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Genetic variation for ruminal starch degradability at silage harvest maturity in a set of 47 maize hybrids using a high through-put measurement approach

*C. Riboulet1, B. Revol1, Frank Technow2

1 Seed Product Development, Corteva Agriscience, Pacé, 35740, France

2 Seed Product Development, Corteva Agriscience, Johnston, IA, 50131, USA

*Corresponding author: E-mail: *cedric.riboulet@corteva.com*

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Abstract

The objective of this study was to evaluate a methodology to characterize ruminal starch degradability of silage maize based on kernel density measurements. A set of 47 European commercial silage hybrids was evaluated in 2024 across six locations in France and Germany for 4 traits: Silage Yield, Dry Matter, Starch content and Ruminal Starch Degradability. The set comprised hybrids from different private companies registered in Europe between 2015 and 2024 and included 12 flint, 11 flint/dent and 24 dent types. We found a high amount of genetic variation and high broad sense heritability ranging from 0.88 to 0.98 for all traits, including Ruminal Starch Degradability. The new measurement protocol for Ruminal Starch Degradability clearly separated hybrids of different grain types and trait values were stable across environment, with little Hybrid by Environment interaction. We finally propose a new trait called Ruminal Starch Degradability Yield, giving the total amount of rumen digestible starch per hectare, as aid to breeders and farmers in identifying promising hybrid products.

Abbreviations

AVG: average
Cor: correlation
DM: Dry Matter
D: Dent Hybrids
EU: European Union
FD: Flint/Dent Hybrids
FFD: Flint Hybrids
H^2: heritability
HxL: Hybrid x Location interaction
MV: Missing Value
NIRS: Near Infrared Reflectance Spectroscopy
RSD: Ruminal Starch Degradability
RSDY: Ruminal Starch Degradability Yield
Starch: Starch content in %
TSS: Total Sums of Squares
SY: Silage Yield

Introduction

With around 8,673,000 hectares in 2024 (FAO.org) and a key role in dairy and beef production, silage maize is a key crop for the European Union. The main traits to characterize European silage hybrids are silage yield (SY), starch content (Starch), dry matter (DM), and cell wall digestibility. Cell wall digestibility is considered as the main factor influencing the valorization of silage maize by the cows (Deinum and Struik, 1985; Dolstra and Medema, 1990; Barrière et al., 1991; Wolf et al., 1993; Coors et al., 1994; Argillier et al., 1995) and has been the subject of numerous scientific investigations (Barrière et al., 2007) and is routinely used by plant breeders to evaluate hybrids. However, while starch content is also an important trait for silage quality, Ruminal Starch Degradability (RSD) has only received minor attention in hybrid evaluation, despite the existence of genetic variability and importance for animal nutrition value (Philippeau et al., 1999; Correa et al., 2002; Mlynekova et al., 2013, Ngonyamo-Majee et al., 2008a; Ngonyamo-Majee et al., 2008b; Santo Rossi et al., 2016). This is partly due to the prohibitive cost and difficulty measuring this trait using fistulated animals or indirectly from kernel vitreousness tests requiring laborious kernel dissection. Instead, breeders and farmers estimate starch degradability with secondary indicator traits like dry matter content (Peyrat et al, 2016) which allows to evaluate a ration based on maize physiological development at harvesting but does not allow either variety differentiation nor hybrid selection or recommendation.

Fig. 1 : Testing locations for a set of 47 silage hybrids: 2 locations in Britany in northwest of France (WF1 and WF2), 2 near Munich in Germany (SG1 and SG2) and 2 in the north of Münster in Germany (NG1 and NG2).

The objective of this research is to develop and test a simple, cost effective, and robust methodology to measure RSD from kernel density, based on a water bath methodology and previous work by Correa et al, 2002, using an experimental data set comprising 47 modern European silage maize hybrids (with different kernel types) evaluated in multi-location field trials.

Materials and methods

Plant material

The set of 47 commercial silage maize hybrids (Table 1) was composed of 12 flints (FFD), 11 flint/dents (FD) and 24 dents (D) according to the European Variety Catalogue (ec.europa.eu/food/plant-variety-portal). Their maturities ranged from Very Early to Early with corresponding FAO Maturity Index values between 195 to 300 derived from seller product descriptions. All hybrids were officially registered in EU between 2015 and 2024 by Corteva agriscience (28 hybrids), Euralis (1 hybrid), KWS (6 hybrids), Limagrain (11 hybrids) and Syngenta (1 hybrid). Their product names were anonymized.

Field experiments

The field trials were conducted in a total of 6 locations (Figure 1): 2 in Britany in Northwest of France (WF1 and

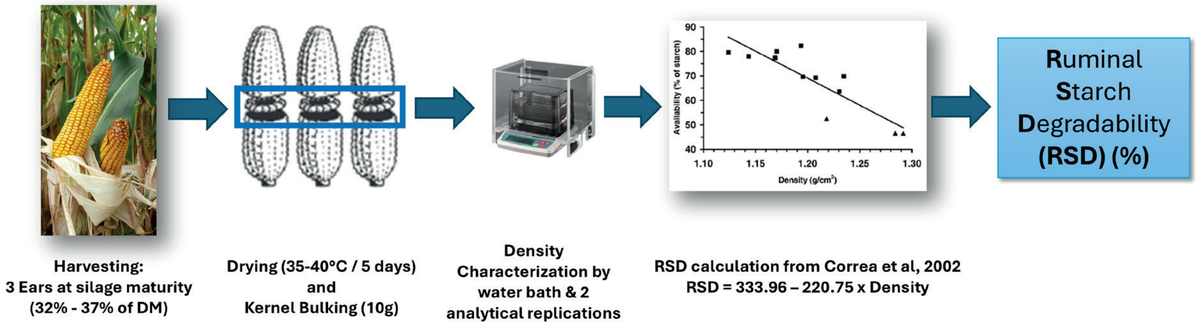

Fig. 2 - RSD Evaluation by water bath methodology: method overview

Fig. 1 - Graphical abstract

Table 1 - Set of 47 hybrids used for this study. The hybrid names were coded according to their Grain Type. Grain types, Maturity groups, FAO maturities came from the European Variety Catalogue and seller product descriptions. SY, DM, Starch, RSD & RSDY values came from BLUPs calculations made for each of the 47 silage maize hybrids evaluated in 2024 in France and Germany in 6 locations.

Hybrid Name (coded)	Grain Type	Maturity Group	FAO Maturity	First EU Registration Year	Hybrid Type	SY (t/ha)	DM (%)	Starch (%)	RSD (%)	RSDY (t/ha)
FF1	FFD	Early	270-280	2022	Single-cross	21.4	33.2	29.6	59.4	3.7
FFD2	FFD	Very Early	240	2018	Single-cross	18.9	36.9	32.7	57.5	3.6
FFD3	FFD	Early	230	2016	Single-cross	18.5	34.5	32.7	59.5	3.6
FFD4	FFD	Early	260	2018	Single-cross	19.5	35.0	31.7	59.5	3.7
FFD5	FFD	Very Early	200-250	2020	Single-cross	19.4	37.2	33.4	61.4	4.0
FFD6	FFD	Very Early	200-250	2018	Single-cross	19.8	37.2	33.0	60.8	4.0
FFD7	FFD	Early	250	2015	Single-cross	19.3	34.9	31.5	63.0	3.8
FFD8	FFD	Very Early	240	2016	Triple-cross	19.5	36.6	31.5	63.7	3.9
FFD9	FFD	Very Early	230	2020	Triple-cross	18.3	37.3	34.6	67.0	4.2
FFD10	FFD	Early	260	2019	Single-cross	20.5	35.5	32.6	67.0	4.5
FFD11	FFD	Very Early	200-250	2018	Triple-cross	20.4	37.4	32.8	70.2	4.7
FFD14	FFD	Very Early	195-220	2020	Single-cross	18.8	39.1	32.9	62.5	3.8
FD13	FD	Very Early	240	2016	Single-cross	20.2	37.6	34.4	61.3	4.2
FD15	FD	Very Early	200-250	2020	Triple-cross	18.8	39.3	34.4	65.0	4.1
FD16	FD	Early	280	2018	Single-cross	21.8	34.7	31.9	64.9	4.6
FD17	FD	Very Early	230	2018	Single-cross	20.6	37.4	34.8	65.7	4.7
FD18	FD	Very Early	220-250	2019	Single-cross	20.1	37.8	33.3	65.9	4.4
FD19	FD	Very Early	240	2018	Single-cross	19.0	36.4	33.2	67.0	4.2
FD20	FD	Very Early	220-250	2022	Single-cross	18.4	38.9	33.6	65.7	4.0
FD21	FD	Early	270	2020	Single-cross	19.8	32.9	30.5	66.9	4.0
FD23	FD	Early	250	2019	Single-cross	20.7	36.9	33.7	67.8	4.7
FD24	FD	Early	275-280	2018	Triple-cross	19.9	33.0	29.6	68.2	4.0
FD26	FD	Early	220-250	2015	Single-cross	20.5	36.7	33.0	70.0	4.7
D27	D	Early	250-300	2021	Single-cross	22.3	34.1	29.8	66.7	4.5
D28	D	Early	250-300	2022	Single-cross	22.2	33.4	29.4	68.2	4.5
D29	D	Early	250-300	2021	Single-cross	20.9	34.6	31.4	71.8	4.6
D30	D	Very Early	220-250	2023	Single-cross	20.7	37.9	32.9	71.5	4.8
D31	D	Early	250-300	2023	Single-cross	20.6	35.8	31.5	71.4	4.6
D32	D	Early	250-300	2024	Single-cross	22.8	33.8	29.6	72.3	4.9
D33	D	Early	250-300	2017	Single-cross	21.6	34.3	31.7	72.6	5.0
D34	D	Early	250-300	2023	Single-cross	21.6	35.4	31.5	73.6	4.9
D35	D	Early	250-300	2017	Single-cross	20.9	33.6	30.3	73.5	4.7
D36	D	Early	250-300	2022	Single-cross	20.9	35.5	31.6	73.9	4.8
D37	D	Early	250-300	2023	Single-cross	21.1	34.0	31.5	74.3	4.9
D38	D	Early	250-300	2022	Single-cross	20.7	34.9	31.3	74.8	4.8
D39	D	Early	250-300	2023	Single-cross	22.5	34.9	30.8	74.9	5.2
D40	D	Early	250-300	2022	Single-cross	21.1	33.4	30.1	76.1	4.8
D41	D	Early	250-300	2020	Single-cross	21.4	33.8	30.4	76.5	4.9
D42	D	Early	250-300	2023	Single-cross	21.3	34.5	30.3	77.3	5.0
D43	D	Early	250-300	2023	Single-cross	21.6	34.4	31.7	77.6	5.3
D44	D	Early	250-300	2024	Single-cross	22.5	34.1	30.9	77.4	5.4
D45	D	Early	250-300	2017	Single-cross	21.7	33.2	30.7	78.7	5.2
D46	D	Early	250-300	2023	Single-cross	19.3	33.4	32.7	80.4	5.0
D47	D	Early	250-300	2024	Single-cross	21.7	35.1	32.8	83.4	5.9
D48	D	Early	250-300	2022	Single-cross	20.8	32.7	30.8	84.3	5.3
D49	D	Early	250-300	2022	Single-cross	21.2	33.6	31.9	85.5	5.7
D50	D	Very Early	220-250	2017	Single-cross	19.9	36.6	34.4	85.3	5.7
					Mean	20.5	35.4	31.9	70.3	4.6
					Mini	18.3	32.7	29.4	57.5	3.6
					Maxi	22.8	39.3	34.8	85.5	5.9

WF2), 2 near Munich in Germany (SG1 and SG2) and 2 in the North of Münster in Germany (NG1 and NG2). The 47 hybrids were planted with two replications in a completely randomized design. Experimental plots were 5.2 m long with two rows of 42 plants each. Row spacing was 0.75 m, and the resulting plant density was 107,000 plants/ha. The plots were harvested with a forage chopper at silage harvest stage. SY was measured directly by the chopper's scales while DM and Starch content were estimated with a Near Infrared Reflectance Spectroscopy (NIRS) using custom calibration.

Ruminal Starch Degradability Evaluation

For the RSD evaluation (Figure 2), the 6 locations were sampled by manually harvesting 3 representative ears per plot at silage maturity. These ears were dried in a ventilated oven between 35 and 40°C for 5 days. A representative kernel sample of 10g was collected from the middle portion of each ear. The density of this bulk was analyzed twice with the electronic densimeter MD-300S provided by BLET Measurement Group S.A.S., using a water bath methodology. The 2 analytical repetitions were averaged. RSD was calculated from this density value following Correa et al, 2002 as:

$RSD\ (\%) = 333.96 - 220.75\ x\ Density\ (g/cm3)$. Then Ruminal Starch Degradability Yield (RSDY) was obtained as:

$$RSDY\ (t/ha) = SY\ (t/ha)\ x\ Starch\ (\%)\ x\ RSD\ (\%)$$

Data analysis

Prior to analysis, the phenotypic observations within each location were adjusted for spatial effects with the moving grid method as implemented in the R package mvngGrAd (Technow, 2015).

Moving grid adjustment is a non-parametric nearest-neighbor spatial adjustment method successfully used in plant breeding field trials (e.g., Lado et al., 2014; Wu et al., 2024). The grid included four plots to the right and left and one above and below the central plot to be adjusted.

Then the following linear mixed model was fit separately for each trait:

$$y_{ijk} = \mu + L_i + H_j + HL_{ij} + e_{ijk}$$

Where $y\__{ijk}$ was the spatially adjusted observed value of hybrid j in location i, μ was the fixed intercept, L_i the random effect of location i, Hj the random effect of hybrid j, HL_{ij} the random hybrid by location interaction effect and e_{ijk} the identical and independently distributed residual with mean zero and variance V_R. The random effects were modeled as normally distributed with mean zero and variance components V_L, V_H and V_{HL}, respectively. The model was fitted with the R package lme4 (Bates et al., 2015). We used μ+H_j as the estimate of across location hybrid performance and refer to these as hybrid BLUPs for brevity.

From the so obtained variance components, broad sense heritability on an entry mean basis was estimated as

$$H^2 = \frac{V_H}{V_H + \frac{V_{HL}}{N_L} + \frac{V_R}{N_L \times N_R}}$$

Where N_L and N_R were the average number of locations and replications, respectively, for each hybrid. Because of missing values, these were slightly lower than 6 and 12, respectively (Table 2). Hypothetical H^2 values were obtained by replacing the observed N_L and N_R with corresponding values for scenarios ranging from 1 - 10 locations and 1 - 4 replications per location.

In addition to the mixed model analysis, the spatially adjusted phenotypic trait values were used to generate Genotype by Environment interaction biplots according to Laffont et al. (2013), using the R package 'gge' (Wright and Laffont, 2024).

Descriptive statistics and graphics (Figure 3, 4, 5, and 7) were built with Spotfire from TIBCO Software (*www.tibco.com/products/tibco-spotfire*).

Results and discussion

Silage Yield (SY), Dry Matter (DM), and Starch - Genetic variation

Genetic variance components (Table 2), for SY, DM and Starch Hybrid components were considerably higher

Table 2 - Model summary with means, variance components and heritability on entry mean basis (H^2) of each analyzed trait.

Traits	mean	hybrid	location	HxL	res	H^2	nloc	nrep
SY (t/ha)	20.5	1.6	3.5	0.4	1.7	0.88	5.9	11.1
DM (%)	35.4	3.4	3.6	0.7	0.7	0.95	5.9	11.1
Starch (%)	31.9	2.3	1.8	0.6	0.7	0.93	5.9	11.1
RSD (%)	70.3	54.3	35.0	1.0	13.0	0.98	5.9	11.1
RSDY (t/ha)	4.6	0.4	0.1	0.05	0.1	0.95	5.9	11.1

Table 3 - Means of analyzed traits for the 6 locations involved in our trial: 2 locations in Britany in northwest of France (WF1 and WF2), 2 near Munich in Germany (SG1 and SG2) and 2 in the north of Münster in Germany (NG1 and NG2).

Location	SY (t/ha)	DM (%)	Starch (%)	RSD (%)	RSDY (t/ha)
WF1	21.1	35.1	30.9	73.7	4.8
WF2	18.2	34.6	29.9	80.5	4.4
NG1	20.3	33.9	32.6	68.2	4.5
NG2	23.7	34.1	32.1	67.7	5.2
SG1	19.3	35.8	32.3	67.1	4.2
SG2	20.6	39.0	33.8	64.2	4.5
Mean	20.5	35.4	31.9	70.3	4.6
Mini	18.2	33.9	29.9	64.2	4.2
Maxi	23.7	39.0	33.8	80.5	5.2

than those for Hybrid x Location interaction effect. We also observed very high entry mean basis heritability's (H^2) for these 3 traits, ranging from 0.88 to 0.95.

The average values of DM content for each location (Table 3) were between 33.9% and 39.0% with a mean at 35.4%. While relatively high, the observed value range was within the expected maize silage DM content and suitable for quality trait investigations. Estimated hybrid BLUPs for DM content ranged from 32.7% for D48 to 39.3% for FD15 (Table 1 and Figure 3) which also cover the expected range of DM for silage maize at harvest maturity. Hybrids from the FD and FFD pools on average showed higher DM values with 36.5% and 36.2% respectively than hybrids from the D group with 34.5% on average (Figure 4B). This difference in DM between Dent and Flint hybrids can be explained by the relative novelty of Dent hybrids in early maturity segment. The gap can be expected to close over time as the Dent germplasm becomes more adapted to this segment.

The location averages for SY (Table 3), ranged between 18.2 t/ha and 23.7 t/ha were higher than the historical yield level in this area (www.agreste.agriculture.gouv.fr). This high yield level indicates optimal and stress-free growing conditions. The range of SY hybrid BLUPs was between 18.3 t/ha for the early maturity hybrid FFD9 and 22.8 t/ha for the late maturity hybrid D32 (Table 1 and Figure 3). With averages of 19.5 t/ha and 20 t/ha, the FDD and FD groups had comparable SY values (Figure 4A). The D group had a significantly higher average SY at 21.3 t/ha. As expected, DM and SY hybrid BLUPs were negatively correlated with -0.56 (Figure 8), which consequently is reflected in the average DM and SY values of the three hybrid pools.

By locations, the average starch content ranged between 29.9% and 33.8% with an overall average of 31.9% (Table 3). These values were those expected for silage maize harvested in normal conditions confirming the lack of stress during this trial. At the hybrid level (Table 1), the range was between 29.4% of starch for hybrid D28 and 34.8% for hybrid FD17. The differences in average starch content of the FFD, FD and D groups (Figure 4C) are consistent with their DM contents (Figure 4B) because, as expected, hybrid BLUPS of these two traits were strongly positively correlated with a value of 0.81 (Figure 8).

Ruminal Starch Degradability (RSD) – a powerful differentiator

Regarding RSD (Table 2), the variance component corresponding to Hybrid effects was considerably higher than for Location effects and Hybrid x Location interaction effects; H^2 was also very high with a value of 0.98. These results highlight the preponderance of genetic vs. environmental and interaction effects for determining phenotypic expression of this trait. Given that, a H^2 model calculation was conducted to identify the optimum number of repetitions and locations necessary to characterize RSD (Table 4). This showed that RSD could be evaluated with very high H^2 at a low number of locations or replications, thus providing opportunities for its utilization in product evaluation with a limited resource investment. In addition, to visualize and compare Genotype and Genotype by Environment effects, a GGE biplot (Figure 6) was generated according to Laffont et al, 2013. As expected from the variance component results, this demonstrated that Hybrids ranked consistently across the locations, with main differences being observed between hybrids and hybrid groups. It should be noted that the high amount of genetic (i.e., between product) variation found in this study is in part due to the diverse panel of hybrids included. This panel reflects entry sets encountered in late-stage evaluation or in registration trials. Lower values should be expected for early generation testing of testcross hybrids between closely related inbred lines.

A large genetic variation of 28 points, ranging from a minimum at 57.5% to a maximum at 85.5%, was observed

Table 4 : H^2 RSD Evaluation by water bath methodology: method overview.

# Rep / # Loc	1	2	3	4	5	6	7	8	9	10
1	0.79	0.89	0.92	0.94	0.95	0.96	0.96	0.97	0.97	0.97
2	0.88	0.94	0.96	0.97	0.97	0.98	0.98	0.98	0.98	0.99
3	0.91	0.95	0.97	0.98	0.98	0.98	0.99	0.99	0.99	0.99
4	0.93	0.96	0.97	0.98	0.98	0.99	0.99	0.99	0.99	0.99

for RSD hybrid BLUPs across the 47 hybrids analyzed in this study (Table 1 and Figure 5). RSD results by grain texture showed a clear ranking between hybrid types (Figure 4D): the FFD group, with an average of 62.6% had lowest RSD values, followed by the FD group with an average of 66.2% and the D group, which had an average of 75.9%, which was considerably above the two Flint based groups. These results were consistent with several previous studies highlighting the advantage of D hybrids compared to FFD or FD for starch degradability (Philippeau et al., 1999; Correa et al., 2002; Mlynekova et al., 2013, Ngonyamo-Majee et al., 2008a; Ngonyamo-Majee et al., 2008b; Santo Rossi et al., 2016). The 13.3 points of difference between D and FFD group for RSD showed that this trait was a very significant differentiator between hybrid types, much more than yield, starch content or maturity. However, there have been exceptions. For example, FFD11, with an RSD value of 70.2%, was comparable to D group hybrids like D31 (Table 1 and Figure 5). On the contrary, D27 and D28 showed lower values than expected regarding their grain type.

Ruminal Starch Degradability Yield - A new trait to characterize Silage Hybrids

Our results show that RSD is a promising trait to evaluate the degradability and hence quality of starch in maize silage. We thus propose a new trait to help both maize breeders and farmers to identify the most promising maize hybrids for dairy production. We define this trait as the Ruminal Starch Degradability Yield (RSDY). It is the quantity of starch by hectare that can be degraded by the rumen, i.e.,

$$RSDY\ (t/ha) = SY\ (t/ha) \times Starch\ (\%) \times RSD\ (\%)$$

For *RSDY*, the Hybrid variance component was considerably larger than the components for Location effects and Hybrid x Location interaction (Table 2). The heritability for *RSDY* (0.95) was also extremely high and the H^2 model calculation showed that the trait could be evaluated with high H^2 at an even lower number of locations and replications. (Table 5).

RSDY hybrid BLUPs values showed a large genetic variation with an average of 4.6 t/ha and a range between 3.6 t/ha and 5.9 t/ha (Table 1 and Figure 7). The average by grain type for *RSDY* highlighted higher values for D group compared to FFD or FD groups with an average of 5, 4.3 and 3.9 t/ha respectively (Figure 4E). Thus, dents compensated for a lower level of starch (Figure 4C) due to their later maturities (Figure 4B) by a better *SY* (Figure 4A) and *RSD* (Figure 4D) and so achieved better RSDY values overall than the 2 flint groups (Figure 4E).

With the 47 early hybrids included in the present research, the correlations between traits (Figure 8) showed that the main driver of *RSDY* is not the DM nor even *SY* or Starch content but *RSD* itself with a correlation value equal to 0.93. This last observation confirmed that the impact of the kernel quality is nowadays underestimated and therefore underused to characterize silage hybrid performance. In Southern Europe, where most maize hybrids are derived from Dent kernel type, less variation for *RSD* should be expected, meaning that differences in *SY* and Starch content might be more important for *RSDY* level.

Conclusions

A large range of genetic variation has been shown for classical traits like *SY*, *DM* and Starch content in the evaluated set of 47 European maize hybrids. These variations highlighted different ideotypes linked to their germplasm types: FFD, FD and D. Thus, the 2 flinty groups had a higher DM and Starch content while the dent group had higher *SY*.

Furthermore, this work described a simple, robust, and cheap method to characterize the *RSD* paving the way for its larger usage in maize breeding and hybrid cha-

Table 5 - H^2 model calculation of RSDY as a function of the number of locations (1 to 10) and the number of replications (1 to 4).

# Rep / # Loc	1	2	3	4	5	6	7	8	9	10
1	0.66	0.79	0.85	0.88	0.90	0.92	0.93	0.94	0.94	0.95
2	0.75	0.86	0.90	0.92	0.94	0.95	0.96	0.96	0.96	0.97
3	0.79	0.88	0.92	0.94	0.95	0.96	0.96	0.97	0.97	0.97
4	0.81	0.90	0.93	0.95	0.96	0.96	0.97	0.97	0.98	0.98

racterization. The high degree of genetic determination suggested that *RSD* can be evaluated accurately with a limited number of locations and so with a reasonable investment. With this method, a broad range of genetic variations was highlighted, showing that it is now possible to better characterize quality of silage maize not only regarding cell wall digestibility as has been done historically, but also regarding starch degradability.

Finally, we proposed a new trait called *RSDY* which quantifies the rumen degradable starch in t/ha by combining *SY*, Starch content and *RSD*. With early hybrids, *RSDY* showed a wide range of phenotypic variability mainly due to *RSD* variability, confirming the interest of this trait. We hope that this *RSD* protocol and the newly defined *RSDY* trait will play a role in helping breeders to develop and identify silage maize hybrids with characteristics more directly linked to the efficiency and sustainability of dairy production.

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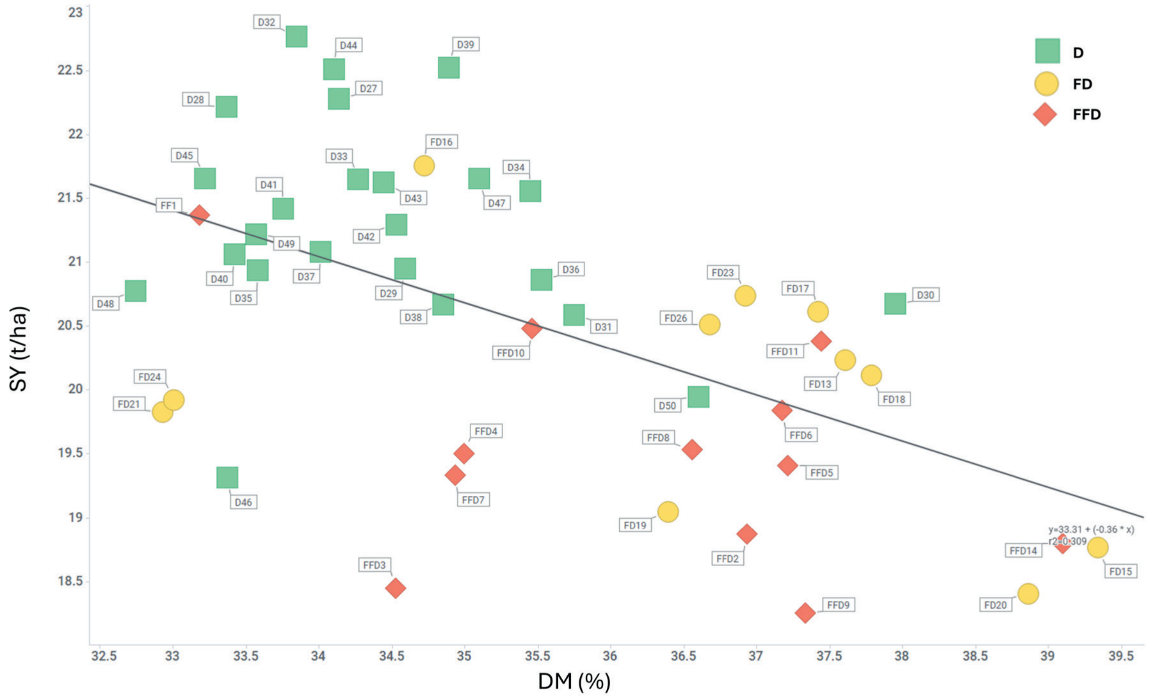
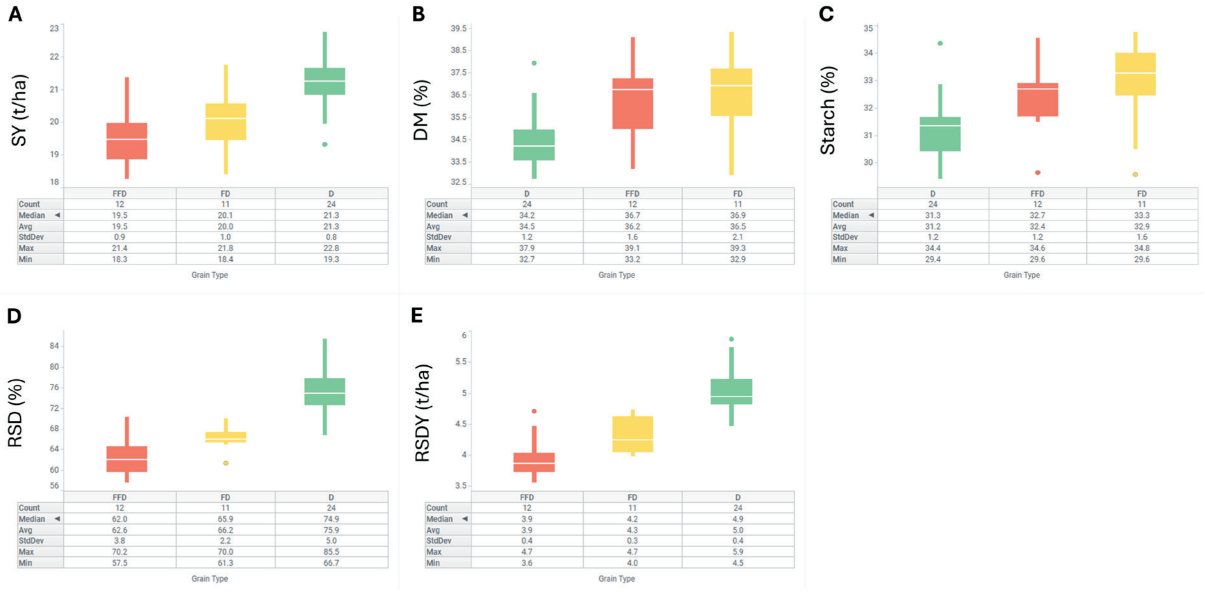


Fig. 3 : Correlation between SY (t/ha) and DM (%) for a set of 47 silage hybrids used for this study. SY and DM values came from BLUPs calculations made for each of the 47 silage maize hybrids evaluated in 2024 in France and Germany in 6 locations



A

	FFD	FD	D
Count	12	11	24
Median ◄	19.5	20.1	21.3
Avg	19.5	20.0	21.3
StdDev	0.9	1.0	0.8
Max	21.4	21.8	22.8
Min	18.3	18.4	19.3

B

	D	FFD	FD
Count	24	12	11
Median ◄	34.2	36.7	36.9
Avg	34.5	36.2	36.5
StdDev	1.2	1.6	2.1
Max	37.9	39.1	39.3
Min	32.7	33.2	32.9

C

	D	FFD	FD
Count	24	12	11
Median ◄	31.3	32.7	33.3
Avg	31.2	32.4	32.9
StdDev	1.2	1.2	1.6
Max	34.4	34.6	34.8
Min	29.4	29.6	29.6

D

	FFD	FD	D
Count	12	11	24
Median ◄	62.0	65.9	74.9
Avg	62.6	66.2	75.9
StdDev	3.8	2.2	5.0
Max	70.2	70.0	85.5
Min	57.5	61.3	66.7

E

	FFD	FD	D
Count	12	11	24
Median ◄	3.9	4.2	4.9
Avg	3.9	4.3	5.0
StdDev	0.4	0.3	0.4
Max	4.7	4.7	5.9
Min	3.6	4.0	4.5

Fig. 4 : Average of each analyzed trait (Box-plots A: SY; B: DM; C: Starch; D: RSD; E: RSDY) by grain type (FFD: Flint; FD: Flint/Dent; D: Dent). For each trait, absolute values came from BLUPs calculations made for each of the 47 silage maize hybrids evaluated in 2024 in France and Germany in 6 locations.

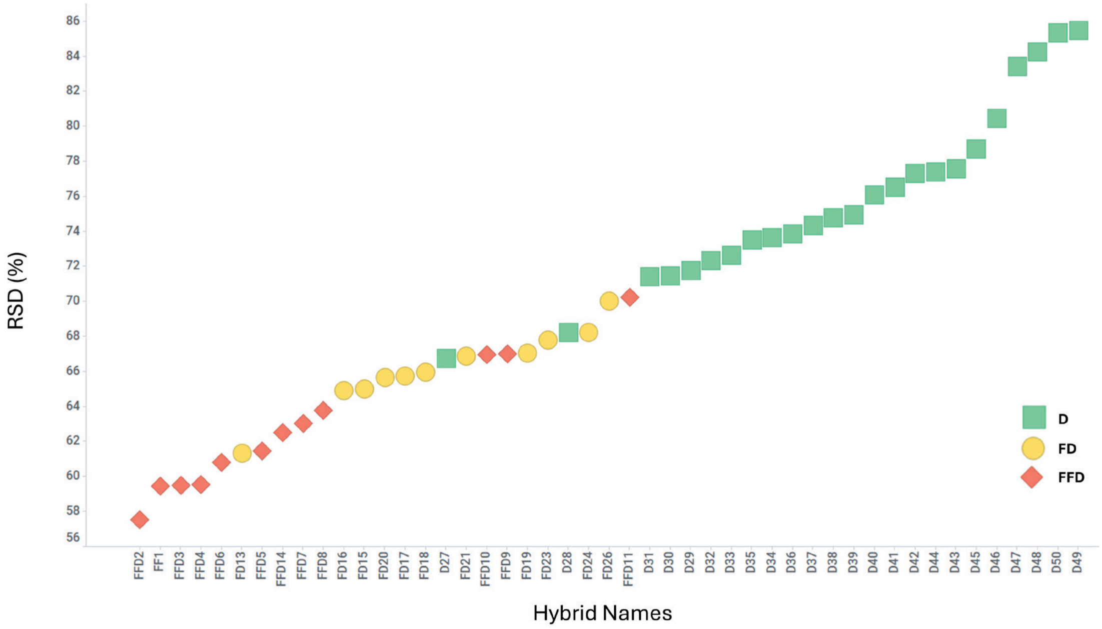


Fig. 5 : RSD means for 47 silage maize hybrids evaluated in 2024 in France and Germany in 6 locations. The hybrids were sorted by RSD values and classified by Dent hybrids (D), Flint/Dent Hybrids (FD) and Flint hybrids (FFD).

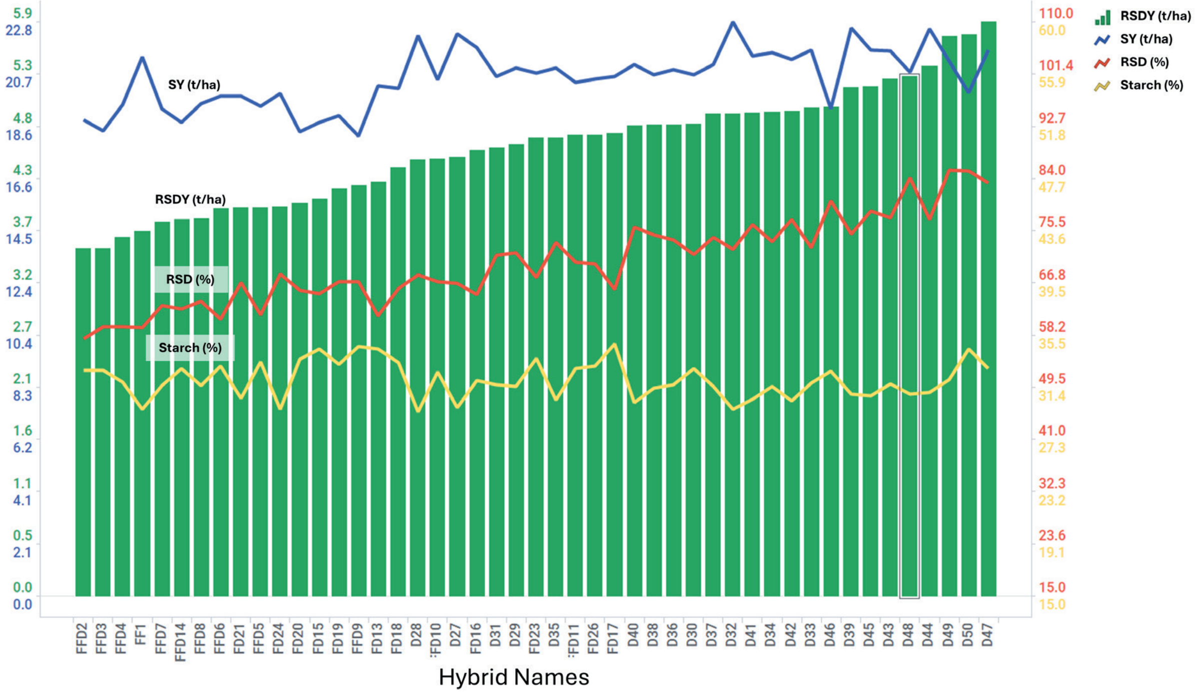


Fig. 7 : RSDY (displayed as bars) for 47 silage maize hybrids evaluated in 2024 in France and Germany. RSDY is the product of the 3 solid lines: SY (t/ha) by starch (%) by RSD (%).

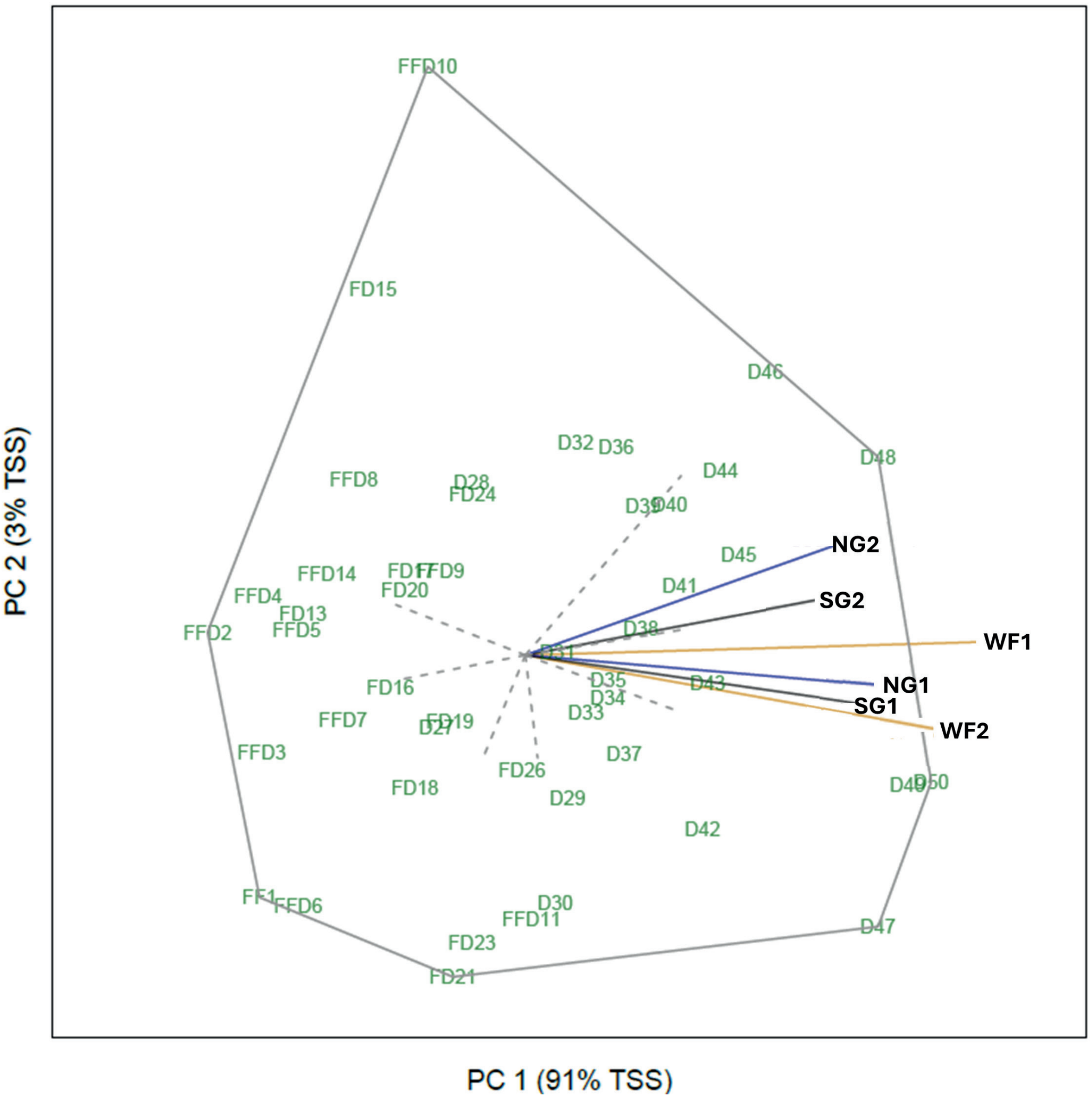


Fig. 6 : GGE Biplot highlighting first two axes of the Genotype (PC1) and Genotype by Environment (PC2) effects for RSD for 47 maize hybrids evaluated in 6 locations. The different field vectors were marked with solid lines with 2 locations in Britany in northwest of France (WF1 and WF2), 2 near Munich in Germany (SG1 and SG2) and 2 in the north of Münster in Germany (NG1 and NG2).

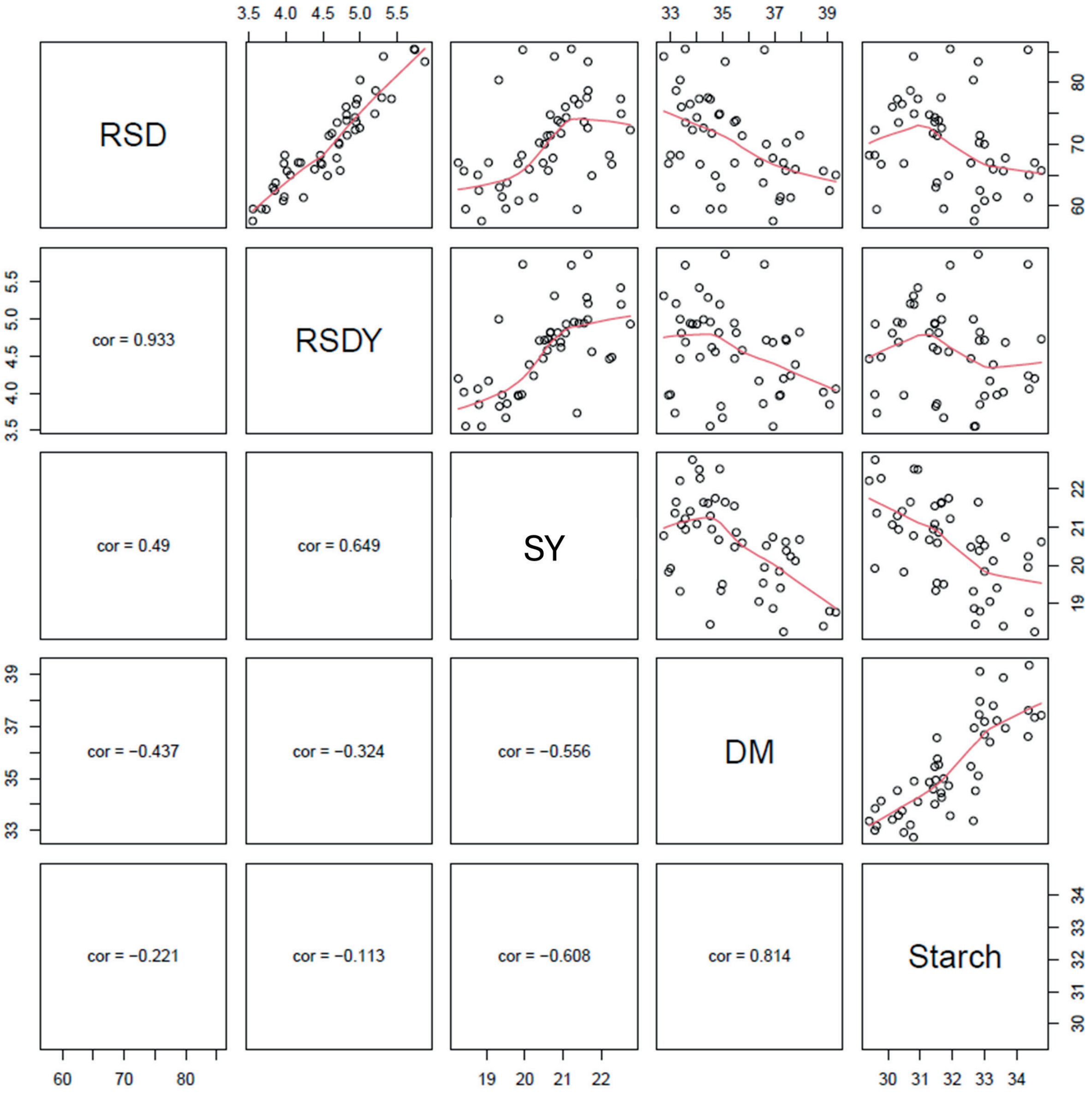


Fig. 8 : BLUPS Correlations between 5 investigated traits for 47 silage maize hybrids evaluated in 2024 in 6 locations distributed across France and Germany.

Maydica's Editor
Dr.ssa Carlotta BALCONI
CREA - Research Centre for Cereal and Industrial Crops
Via Stezzano, 24 24126 Bergamo - ITALY
carlotta.balconi@crea.gov.it

Maydica's Technical Editor
Jacopo Barone
jacopo.barone@masaf.gov.it

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Consiglio per la ricerca in agricoltura
e l'analisi dell'economia agraria