,56	0,27	0,29	0,28	1,00	0,66	0,92
LAI_N0	0,87	0,90	0,90	0,58	0,56	0,57	0,66	1,00	0,90
LAI_Ges	0,77	0,78	0,79	0,46	0,46	0,46	0,92	0,90	1,00

BED (EC stage) = soil coverage; WUFO= plant growht habit

BLH (EC) = leaf inclinatiion; BETF=tillering; LAI=Leaf Area Index

„Organic traits“ – Soil coverage, leaf inclination, LAI Leaf Area Index

- Grain yield and protein yield are negatively correlated with plant height only in the synthetic N (NS) systems, there is no correlation in the N0 systems
- Positive correlations between fusarium susceptibility and yield or protein yield are more pronounced in NS
- Soil coverage and leaf inclination show higher positive correlations with grain yield and protein yield in NO
- Upright plant growth habit is negatively correlated to protein yield in N, but not significant in NO
- Plant growth habit. leaf inclination and LAI are highly correlated in N0, less or not in NS

Relative Selection Efficiency for Yield and Protein YLD:

calculated according to Weber et al. (2012)) – rel SE = rg * $(H1/H2)^{1/2}$

	n	countries (trials; years)	Heritability	rp, phenotypic corr.				rg, genotypic corr.				**rel. SE**				
YLD			***H***	***HIGH***	***LOW***	***NO***	***ORG***	***HIGH***	***LOW***	***NO***	***ORG***	***HIGH***	***LOW***	***NO***	***ORG***	<TARGET H2
HIGH	***10***	***AT(3;3) CH(2;2) FR(1;1) RO (4;3)***	**0,85**	1,00	0,30	0,70	0,39	1,18	0,35	1,14	0,55	**1,00**	**0,36**	**1,39**	**0,64**	
LOW	***7***	***CH(2;2) FR(5;3)***	**0,83**	0,30	1,00	0,28	0,77	0,35	1,20	0,47	1,08	**0,35**	**1,00**	**0,65**	**1,17**	
NO	***6***	***CH(2;2) RO(4;3)***	**0,44**	0,70	0,28	1,00	0,38	1,14	0,47	2,27	0,74	**0,72**	**0,34**	**1,00**	**0,63**	
ORG	***13***	***AT(3;3) FR(7;3) RO(3;3)***	**0,61**	0,39	0,77	0,38	1,00	0,55	1,08	0,74	1,64	**0,46**	**0,86**	**0,87**	**1,00**	

	n	countries (trials; years)	Heritability	rp, phenotypic corr.				rg, genotypic corr.				**rel. SE**				
PYLD			***H***	***HIGH***	***LOW***	***NO***	***ORG***	***HIGH***	***LOW***	***NO***	***ORG***	***HIGH***	***LOW***	***NO***	***ORG***	<TARGET H2
HIGH	***10***	***AT(3;3) CH(2;2) FR(1;1) RO (4;3)***	0,72	1,00	0,18	0,57	0,45	1,40	0,25	1,24	0,67	**1,00**	**0,34**	**1,55**	**0,73**	
LOW	***7***	***CH(2;2) FR(5;3)***	0,40	0,18	1,00	0,14	0,71	0,34	1,87	0,40	1,43	**0,25**	**1,00**	**0,46**	**0,81**	
NO	***6***	***CH(2;2) RO(4;3)***	0,30	0,57	0,14	1,00	0,18	1,24	0,29	3,35	0,42	**0,65**	**0,26**	**1,00**	**0,29**	
ORG	***13***	***AT(2;2) FR(7;3) RO(3;3)***	0,61	0,45	0,71	0,18	1,00	0,67	1,07	0,42	1,63	**0,62**	**1,24**	**0,60**	**1,00**	

^TEST H1

Relative Selection Efficiency for Yield and Protein YLD:

calculated according to Weber et al. (2012) – rel SE = rg * $(H1/H2)^{1/2}$

	n	countries (n)	Heritability	rp, phenotypic corr.		rg, genotypic corr.		rel. SE		
YLD			***H***	***N***	***NO***	***N***	***NO***	***N***	***NO***	<TARGET H2
N	***17***	***AT(3) CH(4) FR(5) RO(4)***	0,86	1,00	0,79	1,16	1,04	1,00	1,14	
NO	***19***	***AT(3) CH(2) FR(7) RO(7)***	0,67	0,79	1,00	1,04	1,50	0,88	1,00	

^TEST H1

	n	countries (n)	Heritability	rp, phenotypic corr.		rg, genotypic corr.		rel. SE		
PYLD			***H***	***N***	***NO***	***N***	***NO***	***N***	***NO***	<TARGET H2
N	***17***	***AT(3) CH(4) FR(5) RO(4)***	0,68	1,00	0,79	1,48	1,26	1,00	1,08	
NO	***17***	***AT(2) CH(2) FR(6) RO(7)***	0,58	0,79	1,00	1,26	1,73	0,92	1,00	

^TEST H1

Relative Selection Efficiency for Yield and Protein YLD:

4 countries rel SE = rg * $(H1/H2)^{1/2}$ (Weber et al. (2012)

	n	system (trials;years)	Heritability	rp, phenotypic corr.				rg, genotypic corr.				**rel. SE**				
YLD			***H***	***AT***	***CH***	***FR***	***RO***	***AT***	***CH***	***FR***	***RO***	***AT***	***CH***	***FR***	***RO***	<TARGET H2
AT	***6***	***ORG(3;3) HI(3;3)***	0,59	1,00	0,65	0,22	0,73	1,69	0,97	0,30	1,04	**1,00**	**0,87**	**0,25**	**0,84**	
CH	***6***	***NI(2;2) LI (2;2) HI(2;2)***	0,74	0,65	1,00	0,59	0,27	0,97	1,34	0,73	0,34	**1,09**	**1,00**	**0,68**	**0,32**	
FR	***13***	***ORG(7;3) LI(6;3)***	0,87	0,22	0,59	1,00	-0,01	0,30	0,73	1,15	-0,01	**0,37**	**0,79**	**1,00**	**-0,01**	
RO	***11***	***ORG(3;3) LI(4;3) HI(4;3)***	0,84	0,73	0,27	-0,01	1,00	1,04	0,34	-0,01	1,19	**1,19**	**0,36**	**-0,01**	**1,00**	

^TEST H1

	n	countries (n)	Heritability	rp, phenotypic corr.				rg, genotypic corr.				**rel. SE**				
PYLD			***H***	***AT***	***CH***	***FR***	***RO***	***AT***	***CH***	***FR***	***RO***	***AT***	***CH***	***FR***	***RO***	<TARGET H2
AT	***5***	***ORG(2;2) HI(3;3)***	0,47	1,00	0,15	-0,05	0,37	2,11	0,26	-0,08	0,62	**1,00**	**0,22**	**-0,07**	**0,50**	
CH	***6***	***NI(2;2) LI (2;2) HI(2;2)***	0,66	0,15	1,00	0,33	0,29	0,26	1,52	0,45	0,42	**0,31**	**1,00**	**0,41**	**0,39**	
FR	***12***	***ORG(6;3) LI(6;3)***	0,79	-0,05	0,33	1,00	0,14	-0,08	0,45	1,27	0,19	**-0,11**	**0,50**	**1,00**	**0,20**	
RO	***11***	***ORG(3;3) LI(4;3) HI(4;3)***	0,73	0,37	0,29	0,14	1,00	0,62	0,42	0,19	1,37	**0,77**	**0,44**	**0,18**	**1,00**	

^TEST H1

Relative Selection Efficiency for Yield and Protein YLD:

3 years

rel SE = rg * $(H1/H2)^{1/2}$ (Weber et al. (2012)

	n	countries (n)	Heritability	rp, phenotypic corr.			rg, genotypic corr.			**rel. SE**			
YLD			***H***	***2006***	***2007***	***2008***	***2006***	***2007***	***2008***	***2006***	***2007***	***2008***	<TARGET H2
2006	***14***	***AT(2) CH(3) FR(6) RO(3)***	0,79	1,00	0,27	0,26	1,27	0,31	0,43	**1,00**	**0,29**	**0,55**	
2007	***15***	***AT(2) CH(3) FR(5) RO(5)***	0,91	0,27	1,00	0,83	0,31	1,10	1,27	**0,34**	**1,00**	**1,39**	
2008	***7***	***AT(2) FR(2) RO(3)***	0,47	0,26	0,83	1,00	0,43	1,27	2,13	**0,33**	**0,72**	**1,00**	

^TEST H1

	n	countries (n)	Heritability	rp, phenotypic corr.			rg, genotypic corr.			**rel. SE**			
PYLD			***H***	***2006***	***2007***	***2008***	***2006***	***2007***	***2008***	***2006***	***2007***	***2008***	<TARGET H2
2006	***12***	***AT(1) CH(3) FR(5) RO(3)***	0,56	1,00	0,24	-0,11	1,78	0,34	-0,30	**1,00**	**0,27**	**-0,44**	
2007	***15***	***AT(2) CH(3) FR(5) RO(5)***	0,86	0,24	1,00	0,73	0,34	1,16	1,54	**0,42**	**1,00**	**1,84**	
2008	***7***	***AT(2) FR(2) RO(3)***	0,26	-0,11	0,73	1,00	-0,30	1,54	3,89	**-0,20**	**0,54**	**1,00**	

^TEST H1

Can we replace „years“ by „locations“ – with equal number of trials?

A: Trials excluded according to repeatability

	n	countries (trials,years)	Herita-bility	rp, phenotypic corr.			rg, genotypic corr.			rel. SE			
YLD			***H***	***2006***	***2007***	***06-08***	***2006***	***2007***	***06-08***	***2006***	***2007***	***06-08***	<TARGET H2
2006	***12***	***AT(1) CH(3) FR(5) RO(3)***	0,77	1,00	0,27	0,30	1,30	0,33	0,38	**1,000**	**0,304**	**0,368**	
2007	***12***	***AT(2) CH(3) FR(5) RO(2)***	0,90	0,27	1,00	0,81	0,33	1,11	0,95	**0,355**	**1,000**	**1,005**	
2006-2008	***12 (3*4)***	***AT (4;3) + RO (8;3)***	0,81	0,30	0,81	1,00	0,38	0,95	1,23	**0,387**	**0,904**	**1,000**	

^TEST H1

B: All trials chosen randomly

	n	countries (n)	Herita-bility	rp, phenotypic corr.			rg, genotypic corr.			rel. SE			
YLD			***H***	***2006***	***2007***	***06-08***	***2006***	***2007***	***06-08***	***2006***	***2007***	***06-08***	<TARGET H2
2006	***12***	***AT(2) CH(2) FR(5) RO(3)***	0,74	1,00	0,23	0,40	1,35	0,28	0,54	**1,000**	**0,259**	**0,530**	
2007	***12***	***AT(2) CH(3) FR(3) RO(4)***	0,89	0,23	1,00	0,84	0,28	1,12	1,02	**0,311**	**1,000**	**1,099**	
2006-2008	***12 (3*4)***	***AT (4;3) + RO (8;3)***	0,76	0,40	0,84	1,00	0,54	1,02	1,32	**0,544**	**0,939**	**1,000**	

^TEST H1

C: Trials 2006+2007 chosen randomly; Trials AT and RO systematically (ORG + HI all 3 years in both countries)

	n	countries (n)	Herita-bility	rp, phenotypic corr.			rg, genotypic corr.			rel. SE			
YLD			***H***	***2006***	***2007***	***06-08***	***2006***	***2007***	***06-08***	***2006***	***2007***	***06-08***	<TARGET H2
2006	***12***	***AT(2) CH(2) FR(5) RO(3)***	0,74	1,00	0,23	0,41	1,35	0,28	0,56	**1,000**	**0,259**	**0,560**	
2007	***12***	***AT(2) CH(3) FR(3) RO(4)***	0,89	0,23	1,00	0,86	0,28	1,12	1,07	**0,311**	**1,000**	**1,180**	
2006-2008	***12 (3*4)***	***AT (6;3) + RO (6;3)***	0,73	0,41	0,86	1,00	0,56	1,07	1,37	**0,553**	**0,968**	**1,000**	

^TEST H1

Relative Selection Efficiency

- High yielding genotypes for Organic and Low Input were more efficiently found by selection in environments with synthetic N; Heritability of the trial series is the major issue!
- Indirect Yield testing in Romania or Switzerland was more efficient than direct testing in Austria (again Heritability!)
- For Protein Yield testing in target country was always best
- Year 2007 results could fully replace year 2008 results
- Years can be replaced by environments –
  - Inclusion of French and Swiss trials into 2007 was more efficient than testing all 3 years 2006-2008 in the „Austria-Romanian“– Mega-Environment

Conclusions – Concept of BFOA (Breeding for organic agriculture)

Organic conditions are variable

→ breeding for broad adaptation helps to find stable genotypes

Commercially sustainable breeding program → market size is important
Royalities sustain our breeding program

Combine direct and indirect selection strategies
<u>Test parallel on organic and conventional conditions</u>
→ find genotypes better suited for organic
→Use a range of testing environments
→ Some traits are better differentiated in organic than in conventional!

Outlook

BFOA combines conventional and organic testing locations

Choose diverse testing environments carefully (e.g. GGE Biplots)

BFOA uses the broad genetic variability available in the conventional breeding program – select for „organic traits“ both on con and org sites

crosses specific for organic and low input.

go through the nursery „open minded“ with an „organic view“

Strategies for Organic and Low-input Integrated Breeding and Management

Solibam

note: In East Austrian agriculture:

convenional is often low input!

Dry climate -> low yield level –> less intensity

VCU test – East Austrian set

– focus is on untreated trials – slowly changing

New challenges: Intensification in conventional farming; we need to nourish the world.

work is going on...

Thank You for your attention!

SAATZUCHT DONAU