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Genotypic variation in maize (*Zea mays*) influences rates of soil organic matter mineralisation and gross nitrification

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Summary

- Agricultural management practices that increase soil organic matter (SOM), such as no-tillage (NT) with crop residue retention, together with crop varieties best able to source nutrients from SOM may help reverse soil degradation and improve soil nutrient supply and uptake by plants in low-input environments of tropical and sub-tropical areas.
- Here, we screened germplasm representing genetic diversity within tropical maize breeding programs in relation to shaping SOM mineralisation. Then we assessed effects of contrasting genotypes on nitrification rates, and genotype by management history interactions on these rates.
- SOM-C mineralisation and gross nitrification rates varied under different maize genotypes. Cumulative SOM-C mineralisation increased with root diameter but decreased with increasing root length. Strong influences of management history and interaction of maize genotype by management history on nitrification were observed. Overall, nitrification rates were higher in NT soil with residue retention.
- We propose that there is potential to exploit genotypic variation in traits associated with SOM mineralisation and nitrification within breeding programs. Root diameter and length could be used as proxies for root-soil interactions driving these processes. Development of maize varieties with enhanced ability to mineralize SOM combined with NT and residue retention to build/replenish SOM could be key to sustainable production.

Key words: Genotype by management history interaction, genotypic variation, maize varieties, nitrification, no-tillage, plant-soil interactions, soil organic matter mineralisation, southern Africa

Introduction

Soil degradation is a major threat to agricultural production (Tully *et al*., 2015). This is particularly critical in tropical and sub-tropical regions (McKenzie *et al*., 2015; Tully *et al*.,

2015). In sub-Saharan Africa (SSA), approximately 494 million ha of land (or over 20% of land in most SSA countries) is affected by soil degradation, typically manifested in the form of soil erosion, soil organic matter (SOM) loss and nutrient depletion (McKenzie *et al*., 2015). In southern Africa, specifically, maize (*Zea mays* L.) accounts for over 75% of the area under cereal production (FAO, 2021), with yields amongst the lowest in the world (Cairns & Prasanna, 2018) and current climate variability has had a significant impact on recent production (Ray *et al*., 2019). Restricted availability and use of fertiliser is also a key factor associated with this large yield gap (Cedrez *et al*., 2020). This gap is largest in female managed plots, with women applying less fertiliser to maize than male managed plots (Burke *et al*., 2018; Burke & Jayne, 2021). Ultimately, increasing fertiliser use in southern Africa will require changes in policy, infrastructure and local manufacturing (Cedrez *et al*., 2020). Technologies such as maize varieties with tolerance to low nitrogen (N) conditions increase yields in this region, but unless higher levels of fertilizer are applied in the long term, they will further deplete soil inorganic N (Pasley *et al*., 2020), thereby further degrading the soil and threatening food security for future generations in southern Africa.

To sustainably improve maize productivity in southern Africa, it is necessary to reverse soil degradation, for example through the build-up/replenishment of SOM (e.g., Amelung *et al*., 2020). The physical, chemical and biological benefits of SOM accrual (Lal, 2015; Maron *et al*., 2018) can confer greater resilience of cropping systems under climate change. Thus, crop management practices that enhance SOM are urgently needed. An example is no-tillage (NT) with retention of crop residues on the soil surface, as utilised in different forms of conservation agriculture (Thierfelder *et al*., 2018), practiced on approximately 180 million ha of arable land worldwide with an increasing trend (Kassam *et al*., 2019). It has been shown that NT with residue retention gradually increases soil C, N and phosphorus (compared with conventional tillage (CT) with crop residue removal) (Yang *et al*., 2016), associated with replenishment of SOM. Selecting maize varieties in these systems that enhance SOM mineralisation and N transformations could help ensure reliable and timely N supply from SOM and organic inputs (e.g., crop residues returned on soil surface) for plant uptake (Mwafulirwa *et al*., 2017). However, there is limited knowledge of the abilities of maize varieties to foster SOM mineralisation, or the potential for integrating these abilities into NT systems through balanced SOM replenishment and utilization (Janzen, 2006), thereby creating what we term a ‘circular nutrient economy’.

Plant species and genotypes vary with respect to the degree to which they mediate SOM mineralisation (Shahzad *et al*., 2015; Mwafulirwa *et al*., 2016; Yin *et al*., 2019). For example, genotypes differ in amount and composition of rhizodeposits that shape rhizosphere microbial community structure (Paterson *et al*., 2007) and increase microbial activities, including mineralisation of SOM (i.e., rhizosphere priming effect, Kuzyakov *et al*., 2000). There is significant potential for manipulating this root-soil interaction through breeding (Mwafulirwa *et al*., 2016; Paterson & Mwafulirwa, 2021). A consequence of SOM mineralisation is the mobilisation of NH_4^+ (following initial immobilisation of N in microbial biomass and subsequent release via the microbial loop, Kuzyakov & Xu, 2013) and subsequent nitrification, both providing N available for plant uptake. Oxidation of NH_3 to NO_2^-, conferred by ammonia oxidising microbes, is typically the rate limiting step of nitrification (Wankel *et al*., 2011), while rhizosphere bacterial communities play a key role in short-term changes in SOM dynamics (Haichar *et al*., 2008; Fontaine *et al*., 2011). Therefore, total bacterial abundance and the size of the ammonia-oxidizing groups (often measured by total bacterial 16S and ammonia monooxygenase (*amoA*) gene abundances, respectively) may reflect SOM mineralisation and nitrification potentials in soil, affecting soil nutrient availability.

Traits such as root diameter, root biomass, root length, specific root length and root density define the nutrient absorption capacity of roots (McCormack *et al*., 2015; Li *et al*., 2016) and are known to affect rhizodeposition (Phillips *et al*., 2011; Guyonnet *et al*., 2018). There is a need to characterize genotypic variation in these traits, for example in maize, in the context of impacts on SOM and N dynamics, especially considering that root traits associated with mobilisation of N from SOM will not necessarily be those that maximise fertiliser N use efficiency. For instance, in the global North, crop breeding under high-input conditions may have resulted in retention of root traits for capture of readily accessible mineral nutrients, such as from inorganic fertilisers, with loss of traits enabling efficient interactions with microbial communities mediating nutrient mobilisation from SOM (Burton *et al*., 2013; Huo *et al*., 2017). However, maize breeding in southern Africa is focussed on selection under low N conditions and there may be more genetic variation remaining within the primary gene pool for root-soil interactions. To explore this potential variation to control SOM and N cycling, it is necessary to (i) identify easily measurable traits with strong influence on root-soil interactions that can be used as proxies for these functional processes, (ii) understand how plant traits, growth and

soil process rates are affected by management practice and interactions with genotype, and (iii) understand the temporal changes of these plant and soil parameters.

In this study, we firstly established genotypic variation in SOM-C mineralisation within an association mapping panel selected to represent genetic diversity within tropical maize breeding programs, and elucidated underpinning root traits associated with this function. We then examined nitrification rates and associated microbial gene abundances under maize genotypes selected for their varying abilities to mineralise SOM-C, and quantified genotype by management history (i.e., NT soil with crop residue retention on cropland *versus* CT soil with crop residue removal) interactions. We hypothesised that (i) genotypic variation associated with SOM-C mineralisation and nitrification rates would be related to root traits, and (ii) the influence of maize germplasm on nitrification rates and associated microbial gene abundances (bacterial 16S and *amoA*) would vary between soils with different management history.

Materials and Methods

Soil

Two soils were collected from the Domboshawa Research Centre (-17.603 S; 31.604 E; 1545 m.a.s.l.) in the highveld of Zimbabwe. The soils are classified as *Lixisols* (Mapfumo *et al*., 2007). One soil was collected from an on-station trial that has been running since 2012 with contrasting soil management practices, from within plots with NT and crop residue retention. The trial is planted with different maize varieties, fertilized with 83kg N ha^{-1}, 28kg P_2O_5 ha^{-1} and 14kg K_2O ha^{-1}, supplied as basal dressing and topdressing. The second soil was collected from a conventionally managed field, with soil tillage (CT) and crop residue removal, bordering the NT plots. Approximately 10 soil sub-samples (0-10cm soil depth) were taken at random within each plot for NT soil and from adjacent locations in the bordering field for CT soil. The sub-samples for each soil were thoroughly mixed into a composite sample and sieved through a 4mm mesh on-site. The sieved soil was then packed in cooler boxes and transported to Aberdeen, United Kingdom, where they were stored at 4°C until experiment setup.

As general soil characterization, the CT and NT soils had silt + clay fractions of 16% and 20% and sand fractions of 84% and 80%, respectively. Total C concentration was 3.0 and 4.7mg g^{-1} soil, total N concentration was 0.2 and 0.4mg g^{-1} soil, NH_4^+-N was 2.6 and 5.4µg N

159 g^{-1} soil and NO_3^--N was 10.0 and 1.7µg N g^{-1} soil for CT and NT soils, respectively. Soil pH
160 (H_2O) was 4.8 and 5.1, cation exchange capacity was 1.0 and 1.6meq 100 g^{-1} soil and electrical
161 conductivity was 94 and 248µS cm^{-1} for CT and NT soils, respectively.
162
163 Maize germplasm
164
165 Ninety-seven maize inbred lines were selected from the Drought Tolerant Maize for Africa
166 association mapping panel (Wen *et al*., 2011). This panel was developed to represent genetic
167 diversity within the International Maize and Wheat Improvement Center (CIMMYT) and
168 International Institute of Tropical Agriculture (IITA) maize breeding programs. These 97 lines
169 were selected based on seed availability, seed quality and yield performance under drought,
170 low N and combined drought and heat stress (Cairns *et al*., 2013) from nine breeding programs
171 (Table 1). Information on the pedigrees of all lines is presented in Supplementary Table S1.
172 Eight medium maturing commercial maize hybrids in Zimbabwe (SC513, SC633, Pan53,
173 Pristine 601, ZAP55, ZAP61, PGS61 and 30G19) were included. These hybrids are widely
174 grown in Zimbabwe. Seeds were imported to Aberdeen, United Kingdom, where they were
175 stored at 4°C until sowing.
176
177 Experiment One: Maize germplasm impacts on SOM mineralisation
178
179 *Setup and measurements*
180
181 A screen of the 97 inbred lines and eight hybrids (i.e., 105 genotypes) was performed utilizing
182 the CT soil. The soil was packed in microcosms (22.5cm x 5.5cm) to a bulk density of 1.44g
183 cm^{-3} to represent field bulk density and adjusted to 65% water holding capacity. A 5cm layer
184 of previously muffle-furnaced sand (0% organic matter) was packed to the bottom of each
185 microcosm before packing the soil, as a strategy to reduce the quantity of soil to import. The
186 systems were left to stabilize over a period of one week. After this initial soil stabilization
187 period, plastic chambers made from syringe tubes (40ml headspace) were inserted to 2.5cm
188 depth into the middle of microcosms for trapping CO_2 efflux from soil. The gas chambers were
189 fitted with inlet and outlet stopper end tubes for controlled gas flow. Systems were maintained
190 at 22°C and 70% relative humidity within a plant growth chamber (Mwafulirwa *et al*., 2016).

Each microcosm was sown with one plant including an unplanted control treatment. Plants were grown over 29 days without fertilizer addition. Due to the large number of genotypes, space limitation and practicability to manage the experiment, treatments were replicated two to four times in a sequential randomized block design. Two hybrids and the control treatment were included in all blocks. Soil water content was maintained by adding deionized water on a mass basis twice a week. A 12-hour daily photoperiod was set with 512µmol m^{-2} s^{-1} PAR within the chamber. Continuous labelling of plants with ^{13}C-CO_2 started at the seedling growth stage, one week after sowing. This was achieved by passing a continuous flow of ^{13}C-enriched CO_2 (20 atom% ^{13}C) through the plant growth chamber over the experiment period (Mwafulirwa *et al*., 2016). CO_2 concentration, including ^{12}C-CO_2 and ^{13}C-CO_2, in the plant growth chamber was monitored multiple times each week.

Soil CO_2 fluxes were sampled at 16, 23 and 29 days after planting (DAP). To collect samples, the gas collection chambers were flushed with CO_2-free air for three minutes, obtaining outlet airflow <10µl L^{-1} CO_2 concentration, then sealed for 40 minutes using stopper end tubes to accumulate soil CO_2 efflux in the headspace. Thereafter, approximately 25ml air was sampled from the headspace with a gas syringe connected to the outlet tubing. Gas chambers remained open except during collection of soil CO_2 efflux. The sampled air was used to determine the CO_2 concentration and $^{12}C/^{13}C$ ratios as described in Mwafulirwa *et al*. (2016). Calculation of total C respired for each treatment per sampling point was achieved using the CO_2-C concentration values and the soil under the surface area covered by the syringe tube. The total CO_2-C was partitioned to two component sources (SOM- and maize root-derived C) based on their $\delta^{13}C$ signatures. The maize root-derived C and SOM-derived C were determined according to Garcia-Pausas & Paterson (2011) and Mwafulirwa *et al*. (2016).

Plants were harvested as root and shoot fractions. Shoots were harvested by cutting at the soil surface, and then freeze-dried. Roots were washed free of soil in deionized water and stored fresh in 50% ethanol at 4°C prior to analysis for average root diameter and total root length. For this, fresh roots were carefully spread onto a clear-bottomed reservoir filled with water to slightly cover the roots. Then, the roots were scanned on an Epson Expression 1640XL flatbed scanner (Epson UK, London), images were cropped to remove the border created by the reservoir, and total root length and average root diameter were measured using the WINrhizo software (Regent Instruments, Quebec City, Canada) (George *et al*., 2014). Thereafter, roots were washed in deionized water and freeze-dried.

223

224 Experiment Two: Impacts of maize genotype and soil management history on nitrification

225

226 *Setup and measurements*

227

228 Five maize inbred lines ((A.T.Z.T.R.L.BA90 5-3-3P-1P-4P-2P-1-1-1-B x G9B C0 R.L.23-1P-
229 2P-3-2P-3-2P-1P-B-B-B)-B-76TL-1-2-4 (ATZTRI), CL-G1837=G18SeqC2-F141-2-2-1-1-1-
230 2-##-2 (CL-G18), [CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-2 (CML444x), La
231 Posta Seq C7-F64-2-6-2-2 (LPSF64) and 95S43SR HG"A"-94-1-1-1 (95S43S)) and two
232 hybrids (SC513 and 30G19), selected based on the range of variation in cumulative SOM-C
233 mineralisation in experiment one (Table 2), were used utilizing both CT and NT soils. The
234 microcosm system, planting, growth conditions, and growth period were as described for
235 experiment one, with the following exceptions: (i) microcosms were packed with soil only
236 without a layer of muffle-furnaced sand, (ii) NT soil was packed to bulk density of 1.38g cm^{-3}, compared to 1.44g cm^{-3} for CT soil, to reflect field conditions, (iii) gas chambers and ^{13}C-CO_2 labelling were not used, and (iv) each microcosm (planted or unplanted) received ^{15}N-enriched fertilizer ($^{14}NH_4{}^{15}NO_3$, 10 atom% ^{15}N), equivalent to 6g N m^{-2} or 60kg N ha^{-1}, at 14 DAP. Microcosms were arranged in a randomized complete block design with four replications, with two microcosms prepared per replicate to allow for two destructive plant and soil harvests. The fertilizer was mixed with deionized water during a watering event and spread onto the soil surface in droplets, ensuring distribution of the fertilizer within the soil. Four extra replicates of unplanted CT and NT soils were also fertilized in the same way and harvested within 15 minutes for determination of initial NO_3^--N concentrations and their ^{15}N-enrichment.

246 Plant root and shoot biomass were measured as described in experiment one, at 23 and
247 29 DAP, with roots and shoots freeze-dried. Following plant harvests, the soil was thoroughly
248 mixed by hand and sub-samples were taken and immediately stored at 4°C for determination
249 of mineral N concentration and, in turn, gross nitrification by ^{15}N isotope pool dilution after
250 the harvesting was completed. Further soil sub-samples were taken and stored at -80°C for
251 DNA extraction. Mineral N (NH_4^+-N and NO_3^--N) concentrations of the harvested soil samples
252 were determined using an autoanalyser (Technicon Traaks 800, Saskatoon, Canada) following
253 extraction of 10g fresh soil with 50ml of 2M KCl solution. The remaining 2M KCl soil extracts
254 were stored frozen at -20°C until preparation for analysis of ^{15}N-enrichment, using a micro-

diffusion technique described by Goerges & Dittert (1998) recovering NO_3^--N. ^{15}N-enrichment of the recovered NO_3^--N was determined on an isotope-ratio mass spectrometer (IRMS; Sercon, UK). Samples taken at 15 minutes after fertiliser application and 23 DAP were used for calculating the gross nitrification rate, according to Hart *et al*. (2018). The calculations are described in Supplementary Methods S1.

Total DNA was extracted from 1g soil using a phenol chloroform method as described in Deng *et al*. (2010) with the addition of a mutated DNA reference fragment to the lysis buffer. This allowed relative real time assessment of gene copy count as described in Daniell *et al*. (2012) controlling for extraction efficiency and variable levels of inhibitors between treatments. Briefly, soil was reduced to a slurry in the extraction buffer before bead beating with 1mm steel beads and treatment with phenol chloroform and chloroform prior to precipitation with isopropanol and sodium acetate. Re-suspended pellets were then further purified through polyvinylpolypyrrolidone (PVPP). This method was selected as proprietary kits had performed poorly in preliminary experiments with soils from this system. Relative real-time PCR targeted the reference fragment using Mut-F and Mut-R primers (CCTACGGGAGGCAGGTC and ATTACCGCGGCTGCACC, Daniell *et al*., 2012) and 16S gene (CCTACGGGAGGCAGCAG and ATTACCGCGGCTGCTGG, Muyzer *et al*., 1993) as described in Daniell *et al*. (2012), as well as the bacterial ammonium monooxygenase gene using amA1F (GGGGTTTCTACTGGTGGT) and amoA2R (CCCCTCKGSAAAGCCTTCTTC) primers (Rotthauwe *et al*., 1997).

Recent research has demonstrated that root traits and rhizosphere properties, including recruitment of microbiomes, during the seedling growth stage (around 2-4 weeks after planting) are predictive of relative rooting and rhizosphere characteristics in mature plants (e.g., Thomas *et al*., 2016).

Statistical analyses

Univariate analyses were performed using the software GenStat 18th Edition (VSN International Ltd). In experiment one, repeated-measures analysis of variance (ANOVA) was used to test the effects of maize genotype and sampling date on root- and SOM-derived CO_2-C efflux rates, with maize genotype as the fixed factor and sampling date as the repeated factor. One-way unbalanced treatment structure (general linear model) was used to assess the effects

of maize genotype on cumulative root-derived C mineralisation, cumulative SOM-C mineralisation, root biomass, shoot biomass, root-to-shoot ratio, root diameter, root length and specific root length. In experiment two, the effects of maize genotype, soil management history and sampling date on root biomass, shoot biomass, soil NH_4^+-N, soil NO_3^--N and bacterial 16S gene copy number in soil were assessed using three-way ANOVA. In addition, two-way ANOVA was used to evaluate the effects of maize genotype and soil management history on gross nitrification, and maize genotype and sampling date on *amoA* gene copy number in soil. For treatments with three or more levels (i.e., maize genotype in both experiments and sampling date in experiment one), where statistically significant (P<0.05) effects were found the least significant difference (LSD) test was used to assess differences between individual means.

In experiment one, the effects of root biomass, shoot biomass, root-to-shoot ratio, root diameter, root length and specific root length on cumulative root-derived C mineralisation or cumulative SOM-C mineralisation were tested using linear regressions (paired relationships). Linear regression was also used to assess the relationship between cumulative root-derived C mineralisation and cumulative SOM-C mineralisation. Furthermore, principal component analysis (PCA) was used to ordinate (eigenvalue scale) the samples to evaluate their associations with the measured traits of root biomass, shoot biomass, root-to-shoot ratio, root diameter, root length, specific root length, cumulative root-derived C mineralisation and cumulative SOM-C mineralisation. Because these variables were measured in different units, PCA was performed applying a correlation matrix to normalise data. In experiment two, paired relationships between variables (root biomass, shoot biomass, NH_4^+-N concentration, NO_3^--N concentration, bacterial 16S gene copy number, bacterial *amoA* gene copy number and gross nitrification) were also evaluated using linear regressions. Furthermore, regression analysis was used to investigate relationships between individual root morphological traits or SOM-C mineralisation measured in experiment one and gross nitrification measured in experiment two for corresponding maize genotypes. All regressions were considered significant at $\alpha = 0.05$. These multivariate analyses were performed using the free software PAST version 4.03 (Palaeontological Association).

Results

Soil CO_2-C efflux and C mineralisation in experiment one

By 29 DAP there were significant (P<0.05) differences among maize genotypes in cumulative SOM-C mineralized and cumulative root-derived C mineralized, measured as surface soil CO_2-C efflux (Table 2, Table S1). Cumulative SOM-C mineralized varied from 12.4 to 29.7µg C g^{-1} soil, whereas cumulative root-derived C mineralized varied from 0.6 to 53.6µg C g^{-1} soil. Lines CL-G1837=G18SeqC2-F141-2-2-1-1-1-2-##-2 (CL-G18) and DTPWC9-F24-4-3-1, derived from the tropical and physiology breeding programs in Mexico, were associated with the highest cumulative SOM-C mineralisation and cumulative root-derived C mineralisation, respectively.

There was also genotypic variation (P<0.05) in SOM- and root-derived soil CO_2-C efflux rates at 16, 23 and 29 DAP, with no significant interaction of maize genotype by time. Rates of root-derived CO_2-C efflux increased over time (Table S2), in line with plant growth increasing root inputs to soil. In contrast, rates of SOM-derived CO_2-C efflux in planted and unplanted soil decreased over time, consistent with low fertility soil and depletion of the available SOM stock over the course of the experiment (Table S3). Nonetheless, rates of SOM-derived CO_2-C efflux in planted soils remained generally higher (P<0.05) compared to the unplanted treatment, indicating positive priming effects of maize genotypes on SOM throughout the experiment period.

Plant characteristics

In experiment one, there was significant (P<0.05) genotypic variation in root and shoot biomass, measured at 29 DAP. Root biomass varied from 0.03 to 0.4g with average of 0.2g, whereas shoot biomass varied from 0.1 to 0.8g with average of 0.4g (Table S1). However, there were no significant differences in root-to-shoot ratio among genotypes. Genotypic variation (P<0.05) was also observed for average root diameter, root length and specific root length, ranging from 0.4 to 0.6mm (0.5mm average), 3.7 to 21.1m (14.8m average) and 40.3 to 175.5m g^{-1} root biomass (81.5m g^{-1} root biomass average), respectively (Table S1).

Likewise, in experiment two there were significant (P<0.05) differences in root and shoot biomass among genotypes (Table 3, Fig. S1a, b). The overall range of root and shoot biomass was 0.1-0.8g (0.4g average) and 0.2-1.0g (0.4g average), respectively, indicating improved growth performance with fertilizer application, relative to experiment one. In

experiment two, the NT soil with residue retention increased (P<0.05) shoot biomass (0.5±0.1g for NT soil and 0.4±0.03g for CT soil) but did not affect root biomass (Table 3). Root biomass increased (P<0.05) from 0.3±0.03g to 0.5±0.04g, measured at 23 and 29 DAP respectively. There was also significant (P<0.05) increase in shoot biomass with time, with a significant interaction effect of genotype by time driven by greater separations in high biomass genotypes (Table 3, Fig. S1c).

Relationships between C mineralisation and plant characteristics

Linear regression analysis in experiment one showed that cumulative SOM-C mineralisation increased with average root diameter (P<0.0001, Fig. 1a) and decreased with increasing root length (P<0.0001, Fig. 1b) or specific root length (P=0.027, Fig. 1c). Specific root length increased with decreasing average root diameter (P<0.0001, Fig. 1d). In contrast, root biomass and root-to-shoot ratio did not significantly affect cumulative SOM-C mineralisation (data not shown). A positive relationship was observed between cumulative SOM-C mineralisation and cumulative root-derived C mineralisation (P=0.0003, Fig. S2a). Cumulative root-derived C mineralisation was positively related to shoot biomass (P<0.0001, Fig. S2b), root biomass (P<0.0001, Fig. S2c) and root length (P<0.0001, Fig. S2d) and negatively related to specific root length (P<0.0001, Fig. S2e), but was not related to root-to-shoot ratio and average root diameter (data not shown).

The PCA plot (Fig. 2) shows an overview of the relationships measured in experiment one. Based on the variation of SOM-C mineralisation, seven maize genotypes (Table 2) were selected to assess microbial community size and nitrification in experiment two. These genotypes are distributed over the PCA plot ordination space, associated with all observed variables, and fall within the 95% ellipse except for one score (Fig. 2). This indicates not only that the selection approach was valid for our stated purpose, but also that the selected genotypes are representative of the variation within the germplasm population for multiple variables.

Nitrification and soil characteristics in experiment two

Overall, gross nitrification rates were increased (P<0.05) by maize plants and the NT soil with residue retention (compared to unplanted soil and CT soil with residue removal, respectively),

383 with a significant interaction between maize genotype and soil management history (Table 3,
384 Fig. 3a). Maize genotype had no effect on gross nitrification in CT soil whereas soil
385 management history did not significantly affect gross nitrification in unplanted soil and the
386 hybrid 30G19 (Fig. 3a), driving the significant interaction. Compared with the maize genotype
387 effect (P=0.017, Table 3), soil management history had a strong effect (P<0.001, Table 3) on
388 gross nitrification.

389 The concentrations of NH_4^+-N and NO_3^--N in soil were affected (P<0.05) by maize
390 genotype, soil management history and time of sampling (Table 3). Soil NH_4^+-N and NO_3^--N
391 concentrations were highest in unplanted soil followed by the line ATZTRI and were lowest in
392 the hybrids (SC513 and 30G19) (Fig. S1d,e), with both N forms decreasing with time (1.9±0.3
393 and 20.8±2 μg N g^{-1} soil for NH_4^+-N and NO_3-N respectively at 23 DAP, and 1.0±0.3 and
394 12.8±2.0 μg N g^{-1} soil for NH_4^+-N and NO_3-N respectively at 29 DAP). Compared with the CT
395 soil with residue removal, the NT soil with residue retention decreased NH_4^+-N concentration
396 (2.3±0.4 and 0.6±0.1 μg N g^{-1} soil for CT soil and NT soil, respectively) but increased NO_3^--N
397 concentration (9.1±1.3 and 25.2±2.3 μg N g^{-1} soil for CT soil and NT soil, respectively). The
398 two-way interaction of maize genotype by soil management history affected both NH_4^+-N and
399 NO_3^--N concentrations (Table 3, Fig. 4). This was driven by the distinct separation of CT and
400 NT soils for both N forms in unplanted soil and maize genotypes except line ATZTRI for NH_4^+-
401 N and hybrid 30G19 for NO_3^--N. Two-way interactions of maize genotype by time and soil
402 management history by time were significant for soil NH_4^+-N but not NO_3^--N, while the three-
403 way interaction of maize genotype by soil management history by time was not significant for
404 any of the N forms (Table 3).

405 Bacterial 16S gene copy number was significantly (P<0.001) affected by maize
406 genotype, but not soil management history or time but with a significant (P<0.05) interaction
407 between genotype and time (Table 3). This was driven by an increase in 16S copy number in
408 30G19 between days 23 and 29 driving the significantly higher overall gene copy count in this
409 line (Fig. 4c). The bacterial *amoA* gene was not detected in CT soil. However, in NT soil
410 bacterial *amoA* gene copy number also varied (P<0.05) among the maize genotypes with
411 testcross lines typically showing lower *amoA* gene copy counts than the hybrids or the
412 unplanted soil (Fig. S1f). Time of sampling and the interaction between genotype and time
413 were not significant for *amoA* gene copy number (Table 3).

Regression analysis, in experiment two, showed that gross nitrification was not related to mineral N (NH_4^+-N and NO_3^--N) concentration or bacterial 16S and *amoA* gene copy numbers in soil, nor to maize plant root and shoot biomass (data not shown). Likewise, regression analysis showed that gross nitrification, measured in experiment two, was not related to root morphological traits (i.e., root diameter, root length and specific root length) measured in experiment one for corresponding maize genotypes (data not shown).

Relationship between SOM mineralisation and nitrification

Regression analysis showed no significant relationship between SOM-C mineralisation and gross nitrification when measured in CT soil (data not shown) for corresponding genotypes and time. However, there was a significant relationship when SOM-C mineralisation measured in experiment one was considered relative to gross nitrification in NT soil for corresponding genotypes and time (Fig. 3b).

Discussion

Genetic variation exists in ability of maize to mineralize SOM

Our results show genotypic variation in the ability of maize plants to influence SOM mineralisation. The largest cumulative SOM-C mineralisation from soil planted with the tropical line CL-G18, 29 DAP, was 2.4-fold greater than the lowest cumulative SOM-C mineralisation associated with the sub-tropical line 95S43S. SOM-C mineralisation was not directly related to root biomass, but was more closely linked to other root traits. In particular, we demonstrate for the first time that SOM-C mineralisation increased with maize root diameter and was less under genotypes having longer, finer root systems.

It is possible that roots with larger diameter supported greater rhizodeposit quantities, as a result of their enhanced assimilate transport capacity (McCormack *et al*., 2015), and that this was coupled to enhanced microbial activity in the rhizosphere (Uren, 2007), increasing SOM mineralisation (Jackson *et al*., 2019). That plants with short, thick roots may have been associated with greater root exudation could be a plant strategy to enhance microbially mediated nutrient mobilisation where root growth/elongation is sacrificed under resource

limitation (Brunner *et al*., 2015). Positive relationships between C-substrate supply via root exudation and SOM priming may also be driven by microbial N-demand (Dijkstra *et al*., 2013) as a consequence of high C-to-N ratio of root-derived C-flow. Indeed, a number of studies have demonstrated that increased microbial N-demand can result in specific mobilisation of N-rich components of SOM (i.e., N-mining, Craine *et al*., 2007), a process that may be particularly important in the context of supporting crop N-demand from organic inputs (e.g., crop residues). These assumptions are in line with the low fertility soil used in this study and the positive priming effect observed throughout the experiment period. A study by Kumar *et al*. (2016), using soil cultivated with a modern maize variety, showed increase of SOM-C mineralisation by up to 126% without N-fertilization. Thus, plant and microbial mediated SOM decomposition could play a beneficial role supporting plant productivity by unlocking nutrients bound in SOM or organic inputs over the crop growing period. However, alone this could ultimately further deplete SOM. Therefore, the declining but still positive SOM priming effect observed over the course of our study as affected by maize genotypes calls for complimentary SOM building measures in this soil, as we discuss in the next section. There is also a need to assess possible physiological trade-offs between short, thick roots with greater exudation for exploitation of SOM sources and deeper roots for drought tolerance.

Larger root diameter and lower specific root length is also a common feature of mycorrhizal plants. This results from enlargement of the root cortex with extra cell layers to accommodate the fungal structures (Fusconi *et al*., 1999; Dreyer *et al*., 2014) with lower biomass investment in root development in mycorrhizal plants (Marschner & Dell, 1994). While mycorrhizal fungi found in many crop plants do not act as saprotrophs, they can access nutrients bound in SOM, and thereby promote its decomposition, through several strategies, mainly direct enzymatic breakdown, oxidation mechanisms, and stimulation of heterotrophic microbes through provision of plant-derived C to the rhizosphere (Frey, 2019). The latter may be particularly important in maize, as arbuscular mycorrhizal fungi do not have the capacity for direct enzymatic breakdown of SOM (Frey, 2019).

Additionally, we observed exceptions to the overall positive relationship between SOM-C mineralisation and root diameter, in that hybrids had the largest root diameter but did not induce highest cumulative SOM-C mineralisation (as compared with lines from the physiology breeding program which overall had large diameter and high cumulative SOM-C mineralisation). Similarly, most genotypes with the largest cumulative root-derived CO_2 efflux

(from root respiration and microbial mineralisation of rhizodeposits) did not have higher cumulative SOM-C mineralisation. This strongly suggests that plant factors besides quantity of root C deposition, such as intraspecies variation in rhizodeposit composition (that can differentially promote or inhibit microbial activity, Paterson *et al*., 2007) or mycorrhizal symbiosis (Frey, 2019), likely also influenced SOM mineralisation.

Genotype by soil management history interactions on nitrification, and the relationship between SOM mineralisation and nitrification

The effects of plants, soil management history and microbial properties on SOM-C mineralisation *versus* gross nitrification are synopsized in Fig. 5. Increasing context-specific understanding of these effects will be vital for designing more sustainable cropping systems.

Studies indicate that variations in nitrification rate exist between plant genotypes (e.g., in ryegrass, clover or forage rape, Bowatte *et al*., 2016) and management practices (e.g., Bi *et al*., 2017). However, there is lack of understanding of plant genotype by management interactions on nitrification. In this study gross nitrification was higher in the NT soil with residue retention, with genotypes differentially affecting gross nitrification in the NT soil but not in the CT soil. It is likely that NT with residue retention history increased nitrification by modifying the soil environment, providing a source of labile SOM to microbial communities and, in turn, maintaining the supply of NH_4^+ (due to decomposition of plant residues) for nitrification. That NH_4^+-N concentration was lower in NT soil compared to CT soil could be due to greater nitrification in the NT soil with residue retention depleting NH_4^+ in soil over the study period, consistent with the observed high concentration of NO_3^- in this soil compared to the CT soil. This is also consistent with bacterial *amoA* detected in NT soil, but which was below the detection limit in CT soil, highlighting the importance of NT and residue management for the abundance of nitrifier communities (e.g., as hypothesized above). This supports our second hypothesis that the influence of maize germplasm on nitrification rates and associated microbial gene abundances would vary as a function of soil management history. However, bacterial 16S gene abundance was not affected by soil management history, consistent with Ng *et al*. (2012) who found that NT did not alter bacterial abundance during a very early vegetative stage of wheat growth.

509 Notably, there was a strong relationship between genotypic effects on SOM-C
510 mineralisation in CT soil (experiment one) and gross nitrification in NT soil (experiment two).
511 As SOM-C mineralisation and gross nitrification were measured using soils with contrasting
512 management history, care should be taken to derive conclusions based on this relationship.
513 However, this relationship supports the positive impact of residue retention on N-supply to the
514 total plant-available N pool. Moore *et al*. (2020) showed that in soil environments dominated
515 with leaf litter, even small amounts of root C inputs could significantly stimulate microbial
516 decomposition of complex C compounds. Surey *et al*. (2020) also demonstrated the importance
517 of organic matter inputs on soil N cycling. Furthermore, in previous ^{13}C and ^{15}N tracer studies
518 it has been shown that rhizodeposition-induced mineralisation of plant residues (Mwafulirwa
519 *et al*., 2017) and native SOM (Murphy *et al*., 2015) can act to supply N for plant uptake.
520 Compared with genotypic variation, soil management history had a stronger effect on
521 gross nitrification, with a significant interaction between genotype and soil management
522 history. That there was no significant change in gross nitrification with planting for all
523 genotypes in the CT soil and for genotypes 30G19 and ATZTRI in the NT soil, and that gross
524 nitrification varied with soil management history for all genotypes but not hybrid maize 30G19
525 highlights the importance of a complimentary approach of crop breeding and management
526 practices that retain organic matter or crop residues on cropland. Residue retention on cropland
527 and NT not only can build SOM stocks and increase nitrification but can also decrease nutrient
528 loss including NO_3^- through reduced leaching (Daryanto *et al*., 2017). In this study gross
529 nitrification was not related to bacterial *amoA* or 16S gene copy numbers in common with other
530 studies. For example, Mao *et al*. (2011) investigating changes in N transforming bacteria and
531 archaea in soil during establishment of bioenergy crops (maize, switchgrass, *Miscanthus x*
532 *giganteus* and mixed tallgrass prairie) also showed that nitrification was not significantly
533 related to the quantity of bacterial *amoA*, and that the archaea community was the major
534 ammonia oxidiser. The archaeal *amoA* gene was not measured in our study as fertilized soils
535 are typically dominated by bacterial ammonia oxidisers (e.g., Shen *et al*., 2011). Our finding
536 of greater bacterial gene copy numbers in soil planted with the hybrid 30G19, especially for
537 16S, may be due to larger plants and larger root diameter leading to greater rhizodeposition.
538 High growth rate of the hybrid variety 30G19 (discussed below) is also in line with the
539 interaction of maize genotype by time being important for 16S gene copy number, although
540 this interaction was not significant for *amoA* gene copy number. That bacterial 16S and *amoA*

gene abundances did not significantly change with time may be due to uniform fertilizer application across treatments, short experiment duration or the fact that autotrophic ammonia oxidisers do not rely solely on C deposition from plants.

Implications for maize breeding

There is increasing attention on plant genotype-specific stimulation of microbial activity in agricultural soil and the impacts on SOM priming (e.g., Mwafulirwa *et al*., 2016, 2017; Yin *et al*., 2019), although the underlying factors have mostly not been elucidated. The large genotypic variation in traits associated with SOM mineralisation observed here suggests that this functional process could be exploited within breeding programs targeting low-input environments. The measurement of SOM mineralisation via continuous ^{13}C-labelling requires dedicated facilities and is too costly to be realistically incorporated routinely into breeding programs. However, SOM mineralisation was significantly related to root morphological traits of root diameter and root length which, therefore, could be used as cheaper proxy traits for SOM mineralisation, especially for context-specific breeding (e.g., under NT and residue retention with low inorganic fertilizer inputs). Lines from the tropical and physiology breeding programs in Mexico were associated with highest C mineralisation rates and could be explored for use as donors for breeding.

In this study, hybrid 30G19 had the largest root and shoot biomass, whereas ATZTRI (from the highland breeding program) had the smallest root and shoot biomass, with size of plants affecting nutrient uptake and residual concentrations of nutrients in soil. For instance, concentrations of soil NH_4^+-N and NO_3^--N were lowest after growth of 30G19 and highest for ATZTRI. This plant biomass data and the significant interaction effect of genotype by time on shoot biomass also show genotypic differences in plant growth rates. It is notable that soil management history influenced shoot biomass but not root biomass. On one hand, shoot biomass increase in the NT soil with residue retention was clearly a consequence of direct nutrient availability in soil. On the other hand, the increase could be explained by a removal of the need to invest extra energy and biomass into roots due to the increased nutrient availability in this soil. Taken together, these findings indicate that maize root and shoot growth can be plastic in response to nutrient status of soil (Junaidi *et al*., 2018), and that their response to

572 management can also depend on nutrient status of soil and plant genotype. This indicates
573 another potential selection/breeding target for specific managements.
574
575 **Conclusions**
576
577 Our study revealed maize genotype-specific effects on SOM-C mineralisation and
578 corresponding effects on nitrification. It provides the first demonstration that SOM
579 mineralisation increases with maize root diameter and decreases with increasing root length
580 and specific root length. Therefore, there is the potential in maize breeding programs for control
581 of SOM mineralisation using root diameter and root length as proxy traits of belowground C-
582 deposition driving this functional process. Lines from the tropical and physiology breeding
583 programs in Mexico were associated with highest C mineralisation and could be utilized as
584 donor parents. Interaction effect of maize genotype by soil management history on nitrification
585 was observed. NH_4^+-N and NO_3^--N concentrations in soil were lower and higher, respectively,
586 in the NT soil with residue retention due to greater nitrification in this soil (compared to the
587 CT soil with residue removal). Total available N was higher in the NT soil, likely due to its
588 history of higher organic matter inputs. Combining management practices that build/replenish
589 SOM and selection of genotypes that enhance SOM mineralisation and organic N
590 transformations could help ensure sustainable production and future food security of
591 smallholder farmers in southern Africa. The extent to which varieties that enhance SOM
592 cycling could enhance soil N supply under residue retention or aggravate SOM depletion in
593 absence of residue retention requires further investigation.
594
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Author Contributions

All authors conceptualised the project and contributed to the data interpretation and writing of this manuscript. LM conducted the experiments and analyses and developed the figures and tables. EB, CT, EP, TD and JC were awarded the funding for this research.

Data Availability

The data used for this study is held in University of Edinburgh and CIMMYT repositories and can be made available on request.

Declaration on Conflict of Interest

All authors declare no conflicts of interest with the current study.

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Tables

Table 1. Origin of maize lines used in experiment one. Cairns *et al*. (2013) and Wen *et al*. (2011) provide more detailed information of the maize lines, breeding programs and breeding targets.

Breeding program	Target of breeding program	Number of lines
Zimbabwe	Drought and low N stress tolerance	31
Nigeria	Drought and striga tolerance	3
Colombia	Soil acidity	11
Highland	Yield potential	3
Entomology	Pest resistance	7
Subtropical	Yield potential	9
Tropical	Yield potential	19
Physiology	Drought and low N stress tolerance	14
Seed companies*	-	8

* Hybrid varieties (from commercial seed companies) adapted to local conditions were included.

Table 2. Selected maize lines used in experiment two. Selection was based on ranking of 105 maize lines and varieties across the range of variation in soil organic matter (SOM) C mineralisation measured in experiment one, as SOM-derived surface soil CO_2-C efflux (mean ± 1SEM). Cairns *et al*. (2013) and Wen *et al*. (2011) provide more detailed information of the maize lines.

Entry number of maize line	Breeding program	Germplasm	Short code	Pedigree	Cumulative SOM-derived CO_2-C (µg C g^{-1} soil)	Rank
211	Tropical	Line	CL-G18	CL-G1837=G18SeqC2-F141-2-2-1-1-1-2-##-2	29.72 ± 9.78	1
24	Zimbabwe	Line	CML444x	[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-2	21.74 ± 5.15	13
-	Seedco*	Hybrid	SC513	-	20.42 ± 2.29	27
-	Physiology	Line	LPSF64	La Posta Seq C7-F64-2-6-2-2	17.45 ± 0.95	63
80	Highland		ATZTRI	(A.T.Z.T.R.L.BA90 5-3-3P-1P-4P-2P-1-1-1-B x G9B C0 R.L.23-1P-2P-3-2P-3-2P-1P-B-B-B)-B-76TL-1-2-4	16.99 ± 0.00	70
-	Pioneer*	Hybrid	30G19	-	16.19 ± 0.28	79
135	Sub-tropical	Line	95S43S	95S43SR HG"A"-94-1-1-1	12.37 ± 2.63	105

* Commercial seed companies.

Table 3. Variance analysis for plant traits and soil parameters measured in experiment two. Significant *P*-values ($P < 0.05$) are shown in bold. df, degrees of freedom.

Source of variation	Plant biomass *P*-values			Soil characteristics and gross nitrification *P*-values					
	df	Root biomass (g)	Shoot biomass (g)	df	NH_4^+-N (µg N g^{-1} soil)	NO_3^--N (µg N g^{-1} soil)	16S gene copies g^{-1} soil	*amoA* gene copies g^{-1} soil*	Gross nitrification (µg N g^{-1} soil day^{-1})†
Maize genotype	6	**<.001**	**<.001**	7	**<.001**	**<.001**	**<.001**	**0.025**	**0.017**
Management history	1	0.057	**0.026**	1	**<.001**	**<.001**	0.117	-	**<.001**
Harvest time	1	**<.001**	**<.001**	1	**<.001**	**<.001**	0.607	0.997	-
Genotype x management history	6	0.955	0.261	7	**<.001**	**<.001**	0.624	-	**0.022**
Genotype x time	6	0.206	**0.047**	7	**<.001**	0.475	**0.007**	0.418	-
Management history x time	1	0.500	0.308	1	**<.001**	0.187	0.204	-	-
Genotype x management history x time	6	0.603	0.454	7	0.098	0.461	0.108	-	-

933 * *amoA* was detected only in the no-tillage soil with crop residue retention, as it was below the
934 detection limit in the conventional tillage soil with residue removal.
935 † Gross nitrification was measured at a single time point, i.e., at the first harvest time (day 23 after
936 planting).
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957 **Figure Captions**
958 **Fig. 1.** Significant ($P < 0.05$) relationships between cumulative soil organic matter (SOM) C
959 mineralized, measured as surface soil CO_2-C efflux, and root diameter (**a**), root length (**b**) and specific
960 root length (**c**), and the relationship between specific root length and root diameter (**d**) in experiment
961 one. Symbols represent different germplasm sources/breeding programs: **plus**, Colombia; **open circle**,
962 Entomology; **star**, Highland; **dot**, Hybrids; **open square**, Nigeria; **filled square**, Physiology; **filled**
963 **triangle**, Sub-tropical; **filled inverted triangle**, Tropical; **filled diamond**, Zimbabwe.
964

Fig. 2. Principal component analysis ordination of the distribution of maize genotypes based on plant traits and root-derived C and soil organic matter (SOM) C mineralized. Symbols represent different germplasm sources: **plus**, Colombia; **open circle**, Entomology; **star**, Highland; **dot**, Hybrids; **open square**, Nigeria; **filled square**, Physiology; **filled triangle**, Sub-tropical; **filled inverted triangle**, Tropical; **filled diamond**, Zimbabwe. Red symbols of the corresponding germplasm source show scores of the selected individual maize genotypes. Solid green lines show the loading (vectors) of the measured traits. The 95% ellipse is shown over the convex hull.

Fig. 3. Interactive effects of maize genotype and soil management history on gross nitrification rates in conventional tillage (CT) soil with crop residue removal and no-tillage (NT) soil with residue retention (**a**) and relationship between soil organic matter (SOM) C mineralization in CT soil *versus* gross nitrification in NT soil (**b**). Letters indicate significant ($P < 0.05$) differences in gross nitrification between maize genotypes or soil management history. Bars show ±1 SEM.

Fig. 4. Interactive effects of maize genotype and soil management history (conventional tillage (CT) with crop residue removal *versus* no-tillage (NT) with residue retention) on soil mineral N (NH_4^+-N and NO_3^--N: **a** and **b**, respectively), and maize genotype and time of sampling on 16S gene copy number in soil (**c**) in experiment two. Letters indicate significant ($P < 0.05$) differences between treatments. Bars show ±1 SEM.

Fig. 5. Effects of maize plant, soil and microbial properties on soil organic matter (SOM) mineralization (experiment one) and nitrification (experiment two) and the impact of no-tillage (NT) soil with residue retention on nitrification (experiment two). Upward pointing arrows indicate a positive effect, downward pointing arrows indicate a negative effect and horizontal arrows indicate no effect. Question marks designate lack of information, i.e., the effect was not assessed in the respective experiment.

Supporting Information

Table S1. Traits measured in experiment one for 105 maize lines and hybrids.

Table S2. Root-derived CO_2-C surface soil efflux rates measured at days 16, 23 and 29 after planting.

998 **Table S3**. Soil organic matter-derived CO_2-C surface soil efflux rates measured at days 16, 23 and 29
999 after planting.
1000
1001 **Fig. S1**. Maize root and shoot biomass, ammonium and nitrate concentrations in soil and
1002 bacterial *amoA* gene copy numbers in soil as measured in experiment two.
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1004 **Fig. S2**. Significant relationships between plant traits and cumulative soil organic matter C mineralized
1005 as measured in experiment one.
1006
1007 **Methods S1**. Calculations for mineralisation and nitrification.

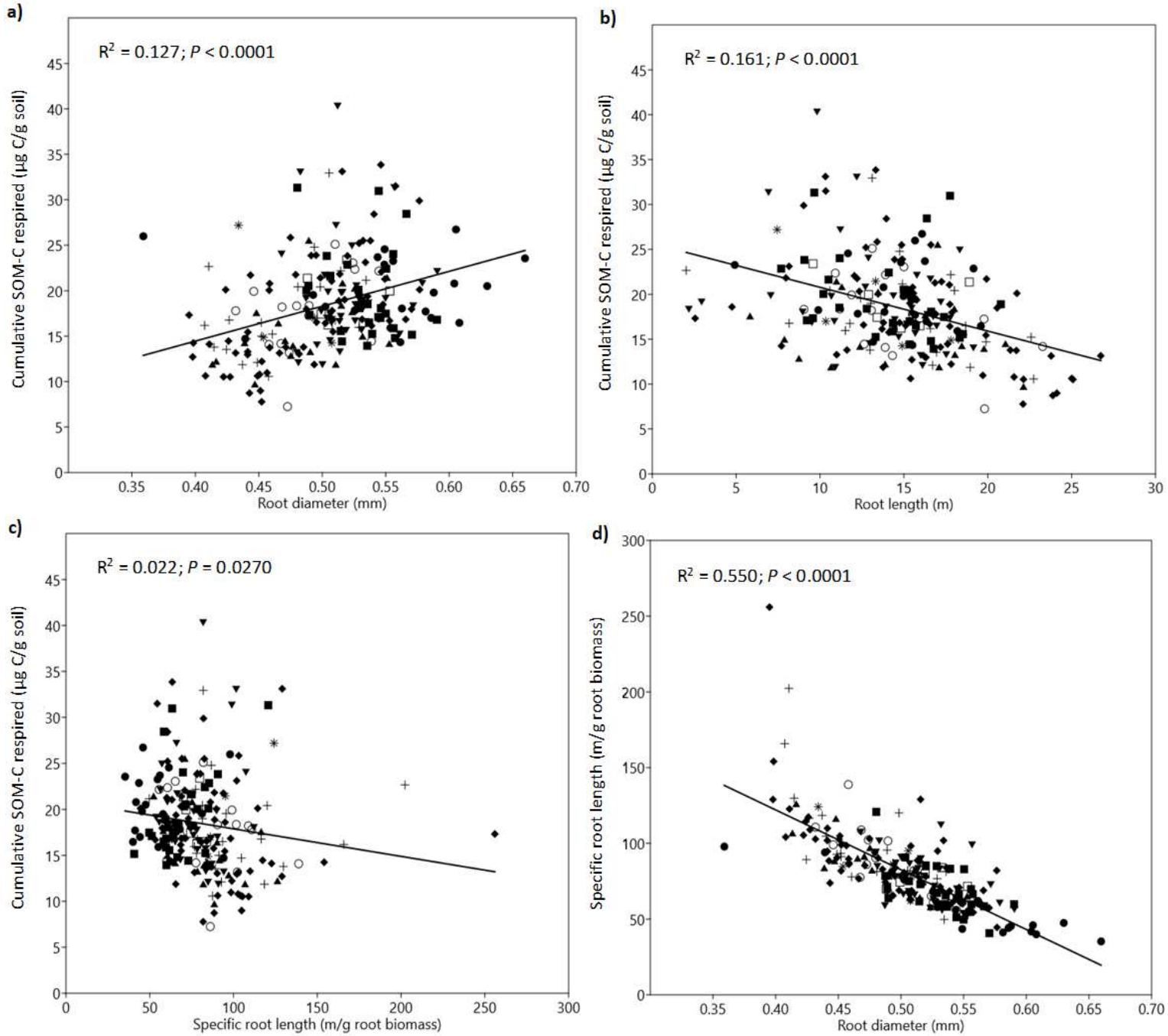
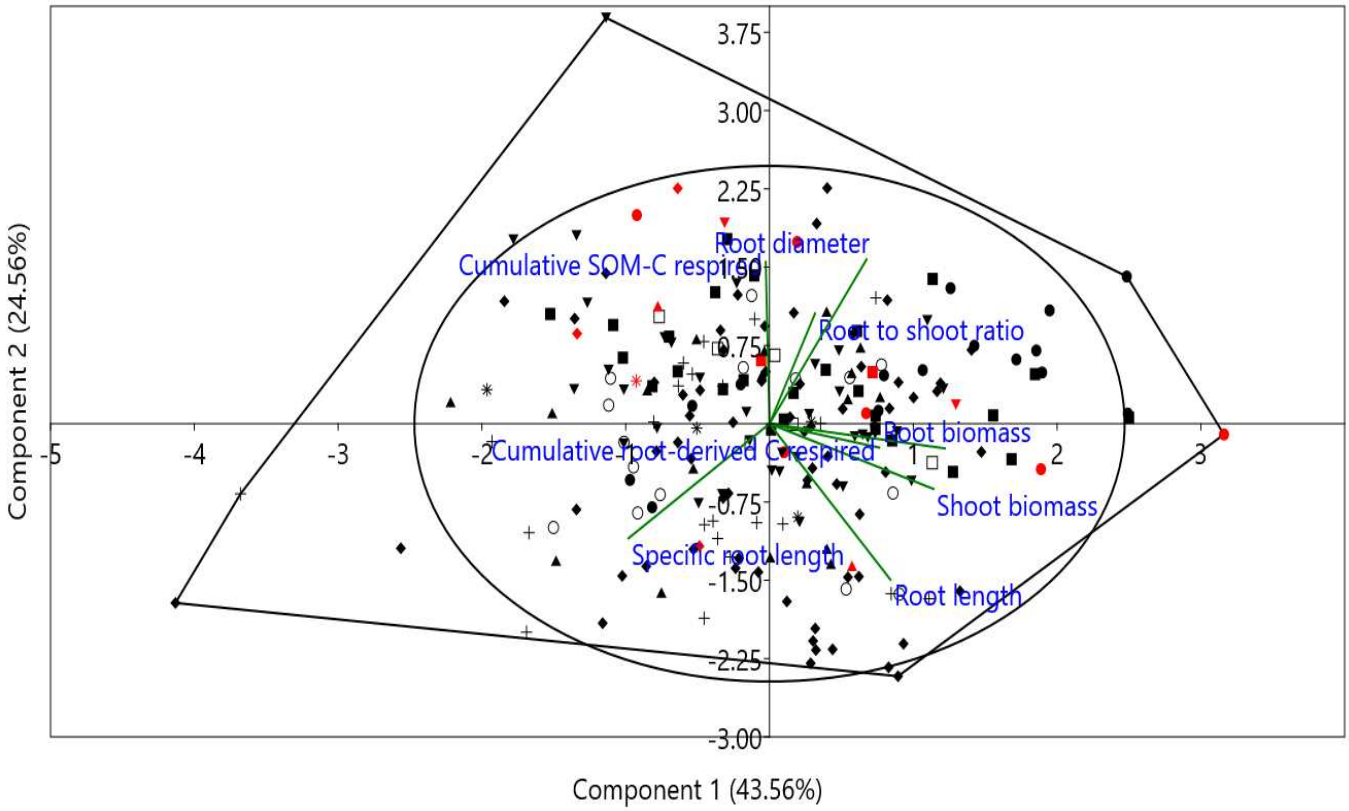


Fig. 1. Significant ($P < 0.05$) relationships between cumulative soil organic matter (SOM) C mineralized, measured as surface soil CO_2-C efflux, and root diameter (**a**), root length (**b**) and specific root length (**c**), and the relationship between specific root length and root diameter (**d**) in experiment one. Symbols represent different germplasm sources/breeding programs: **plus**, Colombia; **open circle**, Entomology; **star**, Highland; **dot**, Hybrids; **open square**, Nigeria; **filled square**, Physiology; **filled triangle**, Sub-tropical; **filled inverted triangle**, Tropical; **filled diamond**, Zimbabwe.



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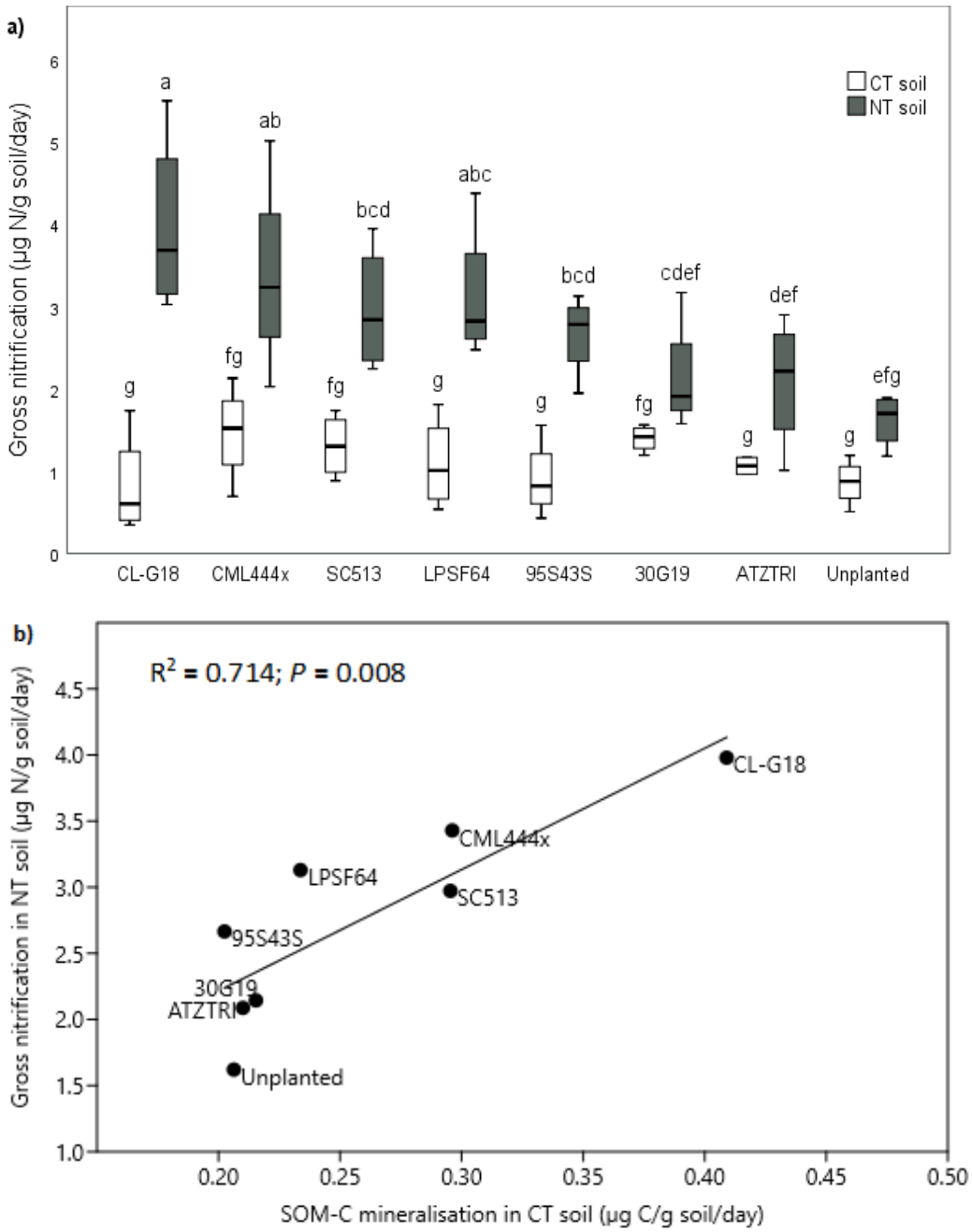

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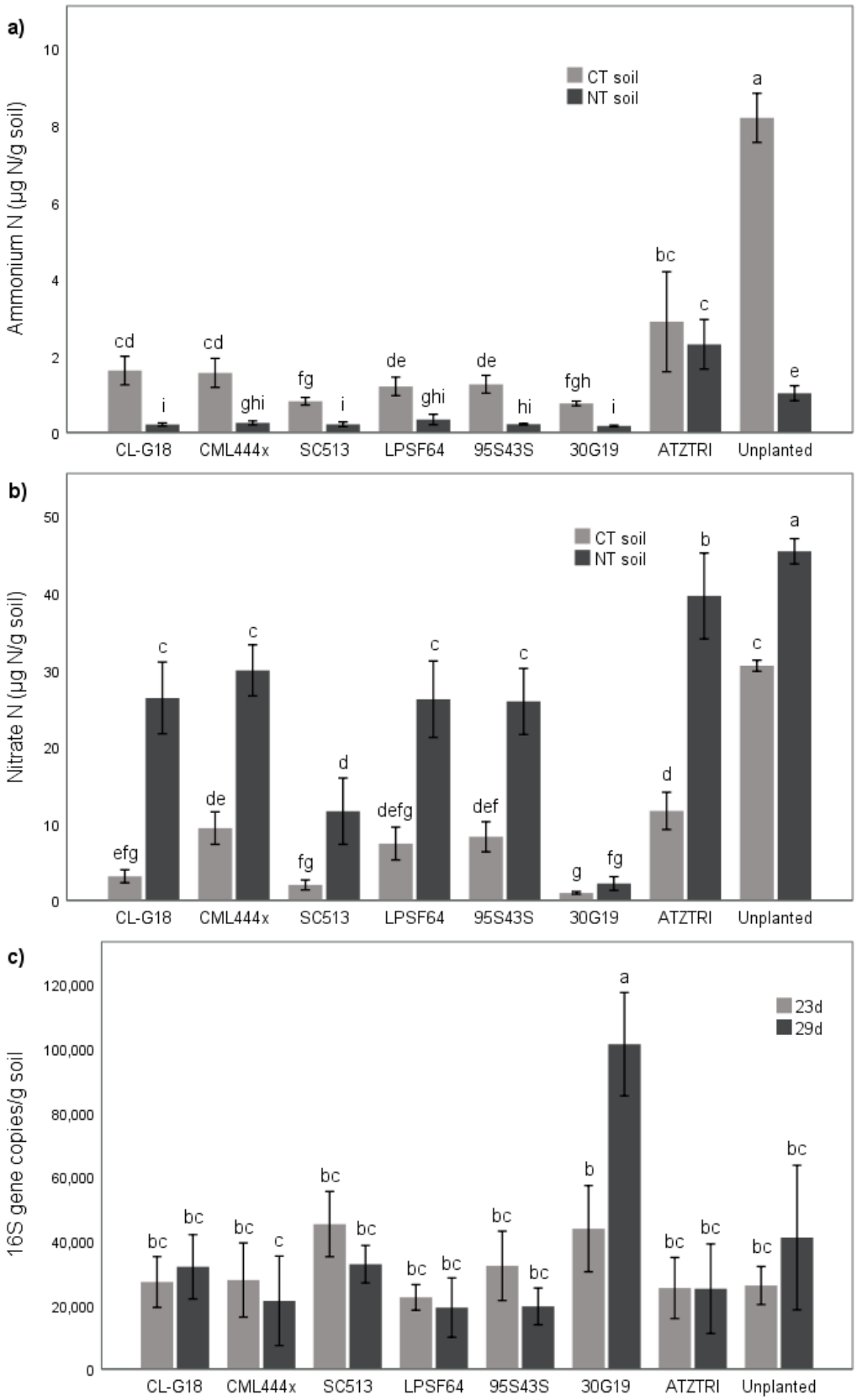

Fig. 4. Interactive effects of maize genotype and soil management history (conventional tillage (CT) with crop residue removal *versus* no-tillage (NT) with residue retention) on soil mineral N (NH_4^+-N and NO_3^--N: **a** and **b**, respectively), and maize genotype and time of sampling on 16S gene copy number in soil (**c**) in experiment two. Letters indicate significant ($P < 0.05$) differences between treatments. Bars show ±1 SEM.

Factors	*Effects on soil processes*	
Plant, soil and microbial properties:	**SOM-C mineralization**	**Gross nitrification**
Shoot biomass	→	→
Root biomass	→	→
Root-to-shoot ratio	→	→
Root diameter	↑	?
Root length	↓	?
Specific root length	↓	?
Soil ammonium	?	→
Soil nitrate	?	→
Bacterial 16S gene copy number	?	→
Bacterial amoA gene copy number	?	→
NT soil with residue retention	?	↑

Fig. 5. Effects of maize plant, soil and microbial properties on soil organic matter (SOM) mineralization (experiment one) and nitrification (experiment two) and the impact of no-tillage (NT) soil with residue retention on nitrification (experiment two). Upward pointing arrows indicate a positive effect, downward pointing arrows indicate a negative effect and horizontal arrows indicate no effect. Question marks designate lack of information, i.e., the effect was not assessed in the respective experiment.

New Phytologist

***New Phytologist* Supporting Information**

Article title: **Genotypic variation in maize (*Zea mays*) influences rates of soil organic matter mineralisation and gross nitrification**

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Article acceptance date: N/A

The following Supporting Information is available for this article:

Fig. S1 Maize root and shoot biomass, ammonium and nitrate concentrations in soil and bacterial *amoA* gene copy numbers in soil as measured in experiment two.

Fig. S2 Significant relationships between plant traits and cumulative soil organic matter C mineralized as measured in experiment one.

Table S1 Traits measured in experiment one for 105 maize lines and hybrids.

Table S2 Root-derived CO_2-C surface soil efflux rates measured at days 16, 23 and 29 after planting.

Table S3 Soil organic matter-derived CO_2-C surface soil efflux rates measured at days 16, 23 and 29 after planting.

Methods S1 Calculations for mineralisation and nitrification.

Fig. S1 Maize root and shoot biomass, ammonium and nitrate concentrations in soil and bacterial *amoA* gene copy numbers in soil as measured in experiment two. (a) Effect of maize genotype on root biomass; (b) effect of maize genotype on shoot biomass; (c) interaction effect of maize genotype and time on shoot biomass; (d) effect of maize genotype on ammonium N; (e) effect of maize genotype on nitrate N; (f) effects of maize genotypes on bacterial *amoA* gene copy numbers in no-tillage soil with crop residue retention.

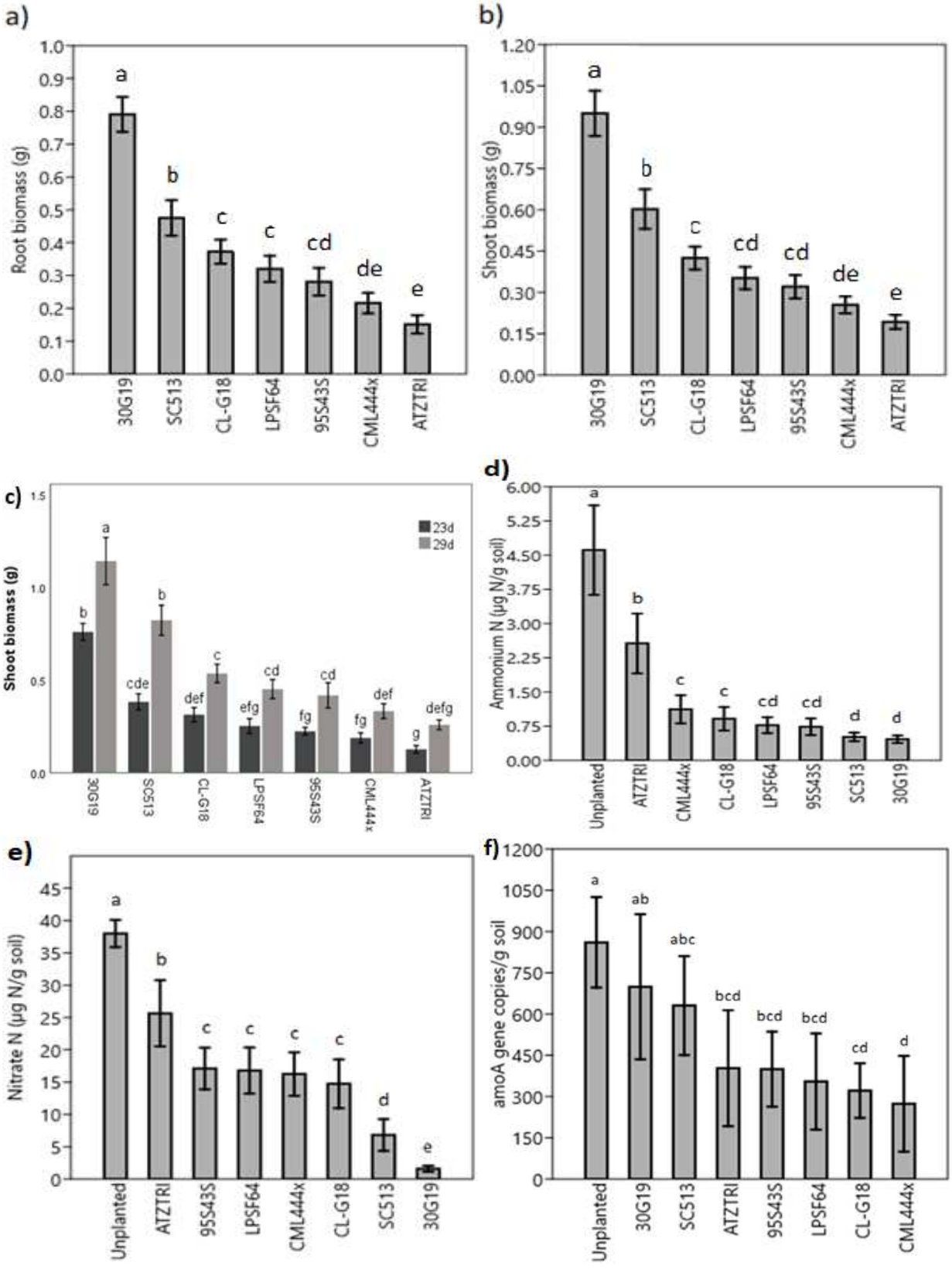

Fig. S2 Significant ($P < 0.05$) relationships between cumulative root-derived C mineralized and cumulative soil organic matter (SOM) C mineralized (a), shoot biomass (b), root biomass (c), root length (d) and specific root length (e) in experiment one. Symbols represent different germplasm sources/breeding programs: **plus**, Colombia; **open circle**, Entomology; **star**, Highland; **dot**, Hybrids; **open square**, Nigeria; **filled square**, Physiology; **filled triangle**, Sub-tropical; **filled inverted triangle**, Tropical; **filled diamond**, Zimbabwe.

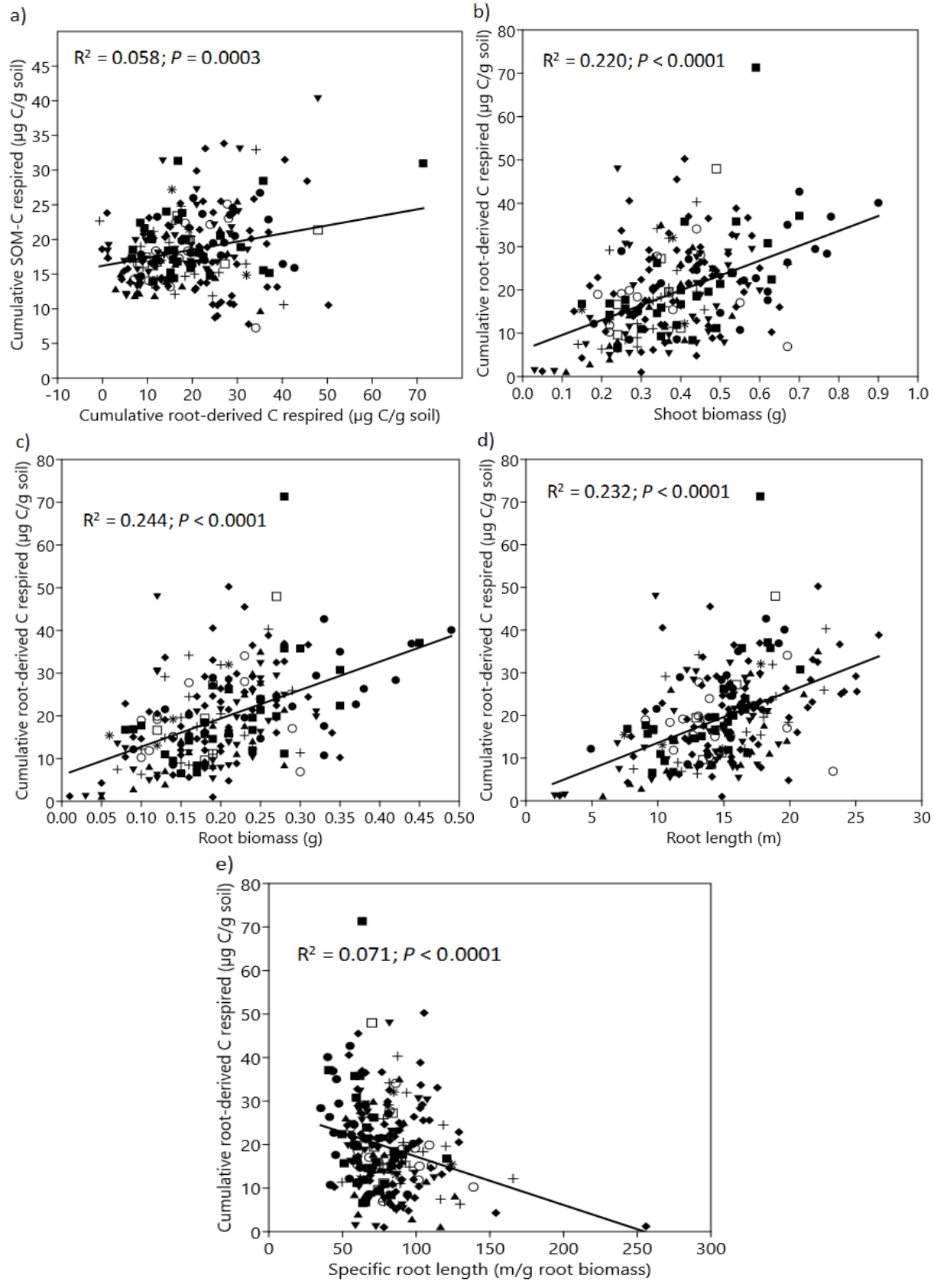

Table S1 Traits measured in experiment one for 105 maize lines and hybrids.

Entry	Pedigree	Cumulative root-derived CO_2-C (µgC/g dry soil)	Cumulative SOM-derived CO_2-C (µgC/g dry soil)	Shoot biomass (g)	Root biomass (g)	Total plant biomass (g)	Root to shoot biomass ratio	Root Length (m)	Specific root length (m g^{-1} root biomass)	Average root diameter (mm)
A) Zimbabwe										
1	[CML444/CML395//DTPWC8F31-4-2-1-6]-2-1-1-1	18.477	19.810	0.312	0.179	0.491	0.550	15.919	102.630	0.500
2	[SYN-USAB2/SYN-ELIB2]-12-1-1-2	17.646	14.423	0.637	0.329	0.966	0.503	19.622	66.440	0.535
3	[(CML395/CML444)-B-4-1-3-1-B/CML395//DTPWC8F31-1-1-2-2]-5-1-2-2	0.577	17.959	0.071	0.029	0.099	0.327	2.479	175.460	0.477
6	00SADVEA-#-28-1-2-1-1-1-2-3	18.210	12.792	0.377	0.209	0.586	0.530	18.252	94.390	0.519
7	CIMCALI8843/S9243-BB-#-B-5-1-BB-2-3-1	26.030	19.219	0.322	0.179	0.501	0.539	16.871	104.150	0.477
8	CIMCALI8843/S9243-BB-#-B-5-1-BB-2-3-2	31.319	16.571	0.396	0.259	0.654	0.592	20.185	85.500	0.472
9	CIMCALI8843/S9243-BB-#-B-5-1-BB-2-3-3	6.968	17.013	0.216	0.104	0.319	0.433	9.726	121.070	0.471
10	CIMCALI8843/S9243-BB-#-B-5-1-BB-2-3-4	12.281	17.144	0.352	0.169	0.521	0.456	16.070	107.800	0.492
11	CIMCALI8843/S9243-BB-#-B-5-1-BB-4-1-3	25.007	13.545	0.542	0.239	0.781	0.421	21.027	94.520	0.471
12	CIMCALI8843/S9243-BB-#-B-5-1-BB-4-3-3	19.249	20.644	0.360	0.179	0.539	0.499	16.420	98.910	0.475
13	CIMCALI8843/S9243-BB-#-B-5-1-BB-4-3-4	27.400	17.193	0.395	0.214	0.609	0.543	19.531	94.620	0.476
14	[[CML198/ZSR923S4BULK-2-2-X-X-X-X-1-BB]-3-3-1-1-B/CML395//DTPWC8F31-1-1-2-2-BBBB]-4-2-5-1-1-B-2-2-1	32.173	18.615	0.406	0.229	0.634	0.570	18.515	84.050	0.475
17	[CML312/CML445//[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-1	14.708	14.785	0.420	0.179	0.599	0.411	15.355	100.130	0.481
19	[CML312/CML445//[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-2	25.845	17.214	0.466	0.244	0.709	0.520	14.133	61.830	0.536
20	[CML312/CML444//[DTP2WC4H255-1-2-2-BB/LATA-F2-138-1-3-1-B]-1-3-2-3-B]-2-1-2	20.646	13.822	0.502	0.224	0.726	0.429	17.572	85.790	0.534
21	[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-BBBB]-1-5-1-1-2	33.700	21.106	0.492	0.259	0.751	0.522	17.547	73.010	0.531
22	P501SRc0-F2-47-3-2-1	20.926	14.737	0.420	0.209	0.629	0.495	16.764	85.440	0.509
24	[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-2	13.045	21.743	0.256	0.144	0.399	0.512	12.247	94.080	0.529
25	[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-1	16.715	21.023	0.442	0.244	0.686	0.563	16.033	71.180	0.492
28	CML489/CML444//ZM521B-66-4-1-1-1-BB]-7-3-1	29.769	20.816	0.465	0.249	0.714	0.561	17.482	72.630	0.516
29	02SADVL2B-#-17-1-1	32.536	16.405	0.511	0.274	0.784	0.565	18.595	65.000	0.516
31	[CML440/[[[K64R/G16SR]-39-1/[K64R/G16SR]-20-2]-5-1-2-B*4/CML390]-B-38-1-B-7-#-B//ZM303c1-243-3-B-1-1-B]-2-1	20.236	19.480	0.455	0.239	0.694	0.526	16.989	73.710	0.510
33	[CML144/[CML144/CML395]F2-5sx]-1-3-1-3	22.877	18.337	0.492	0.254	0.746	0.502	17.218	75.630	0.536
34	[CML198/ZSR923S4BULK-2-2-X-X-X-X-1-BB]-3-3-1-1-2	13.677	24.668	0.380	0.213	0.594	0.583	16.085	73.660	0.519

36	ZEWAc1F2-254-2-1-B-1	13.166	14.712	0.375	0.159	0.534	0.413	12.116	89.200	0.507
37	CML373	23.010	14.817	0.455	0.199	0.654	0.431	15.148	81.840	0.500
38	[CML389/CML176]-B-29-2-2-6-1	18.590	14.752	0.342	0.189	0.531	0.535	15.607	92.920	0.494
40	[CML144/[CML144/CML395]F2-8sx]-1-2-3-2	10.617	17.810	0.245	0.124	0.369	0.558	9.554	85.680	0.516
41	[GQL5/[GQL5/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-4sx]-11-3-1-1	33.483	21.235	0.387	0.214	0.601	0.569	14.923	76.470	0.533
42	[CML150/CML373]-B-2-2	19.146	18.779	0.395	0.229	0.624	0.590	15.071	69.780	0.544
44	CML444	20.108	23.016	0.471	0.254	0.724	0.500	15.508	86.730	0.544
B) Nigeria										
45	1368	13.142	20.416	0.245	0.148	0.394	0.625	11.843	77.110	0.503
48	4001	37.579	18.921	0.411	0.229	0.639	0.547	16.252	76.960	0.525
49	KU1409-SR	15.305	18.095	0.390	0.183	0.574	0.481	14.215	74.810	0.522
C) Colombia										
52	CLA135	20.665	18.699	0.580	0.269	0.849	0.467	19.958	77.600	0.504
57	CLA18	14.250	19.160	0.352	0.199	0.551	0.546	15.742	87.940	0.485
60	CLA37	3.405	19.714	0.117	0.059	0.176	0.350	4.986	159.390	0.444
62	CLA44	19.676	15.702	0.362	0.164	0.526	0.429	15.581	106.970	0.488
65	CLA91	20.207	17.737	0.330	0.189	0.519	0.578	15.626	87.410	0.511
66	CLA99	10.584	16.070	0.305	0.134	0.439	0.431	13.813	121.240	0.485
67	CLA105	23.766	17.556	0.307	0.179	0.486	0.567	15.136	93.040	0.486
68	CLA106	6.600	15.265	0.267	0.144	0.411	0.509	12.275	104.130	0.488
69	CLA113	25.821	15.864	0.425	0.289	0.714	0.690	18.593	68.560	0.513
72	CLA155	25.149	22.519	0.372	0.189	0.561	0.485	14.805	87.360	0.503
73	CLA156	20.054	17.704	0.427	0.194	0.621	0.441	18.027	105.640	0.501
D) Highland										
80	(A.T.Z.T.R.L.BA90 5-3-3P-1P-4P-2P-1-1-1-B x G9B C0 R.L.23-1P-2P-3-2P-3-2P-1P-B-B-B)-B-76TL-1-2-4	13.070	16.991	0.256	0.131	0.388	0.546	12.251	86.210	0.474
82	(A.I.Z.T.V.C. 20-3-1-1-2-B-B x A.I.Z.T.V.C.PR93A-17-1-3-1-1-B-B)-B-14TL-1-3	14.254	22.094	0.282	0.119	0.401	0.389	10.277	109.590	0.495
83	[(P86 S.F*P.S.P.A.A x P.S.P.A.A. TL91A 44-3-1-18-2P-2-1-1-3-1) x A.I.R.L. TL91A 2(3)-1-4-2-2TL-1-1-B]-3-2-3-1	25.629	18.161	0.417	0.244	0.661	0.569	16.248	73.410	0.506
E) Entomology										
85	(200-6 x GUAT189)(51-2-1)F1-B-xP84c1 F26-2-2-4-B-2-B] F102-1-2-2-3 x [KILIMA ST94A]-30/MSV-03-2-10-B-1-B-B-xP84c1 F27-4-1-6-B-5-B]-2-2	17.075	17.465	0.251	0.119	0.369	0.487	11.298	99.210	0.472
88	CML311/MBR C2 Bc F41-2	18.076	19.506	0.487	0.269	0.756	0.540	16.100	64.150	0.539
89	CML311/MBR C2 Bc F4-1	11.181	14.318	0.502	0.259	0.761	0.534	16.986	69.070	0.522
101	P590 C7 Blancos F27-1-1-2	16.725	17.772	0.385	0.194	0.579	0.497	14.428	83.730	0.516
109	[M37W/ZM607#bF37sr-2-3sr-6-2-X]-8-2-X-1-BB-B-xP84c1 F27-4-3-3-B-1-B] F29-1-1-1-7 x [KILIMA ST94A]-30/MSV-03-2-10-B-1-B-B-xP84c1 F27-4-1-6-B-5-B]-1-3-B/CML312SR]-1-1	31.054	15.155	0.381	0.194	0.574	0.497	15.283	84.000	0.506
115	[Cuba/Guad C3 F34-2-1-1-B-B-B x CML264Q]-1-1	19.014	19.596	0.242	0.124	0.366	0.477	12.428	120.210	0.499
118	[Cuba/Guad C3 F44-1-3-2-B-B-B x CML486]-1-1	13.526	18.073	0.425	0.204	0.629	0.477	14.470	83.140	0.505
F) Sub-tropical										

134	MBR C5 Bc F4-1-2-1	23.876	20.338	0.401	0.234	0.634	0.613	16.353	68.910	0.505
135	95S43SR HG"A"-94-1-1-1	21.814	13.712	0.300	0.199	0.499	0.653	14.772	74.530	0.506
136	POB.502c3 F2 9-14-1-2	13.916	16.616	0.351	0.219	0.569	0.656	15.042	71.930	0.505
137	POB.502c3 F2 26-12-1-2	14.568	15.984	0.411	0.189	0.599	0.451	16.601	95.350	0.441
143	[CML-384 X CML-176](F3)100-2-7	9.669	13.264	0.227	0.113	0.339	0.507	12.339	100.740	0.447
148	CML-322	10.695	16.380	0.266	0.153	0.420	0.592	12.749	76.370	0.501
160	90[SPMATC4/P500(SELY)]#-B-48-4	10.339	16.570	0.144	0.073	0.217	0.492	8.103	106.780	0.453
163	S87P69Q(SIYF) 131-2-2-1	7.636	15.777	0.461	0.218	0.680	0.489	16.072	67.320	0.497
166	(CML-329 X CML-287)-F2-11-1	25.591	17.984	0.421	0.203	0.625	0.496	17.412	78.340	0.495
G) Tropical										
175	CLQ-6211=P62QC6HC13-1-3-BBB-6-B-7-6-BBBB-7-9	11.012	15.975	0.471	0.223	0.695	0.485	17.187	72.200	0.483
178	CLQ-RCWQ106=(CML247 x (CLQ-6203xCL-04321)-B-7-1-2)-B-22-1-1-2	17.013	16.779	0.271	0.138	0.410	0.526	11.754	78.410	0.488
180	CML499=(CL-04345*CL-274)-B-15-1-2	11.047	22.756	0.179	0.078	0.257	0.410	8.353	90.000	0.512
181	CML269=P25STEC1F13-6-1-1	18.968	18.605	0.306	0.148	0.455	0.505	14.033	85.170	0.480
183	CL-02143 P21C6S1MH247-5-B-1-1-2	6.706	15.698	0.379	0.163	0.542	0.446	14.084	84.380	0.503
190	CLQ-RCYQ40 = (CML165 x CLQ-6203)-B-9-1-1	5.697	14.524	0.294	0.138	0.432	0.447	13.362	98.450	0.498
191	CLQ-RCYQ28=(CLQ6502*CLQ6601)-B-34-2-2	20.840	17.672	0.571	0.288	0.860	0.514	18.732	61.480	0.498
193	CL-RCY015 = (CML-285*CL-00356)-B-1-1	26.595	21.690	0.519	0.233	0.752	0.446	16.081	66.760	0.518
194	CL-RCY016= (CL-00331*CML-287)-B-6-2-3	12.233	16.898	0.439	0.248	0.687	0.561	17.468	69.860	0.544
195	CL-RCY018=(CL-03618*CML-287)-B-13-1-1	18.967	18.067	0.396	0.213	0.610	0.567	17.963	78.480	0.503
197	CL-RCY007=PIO3011F2-3-5-6-1	13.619	15.659	0.304	0.143	0.447	0.497	10.838	73.340	0.497
199	CML497=[CL-00331*v]-3-B-3-2-1	13.031	18.157	0.339	0.188	0.527	0.539	14.055	75.830	0.499
200	CL-02725=P27(FRRS)C1-248-B-1	3.108	17.994	0.149	0.088	0.237	1.064	8.385	80.160	0.477
201	CML452=Ac8328BNC6-166-1-1-1	29.001	25.266	0.351	0.198	0.550	0.580	16.254	78.390	0.494
208	CL-G1632=G16C20H144#-3-3-1	11.111	16.033	0.324	0.158	0.482	0.461	11.631	80.060	0.551
209	CL-P10201 =P102 C6 S2(B)-34-2	18.256	23.497	0.431	0.198	0.630	0.477	17.069	79.600	0.506
211	CL-G1837=G18SeqC2-F141-2-2-1-1-1-2-##-2	14.602	18.152	0.416	0.213	0.630	0.517	14.204	67.780	0.514
214	CML-423=G18C19MH100#-4-1-1	36.740	28.485	0.481	0.218	0.700	0.464	14.629	61.830	0.535
215	CML421=P31DMR#1-55-2-3-2-1	24.888	18.706	0.424	0.228	0.652	0.540	15.688	67.350	0.515
H) Physiology										
217	DTPWC9-F24-4-3-1	25.973	17.063	0.561	0.283	0.845	0.515	18.828	62.540	0.512
231	DTPYC9-F143-5-4-1-2	51.053	24.933	0.519	0.318	0.837	0.624	19.392	58.880	0.540
232	DTPYC9-F11-2-3-1-2	29.854	21.623	0.444	0.198	0.642	0.436	14.381	70.730	0.524
238	DTPYC9-F46-1-2-1-2	8.865	22.029	0.349	0.138	0.487	0.390	12.403	86.780	0.519
239	DTPYC9-F143-1-6-1	19.560	20.950	0.491	0.258	0.750	0.536	17.393	63.180	0.524
253	La Posta Seq C7-F31-2-3-1-1	15.793	19.126	0.439	0.253	0.692	0.590	14.303	56.730	0.512
269	DTPWC9-F2-3-2-1	11.237	15.877	0.399	0.198	0.597	0.505	16.134	78.970	0.514
283	DTPYC9-F72-1-2-1-1	16.808	17.669	0.376	0.193	0.570	0.531	14.515	71.440	0.531
284	La Posta Seq C7-F153-1-2-1-1	15.749	16.437	0.311	0.198	0.510	0.662	13.942	64.750	0.524
292	La Posta Seq C7-F153-1-1-1-1	21.933	16.834	0.516	0.323	0.840	0.630	17.348	56.010	0.513
299	La Posta Seq C7-F32-2-1-1-1	21.454	18.664	0.279	0.163	0.442	0.567	12.821	90.230	0.527
300	La Posta Seq C7-F32-2-1-1-2	16.242	24.219	0.236	0.163	0.400	0.710	10.886	60.480	0.533
301	DTPWC9-F115-1-2-1-2	15.544	23.438	0.264	0.113	0.377	0.421	9.762	81.890	0.495
302	La Posta Seq C7-F64-2-6-2-2	15.456	18.268	0.366	0.223	0.590	0.617	14.944	62.730	0.516

I) Hybrids										
303	SC513	20.736	20.425	0.451	0.219	0.669	0.519	14.291	47.520	0.542
304	PAN53	23.808	21.411	0.496	0.229	0.724	0.464	13.009	63.610	0.549
305	Pristine 601	19.553	18.916	0.601	0.354	0.954	0.516	13.551	51.830	0.607
306	ZAP61	14.395	21.914	0.364	0.173	0.537	0.473	14.775	52.810	0.434
307	PGS61	28.267	20.458	0.704	0.338	1.042	0.468	17.318	67.530	0.548
308	ZAP55	23.005	21.676	0.691	0.368	1.060	0.539	15.592	50.990	0.607
309	30G19	41.397	16.190	0.804	0.413	1.217	0.508	19.708	40.310	0.573
310	SC633	23.653	18.247	0.519	0.323	0.842	0.620	16.803	82.940	0.549
	LSD	*18.240*	*8.464*	*0.207*	*0.107*	*0.304*	*0.159*	*6.256*	*30.250*	*0.065*

Table S2 Root-derived CO2-C surface soil efflux rates (µg C g-1 soil hr-1) measured at days 16, 23 and 29 after planting.

Entry	Breeding program	Pedigree	16d	23d	29d
1	Zimbabwe	[CML444/CML395//DTPWC8F31-4-2-1-6]-2-1-1-1	0.009	0.041	0.055
2	Zimbabwe	[SYN-USAB2/SYN-ELIB2]-12-1-1-2	0.006	0.031	0.063
3	Zimbabwe	[(CML395/CML444)-B-4-1-3-1-B/CML395//DTPWC8F31-1-1-2-2]-5-1-2-2	0.000	0.000	0.004
6	Zimbabwe	00SADVEA-#-28-1-2-1-1-1-2-3	0.001	0.040	0.062
7	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-2-3-1	0.011	0.054	0.083
8	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-2-3-2	0.014	0.062	0.083
9	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-2-3-3	0.001	0.007	0.020
10	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-2-3-4	0.006	0.022	0.044
11	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-4-1-3	0.006	0.059	0.071
12	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-4-3-3	0.011	0.043	0.056
13	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-4-3-4	0.010	0.059	0.086
14	Zimbabwe	[[CML198/ZSR923S4BULK-2-2-X-X-X-X-1-BB]-3-3-1-1-B/CML395//DTPWC8F31-1-1-2-2-BBBB]-4-2-5-1-1-B-2-2-1	0.013	0.054	0.116
17	Zimbabwe	[CML312/CML445//[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-1	0.007	0.028	0.049
19	Zimbabwe	[CML312/CML445//[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-2	0.013	0.053	0.081
20	Zimbabwe	[CML312/CML444//[DTP2WC4H255-1-2-2-BB/LATA-F2-138-1-3-1-B]-1-3-2-3-B]-2-1-2	0.002	0.045	0.070
21	Zimbabwe	[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-BBBB]-1-5-1-1-2	0.022	0.060	0.109
22	Zimbabwe	P501SRc0-F2-47-3-2-1	0.013	0.034	0.072
24	Zimbabwe	[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-2	0.002	0.021	0.052
25	Zimbabwe	[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-1	0.028	0.028	0.039
28	Zimbabwe	CML489/CML444//ZM521B-66-4-1-1-1-BB]-7-3-1	0.018	0.066	0.085
29	Zimbabwe	02SADVL2B-#-17-1-1	0.019	0.082	0.085
31	Zimbabwe	[CML440/[[[K64R/G16SR]-39-1/[K64R/G16SR]-20-2]-5-1-2-B*4/CML390]-B-38-1-B-7-#-B//ZM303c1-243-3-B-1-1-B]-2-1	0.009	0.042	0.064
33	Zimbabwe	[CML144/[CML144/CML395]F2-5sx]-1-3-1-3	0.024	0.047	0.059
34	Zimbabwe	[CML198/ZSR923S4BULK-2-2-X-X-X-X-1-BB]-3-3-1-1-2	0.013	0.035	0.030
36	Zimbabwe	ZEWAc1F2-254-2-1-B-1	0.003	0.021	0.051
37	Zimbabwe	CML373	0.001	0.031	0.099
38	Zimbabwe	[CML389/CML176]-B-29-2-2-6-1	0.004	0.047	0.054
40	Zimbabwe	[CML144/[CML144/CML395]F2-8sx]-1-2-3-2	0.000	0.019	0.041
41	Zimbabwe	[GQL5/[GQL5/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-4sx]-11-3-1-1	0.012	0.066	0.112
42	Zimbabwe	[CML150/CML373]-B-2-2	0.002	0.034	0.073
44	Zimbabwe	CML444	0.004	0.046	0.064
45	Nigeria	1368	0.001	0.023	0.050
48	Nigeria	4001	0.031	0.101	0.081
49	Nigeria	KU1409-SR	0.014	0.033	0.039
52	Colombia	CLA135	0.012	0.045	0.060
57	Colombia	CLA18	0.004	0.034	0.043
60	Colombia	CLA37	0.000	0.005	0.015
62	Colombia	CLA44	0.002	0.042	0.067
65	Colombia	CLA91	0.017	0.048	0.050
66	Colombia	CLA99	0.002	0.022	0.035
67	Colombia	CLA105	0.002	0.060	0.074
68	Colombia	CLA106	0.002	0.011	0.025
69	Colombia	CLA113	0.013	0.061	0.072
72	Colombia	CLA155	0.023	0.071	0.049

73	Colombia	CLA156	0.013	0.040	0.062
80	Highland	(A.T.Z.T.R.L.BA90 5-3-3P-1P-4P-2P-1-1-1-B x G9B C0 R.L.23-1P-2P-3-2P-3-2P-1P-B-B-B)-B-76TL-1-2-4	0.000	0.011	0.051
82	Highland	(A.I.Z.T.V.C. 20-3-1-1-2-B-B x A.I.Z.T.V.C.PR93A-17-1-3-1-1-B-B)-B-14TL-1-3	0.012	0.030	0.057
83	Highland	[(P86 S.F*P.S.P.A.A x P.S.P.A.A. TL91A 44-3-1-18-2P-2-1-1-3-1) x A.I.R.L. TL91A 2(3)-1-4-2-2TL-1-1-B]-3-2-3-1	0.002	0.033	0.090
85	Entomology	(200-6 x GUAT189)(51-2-1)F1-B-xP84c1 F26-2-2-4-B-2-B] F102-1-2-2-3 x [KILIMA ST94A]-30/MSV-03-2-10-B-1-B-B-xP84c1 F27-4-1-6-B-5-B]-2-2	0.003	0.044	0.063
88	Entomology	CML311/MBR C2 Bc F41-2	0.007	0.038	0.047
89	Entomology	CML311/MBR C2 Bc F4-1	0.008	0.029	0.035
101	Entomology	P590 C7 Blancos F27-1-1-2	0.007	0.046	0.069
109	Entomology	[M37W/ZM607#bF37sr-2-3sr-6-2-X]-8-2-X-1-BB-B-xP84c1 F27-4-3-3-B-1-B] F29-1-1-1-7 x [KILIMA ST94A]-30/MSV-03-2-10-B-1-B-B-xP84c1 F27-4-1-6-B-5-B]-1-3-B/CML312SR]-1-1	0.011	0.061	0.103
115	Entomology	[Cuba/Guad C3 F34-2-1-1-B-B-B x CML264Q]-1-1	0.001	0.027	0.035
118	Entomology	[Cuba/Guad C3 F44-1-3-2-B-B-B x CML486]-1-1	0.003	0.041	0.068
134	Subtropical	MBR C5 Bc F4-1-2-1	0.019	0.042	0.040
135	Subtropical	95S43SR HG"A"-94-1-1-1	0.008	0.032	0.072
136	Subtropical	POB.502c3 F2 9-14-1-2	0.017	0.047	0.060
137	Subtropical	POB.502c3 F2 26-12-1-2	0.005	0.023	0.037
143	Subtropical	[CML-384 X CML-176](F3)100-2-7	0.003	0.026	0.035
148	Subtropical	CML-322	0.005	0.026	0.040
160	Subtropical	90[SPMATC4/P500(SELY)]#-B-48-4	0.000	0.005	0.006
163	Subtropical	S87P69Q(SIYF) 131-2-2-1	0.009	0.040	0.065
166	Subtropical	(CML-329 X CML-287)-F2-11-1	0.009	0.038	0.048
175	Tropical	CLQ-6211=P62QC6HC13-1-3-BBB-6-B-7-6-BBBB-7-9	0.002	0.048	0.071
178	Tropical	CLQ-RCWQ106=(CML247 x (CLQ-6203xCL-04321)-B-7-1-2)-B-22-1-1-2	0.006	0.030	0.039
180	Tropical	CML499=(CL-04345*CL-274)-B-15-1-2	0.003	0.030	0.056
181	Tropical	CML269=P25STEC1F13-6-1-1	0.003	0.019	0.028
183	Tropical	CL-02143 P21C6S1MH247-5-B-1-1-2	0.002	0.016	0.021
190	Tropical	CLQ-RCYQ40 = (CML165 x CLQ-6203)-B-9-1-1	0.004	0.014	0.032
191	Tropical	CLQ-RCYQ28=(CLQ6502*CLQ6601)-B-34-2-2	0.008	0.063	0.072
193	Tropical	CL-RCY015 = (CML-285*CL-00356)-B-1-1	0.008	0.065	0.064
194	Tropical	CL-RCY016= (CL-00331*CML-287)-B-6-2-3	0.008	0.040	0.047
195	Tropical	CL-RCY018=(CL-03618*CML-287)-B-13-1-1	0.010	0.035	0.047
197	Tropical	CL-RCY007=PIO3011F2-3-5-6-1	0.003	0.014	0.025
199	Tropical	CML497=[CL-00331*v]-3-B-3-2-1	0.003	0.031	0.033
200	Tropical	CL-02725=P27(FRRS)C1-248-B-1	0.008	0.035	0.047
201	Tropical	CML452=Ac8328BNC6-166-1-1-1	0.018	0.039	0.054
208	Tropical	CL-G1632=G16C20H144#-3-3-1	0.001	0.019	0.047
209	Tropical	CL-P10201 =P102 C6 S2(B)-34-2	0.007	0.033	0.053
211	Tropical	CL-G1837=G18SeqC2-F141-2-2-1-1-1-2-##-2	0.007	0.066	0.119
214	Tropical	CML-423=G18C19MH100#-4-1-1	0.020	0.056	0.077
215	Tropical	CML421=P31DMR#1-55-2-3-2-1	0.007	0.052	0.048
217	Physiology	DTPWC9-F24-4-3-1	0.049	0.125	0.131
231	Physiology	DTPYC9-F143-5-4-1-2	0.014	0.042	0.133
232	Physiology	DTPYC9-F11-2-3-1-2	0.013	0.029	0.052
238	Physiology	DTPYC9-F46-1-2-1-2	0.003	0.029	0.042
239	Physiology	DTPYC9-F143-1-6-1	0.011	0.026	0.055
253	Physiology	La Posta Seq C7-F31-2-3-1-1	0.005	0.041	0.037
269	Physiology	DTPWC9-F2-3-2-1	0.007	0.031	0.060

283	Physiology	DTPYC9-F72-1-2-1-1	0.008	0.037	0.054
284	Physiology	La Posta Seq C7-F153-1-2-1-1	0.008	0.017	0.028
292	Physiology	La Posta Seq C7-F153-1-1-1-1	0.013	0.081	0.086
299	Physiology	La Posta Seq C7-F32-2-1-1-1	0.005	0.037	0.052
300	Physiology	La Posta Seq C7-F32-2-1-1-2	0.006	0.029	0.049
301	Physiology	DTPWC9-F115-1-2-1-2	0.001	0.024	0.054
302	Physiology	La Posta Seq C7-F64-2-6-2-2	0.009	0.046	0.043
303	Hybrid	SC513	0.007	0.056	0.054
304	Hybrid	PAN53	0.028	0.049	0.059
305	Hybrid	Pristine 601	0.015	0.038	0.058
306	Hybrid	ZAP61	0.017	0.027	0.037
307	Hybrid	PGS61	0.020	0.069	0.072
308	Hybrid	ZAP55	0.019	0.052	0.059
309	Hybrid	30G19	0.044	0.102	0.089
310	Hybrid	SC633	0.026	0.059	0.055
	MEAN		*0.010*	*0.041*	*0.058*
	SE		*0.023*		

Table S3 Soil organic matter-derived CO2-C surface soil efflux rates (µg C g-1 soil hr-1) measured at days 16, 23 and 29 after planting.

Entry	Breeding program	Pedigree	16d	23d	29d
1	Zimbabwe	[CML444/CML395//DTPWC8F31-4-2-1-6]-2-1-1-1	0.044	0.040	0.028
2	Zimbabwe	[SYN-USAB2/SYN-ELIB2]-12-1-1-2	0.033	0.029	0.019
3	Zimbabwe	[(CML395/CML444)-B-4-1-3-1-B/CML395//DTPWC8F31-1-1-2-2]-5-1-2-2	0.038	0.033	0.032
6	Zimbabwe	00SADVEA-#-28-1-2-1-1-1-2-3	0.024	0.030	0.018
7	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-2-3-1	0.048	0.046	0.025
8	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-2-3-2	0.040	0.033	0.025
9	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-2-3-3	0.032	0.027	0.027
10	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-2-3-4	0.035	0.031	0.023
11	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-4-1-3	0.048	0.033	0.016
12	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-4-3-3	0.057	0.036	0.025
13	Zimbabwe	CIMCALI8843/S9243-BB-#-B-5-1-BB-4-3-4	0.034	0.039	0.024
14	Zimbabwe	[[CML198/ZSR923S4BULK-2-2-X-X-X-X-1-BB]-3-3-1-1-B/CML395//DTPWC8F31-1-1-2-2-BBBB]-4-2-5-1-1-B-2-2-1	0.047	0.036	0.023
17	Zimbabwe	[CML312/CML445//[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-1	0.037	0.030	0.017
19	Zimbabwe	[CML312/CML445//[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-2	0.037	0.035	0.026
20	Zimbabwe	[CML312/CML444//[DTP2WC4H255-1-2-2-BB/LATA-F2-138-1-3-1-B]-1-3-2-3-B]-2-1-2	0.030	0.030	0.019
21	Zimbabwe	[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-BBBB]-1-5-1-1-2	0.049	0.037	0.034
22	Zimbabwe	P501SRc0-F2-47-3-2-1	0.039	0.028	0.017
24	Zimbabwe	[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-2	0.042	0.045	0.037
25	Zimbabwe	[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-1	0.062	0.031	0.027
28	Zimbabwe	CML489/CML444//ZM521B-66-4-1-1-1-BB]-7-3-1	0.075	0.027	0.017
29	Zimbabwe	02SADVL2B-#-17-1-1	0.039	0.032	0.023
31	Zimbabwe	[CML440/[[[K64R/G16SR]-39-1/[K64R/G16SR]-20-2]-5-1-2-B*4/CML390]-B-38-1-B-7-#-B//ZM303c1-243-3-B-1-1-B]-2-1	0.046	0.037	0.028
33	Zimbabwe	[CML144/[CML144/CML395]F2-5sx]-1-3-1-3	0.052	0.029	0.023
34	Zimbabwe	[CML198/ZSR923S4BULK-2-2-X-X-X-X-1-BB]-3-3-1-1-2	0.045	0.036	0.059
36	Zimbabwe	ZEWAc1F2-254-2-1-B-1	0.030	0.031	0.022
37	Zimbabwe	CML373	0.027	0.037	0.021
38	Zimbabwe	[CML389/CML176]-B-29-2-2-6-1	0.030	0.032	0.021
40	Zimbabwe	[CML144/[CML144/CML395]F2-8sx]-1-2-3-2	0.026	0.043	0.032
41	Zimbabwe	[GQL5/[GQL5/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-4sx]-11-3-1-1	0.042	0.044	0.034
42	Zimbabwe	[CML150/CML373]-B-2-2	0.032	0.044	0.031
44	Zimbabwe	CML444	0.047	0.045	0.039
45	Nigeria	1368	0.033	0.042	0.042
48	Nigeria	4001	0.053	0.031	0.023
49	Nigeria	KU1409-SR	0.044	0.030	0.029
52	Colombia	CLA135	0.047	0.036	0.023
57	Colombia	CLA18	0.036	0.040	0.033
60	Colombia	CLA37	0.028	0.046	0.038
62	Colombia	CLA44	0.030	0.035	0.024
65	Colombia	CLA91	0.043	0.033	0.025
66	Colombia	CLA99	0.028	0.032	0.031
67	Colombia	CLA105	0.028	0.044	0.028
68	Colombia	CLA106	0.027	0.031	0.029
69	Colombia	CLA113	0.039	0.032	0.020

72	Colombia	CLA155	0.063	0.043	0.022
73	Colombia	CLA156	0.046	0.032	0.023
80	Highland	(A.T.Z.T.R.L.BA90 5-3-3P-1P-4P-2P-1-1-1-B x G9B C0 R.L.23-1P-2P-3-2P-3-2P-1P-B-B-B)-B-76TL-1-2-4	0.027	0.034	0.032
82	Highland	(A.I.Z.T.V.C. 20-3-1-1-2-B-B x A.I.Z.T.V.C.PR93A-17-1-3-1-1-B-B)-B-14TL-1-3	0.065	0.043	0.031
83	Highland	[(P86 S.F*P.S.P.A.A x P.S.P.A.A. TL91A 44-3-1-18-2P-2-1-1-3-1) x A.I.R.L. TL91A 2(3)-1-4-2-2TL-1-1-B]-3-2-3-1	0.028	0.036	0.018
85	Entomology	(200-6 x GUAT189)(51-2-1)F1-B-xP84c1 F26-2-2-4-B-2-B] F102-1-2-2-3 x [KILIMA ST94A]-30/MSV-03-2-10-B-1-B-B-xP84c1 F27-4-1-6-B-5-B]-2-2	0.028	0.044	0.035
88	Entomology	CML311/MBR C2 Bc F41-2	0.038	0.029	0.023
89	Entomology	CML311/MBR C2 Bc F4-1	0.039	0.033	0.032
101	Entomology	P590 C7 Blancos F27-1-1-2	0.036	0.038	0.029
109	Entomology	[M37W/ZM607#bF37sr-2-3sr-6-2-X]-8-2-X-1-BB-B-xP84c1 F27-4-3-3-B-1-B] F29-1-1-1-7 x [KILIMA ST94A]-30/MSV-03-2-10-B-1-B-B-xP84c1 F27-4-1-6-B-5-B]-1-3-B/CML312SR]-1-1	0.045	0.033	0.014
115	Entomology	[Cuba/Guad C3 F34-2-1-1-B-B-B x CML264Q]-1-1	0.029	0.036	0.027
118	Entomology	[Cuba/Guad C3 F44-1-3-2-B-B-B x CML486]-1-1	0.039	0.043	0.031
134	Subtropical	MBR C5 Bc F4-1-2-1	0.044	0.032	0.022
135	Subtropical	95S43SR HG"A"-94-1-1-1	0.034	0.025	0.011
136	Subtropical	POB.502c3 F2 9-14-1-2	0.040	0.034	0.027
137	Subtropical	POB.502c3 F2 26-12-1-2	0.027	0.025	0.023
143	Subtropical	[CML-384 X CML-176](F3)100-2-7	0.031	0.033	0.031
148	Subtropical	CML-322	0.031	0.032	0.028
160	Subtropical	90[SPMATC4/P500(SELY)]#-B-48-4	0.026	0.036	0.025
163	Subtropical	S87P69Q(SIYF) 131-2-2-1	0.033	0.036	0.032
166	Subtropical	(CML-329 X CML-287)-F2-11-1	0.027	0.028	0.027
175	Tropical	CLQ-6211=P62QC6HC13-1-3-BBB-6-B-7-6-BBBB-7-9	0.044	0.036	0.032
178	Tropical	CLQ-RCWQ106=(CML247 x (CLQ-6203xCL-04321)-B-7-1-2)-B-22-1-1-2	0.049	0.034	0.028
180	Tropical	CML499=(CL-04345*CL-274)-B-15-1-2	0.036	0.044	0.041
181	Tropical	CML269=P25STEC1F13-6-1-1	0.029	0.033	0.031
183	Tropical	CL-02143 P21C6S1MH247-5-B-1-1-2	0.031	0.031	0.031
190	Tropical	CLQ-RCYQ40 = (CML165 x CLQ-6203)-B-9-1-1	0.029	0.028	0.028
191	Tropical	CLQ-RCYQ28=(CLQ6502*CLQ6601)-B-34-2-2	0.054	0.036	0.030
193	Tropical	CL-RCY015 = (CML-285*CL-00356)-B-1-1	0.035	0.041	0.035
194	Tropical	CL-RCY016= (CL-00331*CML-287)-B-6-2-3	0.036	0.034	0.030
195	Tropical	CL-RCY018=(CL-03618*CML-287)-B-13-1-1	0.029	0.031	0.027
197	Tropical	CL-RCY007=PIO3011F2-3-5-6-1	0.032	0.034	0.031
199	Tropical	CML497=[CL-00331*v]-3-B-3-2-1	0.031	0.034	0.029
200	Tropical	CL-02725=P27(FRRS)C1-248-B-1	0.048	0.056	0.044
201	Tropical	CML452=Ac8328BNC6-166-1-1-1	0.049	0.031	0.027
208	Tropical	CL-G1632=G16C20H144#-3-3-1	0.055	0.039	0.038
209	Tropical	CL-P10201 =P102 C6 S2(B)-34-2	0.032	0.031	0.031
211	Tropical	CL-G1837=G18SeqC2-F141-2-2-1-1-1-2-##-2	0.061	0.058	0.050
214	Tropical	CML-423=G18C19MH100#-4-1-1	0.041	0.034	0.032
215	Tropical	CML421=P31DMR#1-55-2-3-2-1	0.031	0.037	0.032
217	Physiology	DTPWC9-F24-4-3-1	0.057	0.041	0.035
231	Physiology	DTPYC9-F143-5-4-1-2	0.053	0.036	0.046
232	Physiology	DTPYC9-F11-2-3-1-2	0.038	0.031	0.035
238	Physiology	DTPYC9-F46-1-2-1-2	0.044	0.047	0.040
239	Physiology	DTPYC9-F143-1-6-1	0.032	0.029	0.030
253	Physiology	La Posta Seq C7-F31-2-3-1-1	0.027	0.038	0.034

269	Physiology	DTPWC9-F2-3-2-1	0.038	0.031	0.029
283	Physiology	DTPYC9-F72-1-2-1-1	0.028	0.032	0.029
284	Physiology	La Posta Seq C7-F153-1-2-1-1	0.032	0.032	0.037
292	Physiology	La Posta Seq C7-F153-1-1-1-1	0.036	0.038	0.028
299	Physiology	La Posta Seq C7-F32-2-1-1-1	0.041	0.047	0.048
300	Physiology	La Posta Seq C7-F32-2-1-1-2	0.044	0.037	0.036
301	Physiology	DTPWC9-F115-1-2-1-2	0.039	0.044	0.039
302	Physiology	La Posta Seq C7-F64-2-6-2-2	0.033	0.035	0.031
303	Hybrid	SC513	0.042	0.045	0.030
304	Hybrid	PAN53	0.050	0.037	0.034
305	Hybrid	Pristine 601	0.042	0.036	0.029
306	Hybrid	ZAP61	0.056	0.034	0.035
307	Hybrid	PGS61	0.048	0.036	0.032
308	Hybrid	ZAP55	0.047	0.038	0.038
309	Hybrid	30G19	0.033	0.030	0.029
310	Hybrid	SC633	0.040	0.032	0.031
303	Unplanted		0.026	0.026	0.024
	MEAN		*0.039*	*0.035*	*0.029*
	SE		*0.011*		

Methods S1 Calculations for C mineralisation and gross nitrification.

C mineralisation

Maize root-derived C (C_{plant}) and soil organic matter (SOM)-derived C (C_{soil}) mineralised were determined using the following equations:

$$C_{plant} = C_{total}(\delta^{13}C_{control} - \delta^{13}C_{total})/(\delta^{13}C_{control} - \delta^{13}C_{plant})$$

$$C_{soil} = C_{total} - C_{plant}$$

where $\delta^{13}C_{control}$ is the mean $\delta^{13}C$ value of CO_2 from SOM decomposition measured in the unplanted system, $\delta^{13}C_{total}$ is the measured $\delta^{13}C$ value of total soil respiration, and $\delta^{13}C_{plant}$ is the $\delta^{13}C$ value of plant tissue. These calculations were performed for each point of CO_2 efflux measurement (i.e. at 16, 23 and 29 days after planting). The rates of C mineralisation calculated each week were used to determine cumulative C_{plant} and C_{soil} over the three weeks period of CO_2 measurement.

Nitrification

Gross nitrification rate (N_{gross}) was calculated using the following equation:

$$N_{gross} = (NO3_{Total\ (T0)} - NO3_{Total\ (T1)})/T1 - T0 \cdot \log(^{15}NO3_{T0}/^{15}NO3_{T1})/\log(NO3_{Total\ (T0)}/NO3_{Total\ (T1)})$$

where $NO3_{Total}$ is the total NO_3^- content of soil (μg N g^{-1} soil), $^{15}NO3$ is the ^{15}N abundance within the NO_3^- pool (atom% excess), and T0 and T1 represent time (expressed in days) at initial sample extraction during fertilizer application (hereto 14 days after planting) and that at end of incubation (hereto 23 days after planting). Thus, N_{gross} was expressed as μg N g^{-1} soil day^{-1}.