APPENDIX B: Supplementary figures and tables

Genotype	Year of registration	Breeder	Seed producer	Type of genotype	Included in the Clermont-Ferrand trial
A208	NA	NA	NA	MAGIC	no
A22	NA	NA	NA	MAGIC	yes
A243	NA	NA	NA	MAGIC	no
A398	NA	NA	NA	MAGIC	no
Alauda	2013	Dr. Bertold Heyden (DE)	Keyserlingk-Institut (DE)	organic	yes
Altigo	2007	Nickerson International Research GEIE (FR)	Limagrain Europe (FR)	elite	yes
Apache	1998	Nickerson SA (FR)	Limagrain Europe (FR)	elite	no
Arezzo	2007	R 2n (FR)	RAGT 2n (FR)	elite	yes
Blé autrichien	NA	NA	NA	landrace	yes
Boregar	2007	Serasem (FR)	RAGT 2n (FR)	elite	yes
F236	NA	NA	NA	MAGIC	no
F426	NA	NA	NA	MAGIC	yes
Grapeli	2012	INRA (FR)	Agri Obtentions SA (FR)	elite	yes
Hermes (=Hermion)	2013	Dr. Bertold Heyden (DE)	Keyserlingk-Institut (DE)	organic	yes
Maxi (=SW-Maxi)	2002	Semundo (NL)	Saatzucht Hadmersleben GmbH (DE)	organic	yes
Midas	2008	Saatzucht Donau Ges.m.b.H. & CoKG (AT)	Saatzucht Donau Ges.m.b.H. & CoKG (AT)	organic	yes
Renan	1989	INRA (FR)	Agri Obtentions SA (FR)	elite	yes
Ritter (=Goldritter)	2013	Dr. Bertold Heyden (DE)	Keyserlingk-Institut (DE)	organic	yes
Rouge de Bordeaux	NA	NA	NA	landrace	no

Rouge du Roc	NA	NA	NA	landrace	no
Saint Priest	NA	NA	NA	landrace	no
Skerzzo	2011	INRA (FR)	Agri Obtentions SA (FR)	organic	yes
Sogood	2006	Sogroup (FR)	Caussade (FR)	elite	no
Soissons	1988	Florimond Desprez SA (FR)	Florimond Desprez SA (FR)	elite	yes
Trémie	1992	Serasem (FR)	RAGT 2n (FR)	elite	yes

TABLE B.1: Description of the genotypes composing the panel for the two experiments

Response variable	Model	σ_{GMA}^2	σ_{SMA}^2	σ_e^2	$\sigma_{SMA}^2/\sigma_{GMA}^2$
Number of grains per spike in Le Moulon trial	Model 1	19.93	NA	18.21	NA
	Model 2	19.93	0	18.21	0
	Model 3	19.93	0	18.21	0
TKW in Le Moulon trial	Model 1	14.02	NA	0.98	NA
	Model 2	13.97	0.23	0.78	0.02
	Model 3	13.76	0.90	0.78	0.07
Protein content in Clermont-Ferrand trial	Model 1	1.08	NA	0.28	NA
	Model 2	1.08	0	0.28	0
	Model 3	1.08	0	0.28	0

TABLE B.2: Variance components and ratios for responses variables in Le Moulon and Clermont-Ferrand trials for the three models.

TKW: thousand kernel weight.

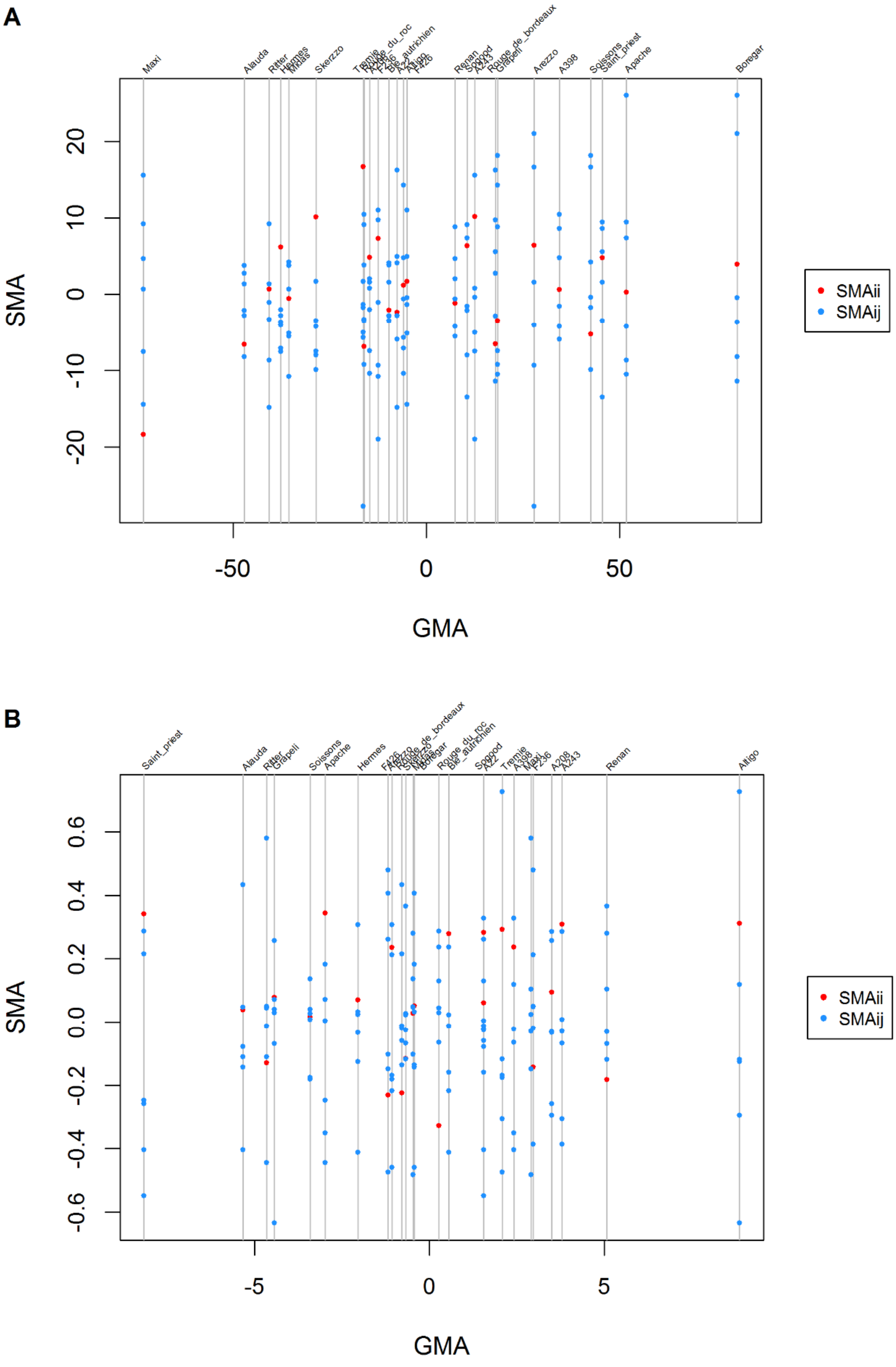

Fig. B.1: SMA and GMA predicted with Model 2 for spike density (A) and thousand kernel weight (B) in LM trial

The red dots represent the intra-genotypic SMA, and the blue dots the inter-genotypic SMA.

Le Moulon					Clermont-Ferrand		
	Yield	Spike density	Grain number per spike	TKW	Yield	Protein content	
Genotype	Model 3	Model 2	Model 1	Model 2	Model 1	Model 1	Genotype
A208	0.26	-14.65	-0.77	3.50			
A22	0.42	-7.55	0.27	1.56	-4.11	-0.48	A22
A243	-0.25	12.60	-4.00	3.79			
A398	2.08	34.53	-3.46	2.42			
Alauda	-7.52	-47.08	3.84	-5.33	-13.57	1.62	Alauda
Altigo	5.39	-5.88	-1.71	8.88	11.99	-0.76	Altigo
Apache	6.89	51.82	0.78	-2.97			
Arezzo	5.80	27.97	1.40	-1.07	10.11	-0.37	Arezzo
Blé Autrichien	-5.93	-9.65	-2.96	0.56	-10.81	-0.25	Blé Autrichien
Boregar	6.57	80.53	-3.50	-0.43	7.08	-0.89	Boregar
F236	4.26	-12.36	1.81	2.97			
F426	-4.88	-4.96	-2.40	-1.18	-4.32	1.02	F426
Grapeli	6.19	18.45	3.97	-4.44	15.18	-1.73	Grapeli
Hermes	-5.73	-37.59	1.76	-2.03	-9.94	1.73	Hermes
Maxi	-4.55	-73.18	4.37	2.91	-12.78	1.33	Maxi
Midas	4.24	-35.57	6.12	-0.47	-0.65	0.05	Midas
Renan	-0.89	7.53	-4.66	5.08	2.11	0.00	Renan
Ritter	-3.55	-40.65	4.88	-4.65	-8.94	0.49	Ritter
Rouge de Bordeaux	-5.41	17.91	-5.04	-0.79			
Rouge du Roc	-18.67	-16.12	-9.34	0.27			
Saint Priest	-7.39	45.56	-3.42	-8.16			
Skerzzo	6.33	-28.50	7.06	-0.67	10.44	-0.25	Skerzzo

Sogood	5.15	10.59	0.78	1.56			
Soissons	3.75	42.56	-0.70	-3.41	2.37	-0.20	Soissons
Trémie	7.41	-16.31	4.93	2.09	5.83	-1.29	Trémie

TABLE B.3: GMA values with the best model for all response variables in LM and CF trials

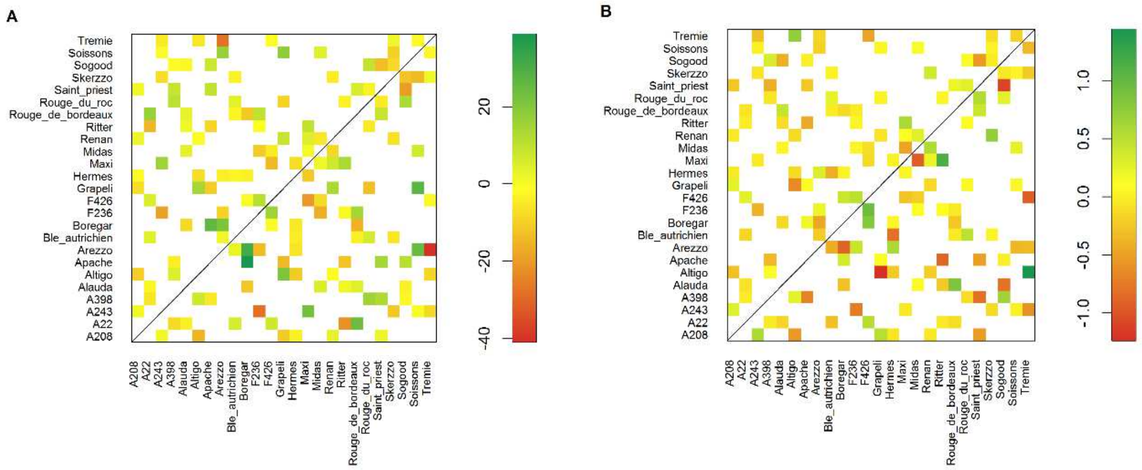

Fig. B.2: SMA values obtained with Models 2 and 3 in LM trial

A. Spike density. B. TKW (thousand kerned weight). The SMA obtained with Model 2 are plotted above the diagonal and the SMA obtained with Model 3 are bellow. The intra-genotypic SMA are not represented on the plots.

Trial	Response variable	Subset for predictions	Model	R²	RMSE	Pearson's correlation	Kendall's correlation
LM	Yield	p	Mean GE	0.471	7.360	0.687	0.481
		m	Model 1	0.610	5.757	0.786	0.590
		m + p	Model 1	0.563	6.690	0.754	0.557
		m	Model 3	0.610	5.757	0.786	0.590
		m + p	Model 3	0.613	6.294	0.790	0.591
LM	Spike density	p	Mean GE	0.127	49.145	0.361	0.244

		m	Model 1	0.515	36.618	0.726	0.532
		m + p	Model 1	0.508	36.908	0.718	0.504
		m	Model 2	0.668	30.295	0.835	0.622
		m + p	Model 2	0.650	31.125	0.821	0.601
LM	TKW	p	Mean GE	0.892	1.016	0.945	0.781
		m	Model 1	0.903	0.879	0.951	0.798
		m + p	Model 1	0.911	0.923	0.954	0.803
		m	Model 2	0.943	0.673	0.972	0.840
		m + p	Model 2	0.941	0.754	0.970	0.841
CF	Yield	p	Mean GE	0.704	4.352	0.840	0.651
		m	Model 1	0.695	4.421	0.834	0.664
		m + p	Model 1	0.728	4.174	0.854	0.669
CF	Protein content	p	Mean GE	0.587	0.539	0.777	0.577
		m	Model 1	0.609	0.525	0.781	0.569
		m + p	Model 1	0.642	0.502	0.802	0.597

TABLE B.4: R^2, RMSE and correlations between observed and predicted values for the response variables in LM and CF trials

The BLUP predictions are based on observations in mixture (*m*) and/or in pure stands (*p*), and the predicted values are calculated for all the observations (*m+p*) using BLUP predictions from Model 1, 2 or 3, or the mean of the genotypic effects (MGE) when predictions are based on pure stands only.

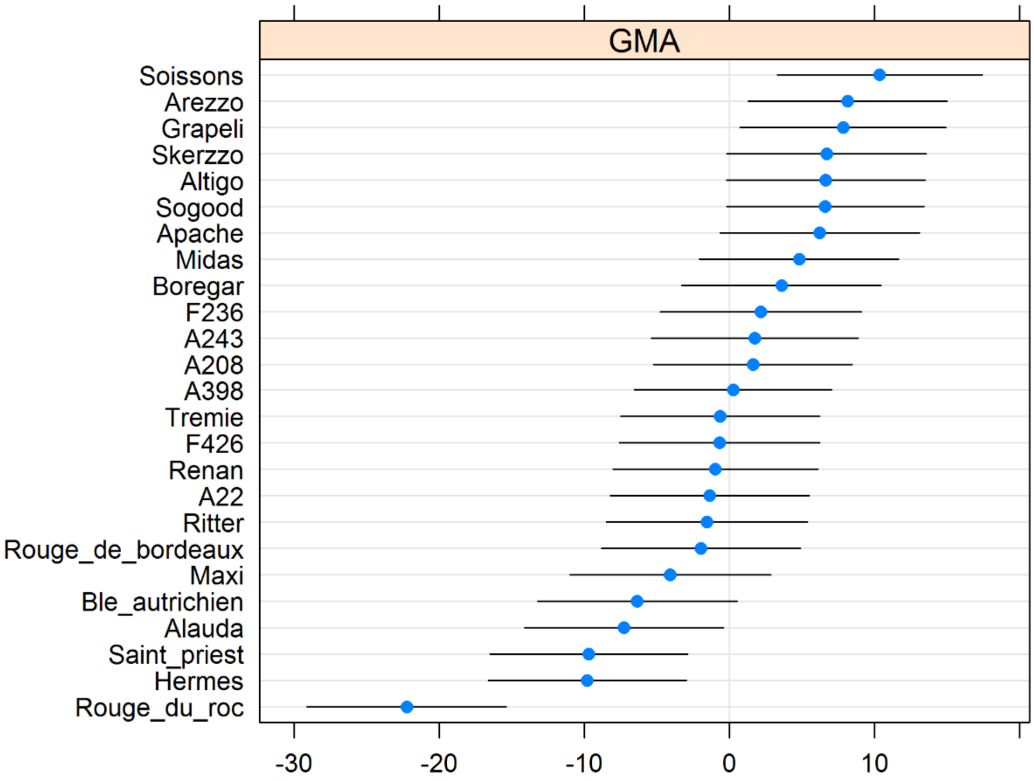

Fig. B.3: GMA for yield of mixtures (excluding the pure stands) in LM trial with Model 1

Response variable	Trial	Correlation GMA_{mp} and genotypic effect in pure stand	Model	Correlation GMA_{mp} and GMA_{m}	Model
Yield	LM	0.8797	Model 1	0.9105	Model 3
Spike density	LM	0.8827	Model 1	0.9477	Model 2
TKW	LM	0.8703	Model 1	0.9428	Model 2
Yield	CF	0.9801	Model 1	0.9629	Model 1
Protein content	CF	0.9668	Model 1	0.9605	Model 1

TABLE B.5: Correlation between the GMA predicted for the mixtures and pure stands (GMA_{mp}) in LM trial with the genotypic effects the pure stands using Model 1, or with the GMA predicted on mixture observations (excluding pure stands, GMA_{m}) using the best model for each response variable