RESEARCH

e-Xtra*

Influence of Environment and Host Plant Genotype on the Structure and Diversity of the *Brassica napus* Seed Microbiota

Aude Rochefort,¹ Martial Briand,² Coralie Marais,² Marie-Hélène Wagner,³ Anne Laperche,¹ Patrick Vallée,¹ Matthieu Barret,² and Alain Sarniguet^{1,†}

¹ INRA, Agrocampus-Ouest, Université de Rennes 1, UMR 1349 IGEPP (Institute of Genetics, Environment and Plant Protection), 35653 Le Rheu, France

² INRA, Agrocampus-Ouest, Université d'Angers, UMR 1345 IRHS (Research Institute on Horticulture and Seeds), SFR4207 QuaSaV, 49071 Beaucouzé, France

³ Groupe d'Etude et de contrôle des Variétés Et des Semences, Beaucouzé, France

Accepted for publication 31 July 2019.

ABSTRACT

Seeds are involved in the transmission of microorganisms from one plant generation to the next and consequently act as reservoirs for the plant microbiota. The driving processes influencing seed microbiota assemblage have not been yet deciphered because of confounding factors related to environmental location, agricultural practices, and host genotype selection. Nine genotypes were chosen among a large panel of genetically diverse *Brassica napus* accessions. The taxonomic structure of the seed microbiota was monitored by amplification and subsequent high-throughput sequencing of *gyrB* and internal transcribed spacer 1 markers for two successive years on seed lots collected from self-pollinated plants. Seed germination capacities were compared between all seed lots. Although harvesting year was the main driver of seed microbiota

composition, the host genotype also significantly altered the structure of seed microbial assemblages. The core microbiota of *B. napus* included nine fungal taxa shared between all the genotypes and years, while no bacterial taxa were conserved across all genotypes and years. The harvesting year had the major effect on seed germination but with some differences between genotypes. The study demonstrated the relative contribution of host- and environmental-filtering on the assemblage of the seed microbiota. It suggested some influence of these assemblages on seed germination.

Keywords: bacteriology, *Brassica napus*, ecosystems, environment, germination, host genotype, microbiome, mycology, seed microbiota, self-pollination

Plants live in association with a diverse and complex set of microorganisms also known as microbiota. The plant microbiota can modify several host traits, such as plant nutrition (Paredes et al. 2018), flowering kinetics (Panke-Buisse et al. 2015), and resistance against plant pathogens and herbivores (Haney et al. 2018; Kwak et al. 2018). Owing to such impacts on plant growth and health, it is of interest to decipher the biological and ecological processes involved in the assembly of the plant microbiota. Several studies have notably investigated the impact of

environmental factors and host genetic variation on the composition of plant microbiota (Bulgarelli et al. 2012; Edwards et al. 2015; Fitzpatrick et al. 2018; Horton et al. 2014; Peiffer et al. 2013; Pérez-Jaramillo et al. 2017). These studies have revealed a major impact of environment on the taxonomic structure of plant microbiota and a limited but significant contribution of the host genotype. Accordingly, it has been recently highlighted that community heritability (H^2_C) (Van Opstal and Bordenstein 2015) of the maize rhizosphere microbiota is low, even if the abundance of some operational taxonomic units (OTUs) is significantly affected by host genetics (Walters et al. 2018). This broad-sense heritability (H^2) of some bacterial taxa is probably linked to host genes involved in the recruitment of its microbiota, for instance genes related to specific plant metabolites and to plant immunity (Hacquard et al. 2017; Sasse et al. 2018).

In contrast to other plant habitats, diversity of seed microbial assemblages is restrained (Adam et al. 2018; Barret et al. 2015; Bergna et al. 2018; Klaedtke et al. 2016; Leff et al. 2017; Rezki et al. 2018; Rodríguez et al. 2018; Rybakova et al. 2017), perhaps as a consequence of a seed bottleneck for microbial transmission

[†]Corresponding author: A. Sarniguet; alain.sarniguet@inra.fr

Funding: Support was provided by the Institut National de la Recherche Agronomique (Metaomics and Microbial Ecosystems metaprogram, Plant Health and Environment division) and the Conseil Régional de Bretagne (ARED).

*The e-Xtra logo stands for “electronic extra” and indicates that six supplementary figures and four supplementary tables are published online.

The author(s) declare no conflict of interest.

(Newcombe et al. 2018; Paredes and Lebeis 2016). In fact, considering that rhizosphere and phyllosphere are plant habitats with a highly diversified and abundant microbiota, seeds act as a filter and select smaller sized and less diversified microbial assemblages. Therefore, the relative importance of vertical transmission from maternal plant to its progeny over horizontal transmission from the environment is probably limited in plants (Leff et al. 2017; Newcombe et al. 2018). Nevertheless, seeds represent the initial inoculum of the plant microbiota and can thus potentially impact plant fitness especially during its early development stages.

Rapidity and uniformity of seed germination and seedling growth together with emergence ability under adverse environmental conditions and performance after storage are collectively referred to as seed vigor (Finch-Savage and Bassel 2016). Seed vigor is determined by seed dormancy (Bentsink and Koornneef 2008) and seed longevity (Leprince et al. 2017); both traits being influenced by genetic and environmental perturbations. For instance, seed dormancy in *Brassica napus* is affected by the genotype and preharvest environmental conditions (Gruber et al. 2009; Gulden et al. 2004). In contrast to physiological and environmental factors, the impact of seed microbiota composition on seed vigor has not yet been explored. However, experimental evidences indicated that some plant-associated bacteria can repress germination through the production of oxyviniglycines (Chahtane et al. 2018; McPhail et al. 2010) or decrease dormancy through free cytokinins production (Goggin et al. 2015; Rodrigues Pereira et al. 1972). Hence, one may argue that changes in seed microbiota structure could ultimately result in differences of seed vigor.

The few studies that have investigated the importance of ecological processes involved in the assembly of the seed microbiota have reported that the environment significantly impacts the structure of the seed microbiota, and especially fungal assemblages (Klaedtke et al. 2016). Part of these studies has also highlighted that the host genotype could have a weaker but significant influence on bacterial endophytes of oilseed rape; however, it is difficult to eliminate environmental variations that could be confounding (Rybakova et al. 2017). In addition, neutral-based processes such as dispersal and ecological drift are also involved in the assembly of seed microbial assemblages (Rezki et al. 2018).

B. napus (oilseed rape) is a cropping plant cultivated worldwide for its oilseed and for protein cattle feed production. *B. napus* is sensitive to a range of soilborne plant pathogens including *Plasmodiophora brassicae*, *Rhizoctonia solani*, and *Verticillium longisporum*, which can cause clubroot, seedling damping-off, and Verticillium wilt, respectively (Hwang et al. 2012; Sturrock et al. 2015; Depotter et al. 2016). In absence of efficient control methods to restrict the populations of these phytopathogenic microorganisms, some biocontrol-based methods based on seed inoculation with microbial consortia have been proposed (Kataria and Verma 1992; Müller and Berg 2008). However, employing these seed inocula requires more basic knowledge on processes involved in assembly and dynamics of the seed microbiota (Barret et al. 2016). In this study, we estimated the impact of host genotypes and environment on the structure of the seed microbiota of nine genotypes representing the diversity of winter oilseed rape (WOSR) during two consecutive years. In addition, we explored the potential effect of seed microbiota composition on seed germination of these nine genotypes.

MATERIALS AND METHODS

Selection of WOSR genotypes. A total of 116 cultivars of winter oilseed rape (*B. napus*), registered in France between the 1950s and

the 2000s, were gathered from the CRB BraCySol (INRA, IGEPP, France) to represent the diversity of inbred lines cultivated in Western Europe. All cultivars were genotyped with the Infinium Brassica 60K SNP array (Clarke et al. 2016). A set of 628 polymorphic single nucleotide polymorphisms presenting a low level of linkage disequilibrium ($r^2 < 0.2$) were selected to analyze the structure of the genetic diversity within the accessions.

The structure of the collection was studied using admixture (Alexander et al. 2009) and 10 cross-validations. The genetic diversity of the collection was analyzed using Darwin software (Perrier and Bonnot 2003). Sokal and Michener genetic distances were estimated between each couple of cultivars, and then clustering was performed using unweighted pair group method with arithmetic mean. Nine *B. napus* genotypes, namely Astrid, Aviso, Boston, Colvert, Express, Major, Mohican, Tenor, and Zorro, were chosen among the collection (Supplementary Fig. S1, Supplementary Table S1) as representatives of *B. napus* diversity.

Seed production. The selected genotypes were cultivated in 2012–2013 (Y0) in the same experimental field (INRA, Le Rheu, France) to minimize the effect of any former environmental difference between genotypes, and under self-pollination cages to ensure autogamy and therefore produce genetically homogenous lines. The 2013 (Y0) seeds, harvested individually for each genotype were sown in 2015 in a field located close to the field dedicated to seed 2013 production. Pollination bags were applied over 20 plants per genotype after cutting off the early emerging flowers. The 2015–2016 (Y1) seeds of 20 plants were harvested and pooled independently for each genotype. In 2016–2017 (Y2), the seeds harvested for each genotype in the Y1 trial were sown in a field near the previous locations (INRA, Le Rheu, France) with the same cropping and harvesting process as Y1. GPS coordinates, distances between fields, and cropping history for each year are available in Supplementary Table S2. Climatic data for the cropping periods Y1 and Y2 are reported in Supplementary Figure S2. All seed lots harvested in Y1 and Y2 were stored in paper bags in dark dry conditions and at room temperature.

Seed phenotyping. Seed imbibition, germination, and early radicle growth were monitored in vitro with an automated phenotyping platform (Phenotic, SFR Quasav, Angers, France), which is described in detail in Ducournau et al. (2004, 2005) and Wagner et al. (2012). Briefly, four subsamples of 25 seeds by genotype and year (Y1 and Y2) were incubated at 20°C on germination test paper (GE Healthcare, type 3644) continuously moistened for 5 days and image acquisition was performed every 2 h. Image acquisition, image analysis, and data analysis methods are described in Demilly et al. (2014). The following parameters were determined: seed area (Area; in mm²), volume 8 h after initiation of imbibition (Imb_Vol; in mm³), radicle elongation after 8 h (Elon_germ, in mm), mean germination time (germination, in hours), and time to reach 50% of germination per seed subsample (T50, in hours). Differences were assessed with Kruskal-Wallis tests and considered as significant at a *P* value of <0.01.

Microbial DNA sample preparation. DNA extraction was performed on five subsamples of 1,000 seeds (~4 g) per genotype (45 subsamples in total per year). First, seeds were soaked in 20 ml of phosphate buffered saline (PBS) supplemented with 0.05% (vol/vol) of Tween 20, for 2 h 30 min under constant agitation (140 rpm) at room temperature. After this seed soak that enables the recovery of epiphytic and endophytic microorganisms (Barret et al. 2015), the suspensions were centrifuged (4,500 × *g*, 10 min) and DNA extraction was performed on the resulting pellets with the DNeasy PowerSoil HTP 96 Kit (Qiagen), following the manufacturer's procedure. Seed suspensions in PBS are classically performed in seed pathology (see International Seed Testing Association –ISTA: <https://www.seedtest.org/en/home.html>) to PCR-amplify bacterial

strains located in the endosperm (e.g., *Acidovorax citrulli* or *Xanthomonas citri*). Numerous antimicrobial compounds are associated to seed tissues and are released during grinding, which therefore can result in underestimation of seed microbial diversity.

Libraries construction and sequencing. An initial PCR amplification was performed with the primer sets *gyrB*_aF64/*gyrB*_aR553 (Barret et al. 2015) and internal transcribed spacer ITS1F/ITS2 (Buée et al. 2009), which target a portion of *gyrB* and the fungal ITS1 region, respectively. The cycling conditions for ITS1F/ITS2, were an initial denaturation at 94°C for 3 min, followed by 35 cycles of amplification at 94°C (30 s), 50°C (45 s), and 68°C (90 s), and a final elongation step at 68°C for 10 min. The cycling conditions for *gyrB* were: initial denaturation at 94°C for 3 min, 35 cycles of amplification at 94°C (30 s), 55°C (45 s), and 68°C (90 s), and final elongation step at 68°C for 10 min. Amplicons were purified with magnetic beads (Sera-Mag, Merck). A second PCR amplification was performed to incorporate Illumina adapters and barcodes. PCR cycling conditions were identical for the two molecular markers: a first denaturation step at 94°C (1 min), followed by 12 cycles at 94°C (1 min), 55°C (1 min), and 68°C (1 min), and a final elongation at 68°C for 10 min. Amplicons were purified as previously described and quantified with the QuantIT PicoGreen dsDNA Assay Kit (ThermoFisher Scientific). All the amplicons were pooled in equimolar concentrations and the concentration of the equimolar pool was monitored with quantitative PCR (KAPA SYBR FAST, Merck). Amplicon libraries were mixed with 10% PhiX and sequenced with MiSeq reagent kit v2 500 cycles (one sequencing cartridge per year).

Sequence processing. Fastq files were processed with DADA2 version 1.6.0 (Callahan et al. 2016), using the parameters described in the workflow for “Big Data: Paired-end” (https://benjjneb.github.io/dada2/bigdata_paired.html). The only modification made relative to this protocol was a change in the `truncLen` argument according to the quality of the sequencing run. Taxonomic affiliations for amplicon sequence variants (ASV) generated with DADA2 were assigned with a naive Bayesian classifier (Wang et al. 2007) on an in-house *gyrB* database (Bartoli et al. 2018) and the UNITE v7.1 fungal database (Abarenkov et al. 2010).

Microbial community analyses. Analyses of diversity were conducted with the R package Phyloseq version 1.22.3 (McMurdie and Holmes 2013). Data were normalized based on sequencing depth, using a rarefaction of 1,100 and 15,000 sequences per sample for *gyrB* and ITS1, respectively. Observed richness (number of ASV per sample), estimated richness (Chao1 index), and inverse Simpson's index were calculated with Phyloseq. Faith's phylogenetic diversity was calculated on *gyrB* dataset with the R package picante version 1.6-2 (Kembel et al. 2010). Differences in alpha-diversity estimators between years and genotypes were assessed with Kruskal-Wallis tests. Differences were considered as significant at a *P* value of <0.01.

Changes in microbial assemblage composition were assessed with Bray-Curtis index and weighted UniFrac (wUF) distance (Lozupone and Knight 2005). Principal coordinate analysis (PCoA) was used for ordination of Bray-Curtis index and wUF distance. To quantify the relative contribution of plant generation and plant genotype in microbial community profiles, canonical analysis of principal coordinates was performed with the function `capscale` of the R package `vegan` 2.4.2 (Oksanen et al. 2017) followed with permutational multivariate analysis of variance (PERMANOVA) (Anderson 2001).

A presence/absence matrix of common ASVs was constructed as follows. Common ASV was recorded as present if detected in all subsamples (*n* = 5) of one seed lot. One seed lot corresponded to seeds collected each year from each plant genotype. Visualization of genotype-specific ASVs and shared ASVs between plant genotypes was assessed for each year with the R package `UpSetR` (Lex et al. 2014). The number of common bacterial and fungal

ASVs between years for each individual genotype was also assessed using Venn diagrams. This binary matrix was used for assessing Jaccard and unweighted UniFrac distance (uUF) between genotypes. Comparisons of Sokal-Michener genetic distance and Jaccard/uUF distances were monitored with coefficient of determination.

Distribution of bacterial and fungal ASVs in other Brassicaceae seeds was assessed by investigating their prevalence in 479 seed samples associated to *B. oleracea*, *B. rapa*, and *Raphanus sativus* (Barret et al. 2015; Rezki et al. 2016, 2018).

The datasets supporting the conclusions of this article are available in the Sequence Read Archive database under accession number PRJEB31617.

RESULTS

Diversity of the seed microbiota of *B. napus*. Overall, 4,451 bacterial and 359 fungal ASVs were detected within *gyrB* and ITS1 datasets. ASV provided a finer resolution than OTU (Callahan et al. 2017), and this descriptor was therefore used for estimating the taxonomic structure of the seed microbiota of *B. napus*.

According to coverage estimates, the number of *gyrB* sequences was not sufficient for reaching the plateau after rarefaction, while saturation was achieved for fungal reads. Hence, predicted richness (Chao1 index) was assessed for bacterial assemblages, while observed richness (number of ASVs) was measured for fungal assemblages. Although bacterial and fungal richness were significantly different between the two harvesting years (*P* < 0.01), seed samples collected in Y2 contained on average fewer bacterial and more fungal ASVs than Y1 seed sample (Fig. 1A and D). The increase of fungal richness in Y2 was associated with a significant decrease in fungal diversity (Fig. 1E). While bacterial diversity did not differ between years (Fig. 1B), bacterial phylogenetic diversity (Faith's PD), was significantly higher in Y2 (*P* < 0.01) (Fig. 1C). In contrast to the harvesting year, no significant differences in α -diversity estimators were observed between plant genotypes (*P* > 0.01).

Similarities in composition of bacterial and fungal assemblages were estimated with weighted UniFrac (wUF) distance and Bray-Curtis index, respectively. Ordination of wUF and Bray-Curtis revealed a significant clustering of seed-associated bacterial and fungal assemblages according to the harvesting year (Fig. 2, Table 1). The relative influence of the harvesting year and the plant genotype in assemblage composition was further inspected through canonical analysis of principal coordinates followed by PERMANOVA. Based on canonical analysis of principal coordinates, 16.4 and 65.5% of variances in bacterial and fungal assemblage compositions, respectively, were explained by the harvesting year (*P* < 0.01). Changes in bacterial and fungal assemblage compositions were also significantly (*P* < 0.01) explained by the plant genotype, with 19.3 and 11.5% of variances driven by this factor, respectively (Table 1). Interaction between harvesting year and genotype was significant (*P* < 0.01) and explained 16.6 and 13.3% of variances of bacterial and fungal assemblage compositions, respectively. When each year is analyzed separately, the impact of plant genotype (*P* < 0.01) ranged from 40 to 90% of explained variance (Table 1, Supplementary Fig. S3). However, similarity in assemblage compositions between genotypes were different in Y1 and Y2.

Core and specific fractions of the *B. napus* microbiota. Differences in relative abundance of bacterial orders between genotypes were mostly observed within Y1 (Fig. 3A). Notably we detected a higher abundance of Sphingomonadales and Pseudomonadales in Astrid, Aviso, and Boston in comparison with the other genotypes (Fig. 3A). However, these differences between genotypes were not detected in Y2, where principal variations were related to increase in relative

abundance of Enterobacteriales in Express and Zorro. Regarding fungal assemblages, differences in relative abundance of fungal orders were mostly observed between harvesting years, with a decrease in relative abundance of Tremellales and Helotiales in Y2 (Fig. 3B).

The distribution of ASVs between plant genotypes for each year of production was also assessed (Figs. 4 and 5). Among the 15 bacterial ASVs systematically detected in at least one genotype in Y1, none were shared between all genotypes (Fig. 4A). In Y2, six bacterial ASVs (out of 268) were shared between all genotypes (Fig. 4B). Four of these six ASVs have been already detected in more than 10% of seed samples ($n = 479$) collected from various

Brassicaceae including *B. oleracea*, *B. rapa*, and *R. sativus* (Table 2). The inheritance of bacterial ASVs between years was quite low, since only three genotypes (Astrid, Aviso, and Boston) possessed four and five ASVs in common in Y1 and Y2, respectively (Supplementary Fig. S4). These ASVs shared between both years are related to *Sphingomonas*, *Pseudomonas*, and *Frigoribacterium*.

Fungal assemblages shared more ASVs between all genotypes in comparison with bacterial assemblages. Indeed, 18 (out of 37) and 19 (out of 52) fungal ASVs were shared between all the genotypes in Y1 and Y2, respectively (Fig. 5). For each genotype, 35

Fig. 1. Diversity of seed-associated microbial assemblages of *Brassica napus*. Seed samples of nine genotypes were collected during two consecutive years (Y1 and Y2). Community profiling of the seed microbiota was performed on five seed subsamples per genotype. **A**, Estimated richness (Chao1 index), **B**, diversity (inverse Simpson's index), and **C**, phylogenetic diversity (Faith's phylogenetic diversity index) were monitored with *gyrB* amplicon sequence variants (ASVs) for bacteria. **D**, Observed richness (number of detected ASVs) and **E**, diversity (inverse Simpson's index) were assessed with internal transcribed spacer 1 ASVs for fungi.

Fig. 2. Similarities in microbial composition between *Brassica napus* genotypes seed-associated microbial assemblages. Similarities in seed microbial composition were estimated with **A**, weighted UniFrac distance and **B**, Bray-Curtis index for bacterial and fungal assemblages, respectively. Principal coordinate analysis was used for ordination of weighted UniFrac distance and Bray-Curtis index. Samples are colored according to their genotypes, while shape corresponded to the 2 years of production.

to 40% fungal ASVs were conserved from Y1 to Y2. In addition, nine fungal ASVs were systematically detected during both years. These fungal ASVs are also highly prevalent in seed samples of other Brassicaceae species (Table 2). There were very few bacterial ASVs specifically associated to one genotype in Y1, while there were in general more specific bacterial ASVs per genotype in Y2. Conversely, very few genotypes harbor specific fungal ASVs in Y1 as in Y2 (Supplementary Table S3 and S4).

Relationship between *B. napus* genotypes and seed microbiota composition. To assess if the composition of the seed microbiota could be related to genetic relatedness of *B. napus*, we compared Sokal-Michener genetic distance to Jaccard and uUF distances calculated with ITS1 and *gyrB* sequences, respectively (Supplementary Fig. S5). Coefficient of determination between Jaccard/uUF distances and Sokal-Michener distance were low for bacterial ($r^2 = 0.026$ in Y1; $r^2 = 0.009$ in Y2) and fungal ($r^2 = 0.005$ in Y1; $r^2 = 0.117$ in Y2) assemblages. While a significant ($P = 0.002$) positive correlation between genetic distance and fungal assemblage composition was detected in Y2, the overall genetic

similarities between the *B. napus* genotypes employed in this work is not a robust predictor of seed microbiota composition.

Impact of production year and host genotype on seed phenotypes. There were no significant differences between years and genotypes for seed area, radicle elongation and imbibition speed (Supplementary Fig. S6). However, according to average germination rate ($n = 100$), germination of seed samples harvested in Y1 was significantly ($P < 0.01$) slower than germination of seed samples harvested in Y2 (Fig. 6). Significant differences were also observed between genotypes within specific year. For instance, seeds from Astrid germinated on average earlier ($P < 0.01$) than the other genotypes in Y1 but not in Y2 (Fig. 6). Seeds from Tenor had a slower mean germination time ($P < 0.01$) in comparison with the other genotypes but only for samples collected in Y2 (Fig. 6). Thus, another metric, T50, varied in the same way as mean germination time. Of note, three bacterial ASVs were specifically associated with Astrid in Y1. Moreover, three bacterial ASVs and five fungal ASVs were specifically associated to Tenor in Y2.

DISCUSSION

The aim of this study was to assess the relative influence of the environment (i.e., year) and the host genotype on the structure of the *B. napus* seed microbiota. To eliminate environmental variations within a year, we sowed seeds of nine *B. napus* genotypes in the same field. In addition, to ensure homogeneous genetic material and preserve genotype specificities, each individual plant was cultivated in self-pollination.

Over two years we observed a decrease in bacterial richness for seed samples collected during the second year. This loss of bacterial

TABLE 1 Percentage of explained variance for beta-diversity estimators ^a					
	Year	Genotype	Year: Genotype	Genotype (Y1)	Genotype (Y2)
<i>gyrB</i>	16.4	19.3	16.6	44.0	40.8
ITS1	65.5	11.5	13.3	66.2	90.7

^a Percentage of explained variance estimated with permutational multivariate analysis of variance ($P < 0.01$) for β -diversity of bacterial (*gyrB*) and fungal (internal transcribed spacer 1 [ITS1]) assemblages.

Fig. 3. Taxonomic composition of *Brassica napus* seed microbiota. Relative abundance of the most abundant **A**, bacterial and **B**, fungal orders within *B. napus* seed samples collected from nine genotypes across two successive generations (Y1 and Y2). Taxonomic affiliation of bacterial and fungal amplicon sequence variants (ASVs) was performed with an in-house *gyrB* database (Bartoli et al. 2018) and the UNITE v7.1 database (Abarenkov et al. 2010), respectively. Unknown taxa represented ASVs that are not affiliated at the order level.

dispersal of individuals among local bacterial assemblages (Vannette and Fukami 2017). If this assumption was correct, a similar reduction of richness would be expected within seed fungal assemblages. However, fungal richness increased in Y2. Therefore,

alteration of richness could be solely due to differences in richness of local microbial assemblages between years. Influence of the harvesting year was the main driving factor of seed fungal assemblage composition with 65.5% of explained variance. These

results agree with a previous report showing that seed fungal assemblages of common bean are mostly shaped by crop management practices and geographical locations (Klaedtke et al. 2016). The high impact of environmental filtering on composition of the fungal

Fig. 5. Generalist and specific fungal amplicon sequence variants (ASVs). Prevalence of fungal ASVs across plant genotypes were investigated with UpSetR (Lex et al. 2014). Upper histograms represent the number of ASVs associated with one specific intersection in **A**, year 1 (Y1) or **B**, year 2 (Y2). Plant genotype associated with each particular intersection is highlighted with a dot. Intersection associated with all genotypes is displayed in red. The histogram located on the left of each UpSetR representation indicates the number of ASVs per genotype. Finally, boxplot represents the median relative abundance (log10) of fungal ASVs associated with each intersection.

fraction of the seed microbiota could be related to local biogeographical patterns of fungal assemblages (Peay et al. 2016).

Diversity and composition of the *B. napus* seed microbiota was different between years but also between the host genotypes used in this study. Host genotype is an important driver in the assembly of the seed microbiota, especially for the bacterial fraction. The impact of host genotypes on the structure of *B. napus* microbiota was already highlighted for endophytic bacteria (Rybakova et al. 2017). Since seed lots employed by Rybakova et al. (2017) were collected from different geographical regions, the influence of host genotype was therefore inseparable from the influence of the environment.

Our study confirmed without any confounding factor that the structure of the *B. napus* seed bacterial assemblage are partly genotype-dependent. Since interaction between year and genotype was significantly influencing β -diversity, we assessed the influence of host genotypes on microbiota compositions for each year. According to these analyses, the plant genotype explained a major part of variation in seed microbial assemblage composition, therefore suggesting an important influence of host-filtering in the assembly of the seed microbiota. However, composition of seed microbial assemblage differed greatly between harvesting years. In addition, a small part of the *B. napus* seed bacterial assemblage is

TABLE 2
Core members of *Brassica napus* seed microbiota^a

ASV	Taxonomy	Y1 (%)	Y2 (%)	Others (%)
Bacteria				
ASV00001	<i>Pantoea agglomerans</i>	0.0	100.0	90.6
ASV00003	<i>Ralstonia pickettii</i>	0.0	100.0	0.6
ASV00028	<i>Pseudomonas</i>	20.0	100.0	34.9
ASV00038	<i>Sphingomonas</i>	0.0	100.0	10.6
ASV00046	<i>Frigoribacterium</i>	10.0	100.0	11.1
ASV00124	<i>Burkholderiales</i>	0.0	100.0	0.0
Fungi				
ASV00001	<i>Alternaria infectoria</i>	100.0	100.0	72.6
ASV00002	<i>Cladosporium</i>	100.0	100.0	97.6
ASV00003	<i>Cladosporium delicatulum</i>	100.0	100.0	100.0
ASV00004	<i>Botrytis fabae</i>	100.0	100.0	47.9
ASV00005	<i>Sporidiobolales</i>	100.0	100.0	60.1
ASV00006	<i>Alternaria infectoria</i>	100.0	100.0	66.2
ASV00007	<i>Alternaria brassicae</i>	100.0	90.0	95.4
ASV00008	<i>Cryptococcus victoriae</i>	100.0	0.0	34.8
ASV00009	<i>Cryptococcus victoriae</i>	100.0	0.0	37.5
ASV00010	<i>Cryptococcus oeirensis</i>	100.0	0.0	37.8
ASV00011	<i>Filobasidium stepposum</i>	100.0	100.0	95.4
ASV00012	<i>Alternaria infectoria</i>	100.0	100.0	62.8
ASV00013	<i>Alternaria infectoria</i>	0.0	100.0	47.0
ASV00014	<i>Bulleromyces</i>	100.0	0.0	0.3
ASV00015	<i>Bensingtonia</i>	100.0	90.0	58.5
ASV00017	<i>Erysiphe cruciferarum</i>	100.0	20.0	12.8
ASV00018	<i>Cryptococcus oeirensis</i>	0.0	100.0	0.0
ASV00019	<i>Udeniomyces pannonicus</i>	60.0	100.0	14.0
ASV00021	<i>Cladosporium aggregatocaticratum</i>	100.0	100.0	47.3
ASV00022	<i>Alternaria</i>	90.0	100.0	0.3
ASV00025	<i>Cryptococcus victoriae</i>	0.0	100.0	0.0
ASV00028	<i>Cryptococcus tephrensensis</i>	100.0	90.0	32.9
ASV00029	<i>Cryptococcus carnesensis</i>	90.0	100.0	32.9
ASV00030	<i>Cladosporium perangustum</i>	0.0	100.0	4.6
ASV00038	<i>Phaeosphaeria caricicola</i>	100.0	0.0	11.9
ASV00041	<i>Cladosporium ramotenellum</i>	0.0	100.0	5.2
ASV00044	<i>Cryptococcus victoriae</i>	0.0	100.0	0.0
ASV00054	<i>Ramularia vizellae</i>	0.0	100.0	0.9

^a Prevalence (expressed as a percentage) of each amplicon sequence variants (ASV) in *B. napus* seed samples collected in year 1 (Y1), year 2 (Y2), and in seed samples (Others) of *B. oleracea*, *B. rapa*, and *Raphanus sativus* reported by Barret et al. (2015) and (Rezki et al. 2016, 2018).

inherited from one generation to the next. Overall, our study highlighted a low inheritance of bacterial and fungal assemblages across *B. napus* generations. Indeed, no bacterial ASV were consistently detected between plant generations, while nine fungal ASVs were conserved between years. The absence of conserved bacterial ASV between year and genotypes could be explained by a stronger impact of host-filtering on assembly of the bacterial fraction of the seed microbiota. Alternatively, the absence of generalist bacterial ASV observed between years could be partly explained by the weak number of bacterial ASVs detected in Y1. The inheritance of seed-borne microbial taxa is quite low, therefore confirming previous observations performed on *R. sativus* over three consecutive generations (Rezki et al. 2018) and *Solanum lycopersicum* over two generations (Bergna et al. 2018). Hence, the main acceptable conclusion is that few microbial taxa associated with seeds are inherited and that most of seed-borne taxa represented cases of horizontal transmission (Leff et al. 2017). Despite these changes in assemblage compositions, the ASVs detected on seed samples corresponded to microbial taxa frequently associated with other seed samples. For instance, four of the bacterial generalists detected in Y2, namely *Pantoea agglomerans*, *Pseudomonas*, *Sphingomonas*, and *Frigoribacterium*, were already detected in more than 10% of other Brassicaceae seed lots (Barret et al. 2015; Rezki et al. 2018). Hence, these taxa might be adapted to the seed habitat. The case was different for fungi with a significant number of fungal ASVs recovered through generations. However this does not mean that these taxa are vertically transmitted. Assessing the relative importance of vertical and horizontal transmission will require an in-depth analysis of the seed transmission pathways (internal, floral and external) employed by these fungal taxa. Therefore, it is tempting to speculate that these

differences in seed microbiota composition between years are the result of fluctuations of the local microbial reservoir. In this way, specific microbial recruitment and selection by the genotypes are modulated among years. Consequently, the relative impact of the host genotype on the structure of seed microbial assemblages is difficult to predict, as it is dependent of fluctuations of the local reservoir.

Previous works performed on the rhizosphere and phyllosphere of multiple maize genotypes have highlighted a relatively low H^2 of microbial taxa (Wallace et al. 2018; Walters et al. 2018). Although the number of genotypes employed in our study precluded the measurement of this broad-sense heritability, we did not establish any significant link between the genetic distance of the nine genotypes and their microbial distances. While considering the variability between subsamples collected from plants of the same genotype and cultivated on the same field, in addition to the relative influence of environment and host genotype, there is a contribution of other neutral-based processes on the assembly of the seed microbiota (Rezki et al. 2018). However, some specific plant functions and traits, and especially genes implicated in plant immune system, shape the structure and diversity of their own microbiota (Horton et al. 2014; Li et al. 2018). Thus, it would be necessary to use a larger number of genetically diverse genotypes of WOSR to explore this hypothesis at a finer resolution (i.e., intraspecies). To date, some studies failed to establish this link even when microbial diversification due to genetic diverse plant species was demonstrated (Bouffaud et al. 2012; Schlaeppi et al. 2014). However, establishing a direct correlation between genotypes and their microbiota would be of great interest for selecting genotypes with a specific microbiota in which certain taxa would ensure positive functions for the plant fitness.

Fig. 6. Dynamics of seed germination of each genotype and year. Germination was monitored in vitro with an automated phenotyping platform (Phenotic; Ducournau et al. 2004, 2005; Wagner et al. 2012). Four subsamples of 25 seeds by genotype and year (Y1 and Y2) were incubated at 20°C on germination paper (GE Healthcare, type 3644) continuously moistened for 5 days, and image acquisition was performed every 2 h.

Among different observed seed phenotypes, only the mean germination time and T50 (half-mean germination time) varied between years. Seed germination progresses through three phases (Bewley 1997). The first phase, known as imbibition, is a physical process driven by difference in water potential between the inside and the outside of the seed. Based on seed volume monitored during 8 h after initiation of imbibition, no significant differences in imbibition was observed between seed samples. This observation suggested that seed moisture was quite comparable between seed samples and that the resulting differences in germination kinetics are related to later phases. Since the environmental factor (year) more strongly shapes the bacterial and fungal communities, we assessed whether the change in microbiota composition could explain variation in germination rates. Authors demonstrated that the environmental conditions, age of seed and genotype (He et al. 2014; Leprince et al. 2017; Nagel et al. 2015) affect different seed performances like secondary dormancy and seed vigor. The requirement to perform germination assays for all seed samples simultaneously ultimately results in differences in longevity of seed collected in Y1 and Y2. However, long-term storage (i.e., several years) of *B. napus* seeds samples does not impact germination time but rather germination percentage (Nagel et al. 2011), which was not different between Y1 and Y2. Moreover, Astrid and Tenor genotypes did not support the ageing effect hypothesis as their germination rates were either similar or inverted, respectively, between Y1 and Y2 compared with the other genotypes. In addition, for Tenor different bacterial and fungal ASVs were effectively described in seed assemblages. Seed moisture cannot be involved as there was no significant differences during imbibition phase. Therefore, because of the most probable assumption of microbiota involvement, further experiments are required to investigate further the implication of microbial assemblages in germination or extended seed phenotypes variations.

In conclusion, the microbial assemblages of *B. napus* seeds are mainly influenced by the environment but to a lesser extent by the plant genotype. The inheritance of some abundant bacterial and fungal ASVs also differs between genotypes. Further studies will explore more extensively the host genetic determinants driving the microbial assemblages and the impact of such assemblages on seed vigor.

ACKNOWLEDGMENTS

We thank Muriel Bahut from the ANAN platform (SFR Quasav) for amplicon sequencing, the Phenotic Platform for performing seed germination experiments, and Thomas Baldwin for English proofreading. We apologize to authors whose relevant work was not included in this article due to space constraints.

LITERATURE CITED

- Abarenkov, K., Nilsson, R. H., Larsson, K.-H., Alexander, I. J., Eberhardt, U., Erland, S., Høiland, K., Kjeller, R., Larsson, E., Pennanen, T., et al. 2010. The UNITE database for molecular identification of fungi—Recent updates and future perspectives. *New Phytol.* 186:281-285.
- Adam, E., Bernhart, M., Müller, H., Winkler, J., and Berg, G. 2018. The *Cucurbita pepo* seed microbiome: Genotype-specific composition and implications for breeding. *Plant Soil* 422:35-49.
- Alexander, D. H., Novembre, J., and Lange, K. 2009. Fast model-based estimation of ancestry in unrelated individuals. *Genome Res.* 19:1655-1664.
- Anderson, M. J. 2001. A new method for non-parametric multivariate analysis of variance. *Austral. Ecol.* 26:32-46.
- Barret, M., Briand, M., Bonneau, S., Préveaux, A., Valière, S., Bouchez, O., Hunault, G., Simoneau, P., and Jacques, M.-A. 2015. Emergence shapes the structure of the seed microbiota. *Appl. Environ. Microbiol.* 81:1257-1266.
- Barret, M., Guimbaud, J.-F., Darrasse, A., and Jacques, M.-A. 2016. Plant microbiota affects seed transmission of phytopathogenic microorganisms. *Mol. Plant Pathol.* 17:791-795.
- Bartoli, C., Frachon, L., Barret, M., Rigal, M., Huard-Chauveau, C., Mayjonade, B., Zanchetta, C., Bouchez, O., Roby, D., Carrère, S., et al. 2018. In situ relationships between microbiota and potential pathobiota in *Arabidopsis thaliana*. *ISME J.* 12:2024-2038.
- Bentsink, L., and Koornneef, M. 2008. Seed dormancy and germination. *The Arabidopsis Book* 6:e0119.
- Bergna, A., Cernava, T., Rändler, M., Grosch, R., Zachow, C., and Berg, G. 2018. Tomato seeds preferably transmit plant beneficial endophytes. *Phytobiomes J.* 2:183-193.
- Bewley, J. D. 1997. Seed germination and dormancy. *Plant Cell* 9:1055-1066.
- Bouffaud, M.-L., Kyselková, M., Gouesnard, B., Grundmann, G., Müller, D., and Moëgne-Loccoz, Y. 2012. Is diversification history of maize influencing selection of soil bacteria by roots? *Mol. Ecol.* 21:195-206.
- Buée, M., Reich, M., Murat, C., Morin, E., Nilsson, R. H., Uroz, S., and Martin, F. 2009. 454 Pyrosequencing analyses of forest soils reveal an unexpectedly high fungal diversity. *New Phytol.* 184:449-456.
- Bulgarelli, D., Rott, M., Schlaeppi, K., Ver Loren van Themaat, E., Ahmadinejad, N., Assenza, F., Rauf, P., Huettel, B., Reinhardt, R., Schmelzer, E., et al. 2012. Revealing structure and assembly cues for *Arabidopsis* root-inhabiting bacterial microbiota. *Nature* 488:91-95.
- Callahan, B. J., McMurdie, P. J., and Holmes, S. P. 2017. Exact sequence variants should replace operational taxonomic units in marker-gene data analysis. *ISME J.* 11:2639-2643.
- Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J. A., and Holmes, S. P. 2016. DADA2: High-resolution sample inference from Illumina amplicon data. *Nat. Methods* 13:581-583.
- Chahtane, H., Nogueira-Füller, T., Allard, P.-M., Marcourt, L., Ferreira Queiroz, E., Shanmugabala, V., Falquet, J., Wolfender, J.-L., and Lopez-Molina, L. 2018. The plant pathogen *Pseudomonas aeruginosa* triggers a DELLA-dependent seed germination arrest in *Arabidopsis*. C. S. Hardtke and D. J. Kliebenstein, eds. *eLife* 7:e37082.
- Clarke, W. E., Higgins, E. E., Plieske, J., Wieseke, R., Sidebottom, C., Khedikar, Y., Batley, J., Edwards, D., Meng, J., Li, R., et al. 2016. A high-density SNP genotyping array for *Brassica napus* and its ancestral diploid species based on optimized selection of single-locus markers in the allotetraploid genome. *Theor. Appl. Genet.* 129:1887-1899.
- Demilly, D., Ducournau, S., Wagner, M.-H., and Dürr, C. 2014. Digital imaging of seed germination. Pages 147-164 in: *Plant Image Analysis*. S. Gupta and Y. Ibaraki, eds. CRC Press, Boca Raton, FL.
- Depotter, J. R. L., Deketelaere, S., Inderbitzin, P., Tiedemann, A. V., Höfte, M., Subbarao, K. V., Wood, T. A., and Thomma, B. P. H. J. 2016. *Verticillium longisporum*, the invisible threat to oilseed rape and other brassicaceous plant hosts. *Mol. Plant Pathol.* 17:1004-1016.
- Ducournau, S., Feutry, A., Plainchault, P., Revollon, P., Vigouroux, B., and Wagner, M. H. 2004. An image acquisition system for automated monitoring of the germination rate of sunflower seeds. *Comput. Electron. Agric.* 44: 189-202.
- Ducournau, S., Feutry, A., Plainchault, P., Revollon, P., Vigouroux, B., and Wagner, M. H. 2005. Using computer vision to monitor germination time course of sunflower (*Helianthus annuus* L.) seeds. *Seed Sci. Technol.* 33: 329-340.
- Edwards, J., Johnson, C., Santos-Medellín, C., Lurie, E., Podishetty, N. K., Bhatnagar, S., Eisen, J. A., and Sundaresan, V. 2015. Structure, variation, and assembly of the root-associated microbiomes of rice. *Proc. Natl. Acad. Sci. USA* 112:E911-E920.
- Finch-Savage, W. E., and Bassel, G. W. 2016. Seed vigour and crop establishment: extending performance beyond adaptation. *J. Exp. Bot.* 67: 567-591.
- Fitzpatrick, C. R., Copeland, J., Wang, P. W., Guttman, D. S., Kotanen, P. M., and Johnson, M. T. J. 2018. Assembly and ecological function of the root microbiome across angiosperm plant species. *Proc. Natl. Acad. Sci.* 115: E1157-E1165.
- Goggin, D. E., Emery, R. J. N., Kurepin, L. V., and Powles, S. B. 2015. A potential role for endogenous microflora in dormancy release, cytokinin metabolism and the response to fluridone in *Lolium rigidum* seeds. *Ann. Bot. (Lond.)* 115:293-301.
- Gruber, S., Emrich, K., and Claupein, W. 2009. Classification of canola (*Brassica napus*) winter cultivars by secondary dormancy. *Can. J. Plant Sci.* 89:613-619.
- Gulden, R. H., Thomas, A. G., and Shirliff, S. J. 2004. Relative contribution of genotype, seed size and environment to secondary seed dormancy potential in Canadian spring oilseed rape (*Brassica napus*). *Weed Res.* 44:97-106.

- Hacquard, S., Spaepen, S., Garrido-Oter, R., and Schulze-Lefert, P. 2017. Interplay between innate immunity and the plant microbiota. *Annu. Rev. Phytopathol.* 55:565-589.
- Haney, C. H., Wiesmann, C. L., Shapiro, L. R., Melnyk, R. A., O'Sullivan, L. R., Khorasani, S., Xiao, L., Han, J., Bush, J., Carrillo, J., et al. 2018. Rhizosphere-associated *Pseudomonas* induce systemic resistance to herbivores at the cost of susceptibility to bacterial pathogens. *Mol. Ecol.* 27:1833-1847.
- He, H., de Souza Vidigal, D., Snoek, L. B., Schnabel, S., Nijveen, H., Hilhorst, H., and Bentsink, L. 2014. Interaction between parental environment and genotype affects plant and seed performance in *Arabidopsis*. *J. Exp. Bot.* 65:6603-6615.
- Horton, M. W., Bodenhausen, N., Beilsmith, K., Meng, D., Muegge, B. D., Subramanian, S., Vetter, M. M., Vilhjálmsson, B. J., Nordborg, M., Gordon, J. I., et al. 2014. Genome-wide association study of *Arabidopsis thaliana*'s leaf microbial community. *Nat. Commun.* 5:5320.
- Hwang, S.-F., Strelkov, S. E., Feng, J., Gossen, B. D., and Howard, R. J. 2012. *Plasmodiophora brassicae*: A review of an emerging pathogen of the Canadian canola (*Brassica napus*) crop. *Mol. Plant Pathol.* 13:105-113.
- Kataria, H. R., and Verma, P. R. 1992. Rhizoctonia solani damping-off and root rot in oilseed rape and canola. *Crop Prot.* 11:8-13.
- Kembel, S. W., Cowan, P. D., Helmus, M. R., Cornwell, W. K., Morlon, H., Ackerly, D. D., Blomberg, S. P., and Webb, C. O. 2010. Picante: R tools for integrating phylogenies and ecology. *Bioinformatics* 26:1463-1464.
- Klaedtke, S., Jacques, M.-A., Raggi, L., Préveaux, A., Bonneau, S., Negri, V., Chable, V., and Barret, M. 2016. Terroir is a key driver of seed-associated microbial assemblages. *Environ. Microbiol.* 18:1792-1804.
- Kwak, M.-J., Kong, H. G., Choi, K., Kwon, S.-K., Song, J. Y., Lee, J., Lee, P. A., Choi, S. Y., Seo, M., Lee, H. J., et al. 2018. Rhizosphere microbiome structure alters to enable wilt resistance in tomato. *Nat. Biotechnol.* 36:1100-1109.
- Leff, J. W., Lynch, R. C., Kane, N. C., and Fierer, N. 2017. Plant domestication and the assembly of bacterial and fungal communities associated with strains of the common sunflower, *Helianthus annuus*. *New Phytol.* 214:412-423.
- Leprince, O., Pellizzaro, A., Berri, S., and Buitink, J. 2017. Late seed maturation: Drying without dying. *J. Exp. Bot.* 68:827-841.
- Lex, A., Gehlenborg, N., Strobelt, H., Vuilleumot, R., and Pfister, H. 2014. UpSet: Visualization of intersecting sets. *IEEE Trans. Vis. Comput. Graph.* 20:1983-1992.
- Li, Y., Wu, X., Chen, T., Wang, W., Liu, G., Zhang, W., Li, S., Wang, M., Zhao, C., Zhou, H., et al. 2018. Plant phenotypic traits eventually shape its microbiota: A common garden test. *Front. Microbiol.* 9:2479.
- Lozupone, C., and Knight, R. 2005. UniFrac: A new phylogenetic method for comparing microbial communities. *Appl. Environ. Microbiol.* 71:8228-8235.
- McMurdie, P. J., and Holmes, S. 2013. phyloseq: An R package for reproducible interactive analysis and graphics of microbiome census data. *PLoS One* 8: e61217.
- McPhail, K. L., Armstrong, D. J., Azevedo, M. D., Banowetz, G. M., and Mills, D. I. 2010. 4-Formylaminoxyvinylglycine, an herbicidal germination-arrest factor from *Pseudomonas* rhizosphere bacteria. *J. Nat. Prod.* 73:1853-1857.
- Müller, H., and Berg, G. 2008. Impact of formulation procedures on the effect of the biocontrol agent *Serratia plymuthica* HRO-C48 on Verticillium wilt in oilseed rape. *BioControl* 53:905-916.
- Nagel, M., Kranner, I., Neumann, K., Rolletschek, H., Seal, C. E., Colville, L., and Fernández-Marín, B., Börner, A. 2015. Genome-wide association mapping and biochemical markers reveal that seed ageing and longevity are intricately affected by genetic background and developmental and environmental conditions in barley. *Plant Cell Environ.* 38:1011-1022.
- Nagel, M., Rosenhauer, M., Willner, E., Snowdon, R. J., Friedt, W., and Börner, A. 2011. Seed longevity in oilseed rape (*Brassica napus* L.)—Genetic variation and QTL mapping. *Plant Genet. Resour.* 9:260-263.
- Newcombe, G., Harding, A., Ridout, M., and Busby, P. E. 2018. A hypothetical bottleneck in the plant microbiome. *Front. Microbiol.* 9:1645.
- Oksanen, J., Blanchet, F., Kindt, R., Legendre, P., Minchin, P., O'Hara, R., Simpson, G., Solymos, P., Stevens, M., and Wagner, H. 2017. Vegan: Community ecology package. R package version 2.4-2.
- Panke-Buisse, K., Poole, A. C., Goodrich, J. K., Ley, R. E., and Kao-Kniffin, J. 2015. Selection on soil microbiomes reveals reproducible impacts on plant function. *ISME J.* 9:980-989.
- Paredes, S. H., Gao, T., Law, T. F., Finkel, O. M., Mucyn, T., Teixeira, P. J. P. L., González, I. S., Feltcher, M. E., Powers, M. J., Shank, E. A., et al. 2018. Design of synthetic bacterial communities for predictable plant phenotypes. *PLoS Biol.* 16:e2003962.
- Paredes, S. H., and Lebeis, S. L. 2016. Giving back to the community: Microbial mechanisms of plant–soil interactions. *Funct. Ecol.* 30:1043-1052.
- Peay, K. G., Kennedy, P. G., and Talbot, J. M. 2016. Dimensions of biodiversity in the Earth mycobiome. *Nat. Rev. Microbiol.* 14:434-447.
- Peiffer, J. A., Spor, A., Koren, O., Jin, Z., Tringe, S. G., Dangl, J. L., Buckler, E. S., and Ley, R. E. 2013. Diversity and heritability of the maize rhizosphere microbiome under field conditions. *Proc. Natl. Acad. Sci.* 110: 6548-6553.
- Pérez-Jaramillo, J. E., Carrión, V. J., Bosse, M., Ferrão, L. F. V., de Hollander, M., García, A. A. F., Ramírez, C. A., Mendes, R., and Raaijmakers, J. M. 2017. Linking rhizosphere microbiome composition of wild and domesticated *Phaseolus vulgaris* to genotypic and root phenotypic traits. *ISME J.* 11: 2244-2257.
- Perrier, X., and Bonnot, O. 2003. Methods of data analysis. Genetic Diversity of Cultivated Tropical Plants, CRC Press, Boca Raton, FL.
- Rezki, S., Campion, C., Iacomí-Vasilescu, B., Preveaux, A., Toubalia, Y., Bonneau, S., Briand, M., Laurent, E., Hunault, G., Simoneau, P., et al. 2016. Differences in stability of seed-associated microbial assemblages in response to invasion by phytopathogenic microorganisms. *PeerJ* 4:e1923.
- Rezki, S., Campion, C., Simoneau, P., Jacques, M.-A., Shade, A., and Barret, M. 2018. Assembly of seed-associated microbial communities within and across successive plant generations. *Plant Soil* 422:67-79.
- Rodrigues Pereira, A. S., Houwen, P. J. W., Deurenberg-Vos, H. W. J., and Pey, E. B. F. 1972. Cytokinins and the bacterial symbiosis of *Ardisia* species. *Z. Pflanzenphysiol.* 68:170-177.
- Rodríguez, C. E., Mitter, B., Barret, M., Sessitsch, A., and Compant, S. 2018. Commentary: Seed bacterial inhabitants and their routes of colonization. *Plant Soil* 422:129-134.
- Rybakova, D., Mancinelli, R., Wikström, M., Birch-Jensen, A.-S., Postma, J., Ehlers, R.-U., Goertz, S., and Berg, G. 2017. The structure of the *Brassica napus* seed microbiome is cultivar-dependent and affects the interactions of symbionts and pathogens. *Microbiome* 5:104.
- Sasse, J., Martinoia, E., and Northen, T. 2018. Feed your friends: Do plant exudates shape the root microbiome? *Trends Plant Sci.* 23:25-41.
- Schlaeppli, K., Dombrowski, N., Oter, R. G., Ver Loren van Themaat, E., and Schulze-Lefert, P. 2014. Quantitative divergence of the bacterial root microbiota in *Arabidopsis thaliana* relatives. *Proc. Natl. Acad. Sci.* 111: 585-592.
- Sturrock, C. J., Woodhall, J., Brown, M., Walker, C., Mooney, S. J., and Ray, R. V. 2015. Effects of damping-off caused by *Rhizoctonia solani* anastomosis group 2-1 on roots of wheat and oil seed rape quantified using X-ray computed tomography and real-time PCR. *Front. Plant Sci.* 6:461.
- van Opstal, E. J., and Bordenstein, S. R. 2015. Rethinking heritability of the microbiome. *Science* 349:1172-1173.
- Vannette, R. L., and Fukami, T. 2017. Dispersal enhances beta diversity in nectar microbes. *Ecol. Lett.* 20:901-910.
- Wagner, M.-H., Ducournau, S., Luciani, A., and Léchappé, J. 2012. From knowledge-based research towards accurate and rapid testing of seed quality in winter rape. *Seed Sci. Res.* 22:S80-S85.
- Wallace, J. G., Kremling, K. A., Kovar, L. L., and Buckler, E. S. 2018. Quantitative genetics of the maize leaf microbiome. *Phytobiomes J.* 2: 208-224.
- Walters, W. A., Jin, Z., Youngblut, N., Wallace, J. G., Sutter, J., Zhang, W., González-Peña, A., Peiffer, J., Koren, O., Shi, Q., et al. 2018. Large-scale replicated field study of maize rhizosphere identifies heritable microbes. *Proc. Natl. Acad. Sci.* 115:7368-7373.
- Wang, Q., Garrity, G. M., Tiedje, J. M., and Cole, J. R. 2007. Naïve Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Appl. Environ. Microbiol.* 73:5261-5267.
- Zhao, Q., Xiong, W., Xing, Y., Sun, Y., Lin, X., and Dong, Y. 2018. Long-term coffee monoculture alters soil chemical properties and microbial communities. *Sci. Rep.* 8:6116.