From standard to region-specific monocrops : localizing industrial agriculture through microbes' taste of place

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SPECIAL ISSUE

FROM STANDARD TO REGION-SPECIFIC MONOCROPS

Localizing Industrial Agriculture through Microbes' Taste of Place

Diego Silva Garzón

Abstract

Industrial agriculture has promoted the expansion of monocrops around the world, aided by the circulation of highly standardized plant varieties. However, given the adverse environmental effects of this agricultural approach (such as genetic erosion) and the challenges posed by climate change, some biotech companies are trying to complexify industrial agriculture's relationship to "place". They are beginning to consider local particularities in the design of seed products. Focusing on the experience of an Argentinian biotech company, this article explores the creation of microbial seed treatments that claim to be "region-specific" and whose production is mediated by novel meta-genomic techniques. Through the notions of association and mediation, the article reflects on the diverse meanings of region-specificity (geographical, environmental, relational) that are mobilized in the creation of these products. In this way, the article highlights the role of computational technologies, plants, and microorganisms in the shaping of scientific and corporate meanings of place.

Keywords: *climate change, climate resilient crops, locally adapted crops, microbial seed treatments, plant-microbial interspecies associations, postfordist agriculture*

Introduction

Industrial agriculture has promoted the expansion of monocrops around the world, aided by the circulation of highly standardized plant varieties. Today, some biotech companies are trying to complexify industrial agriculture's relation to "place" by taking into account local particularities in the design of microbial seed treatments. A crucial promise of these treatments is their claim to "region-specificity". For example, the US company Indigo AG takes microbial samples from farmers' crops to produce a diagnosis of underground microbial diversity. This diagnosis serves as guidance to prescribe bacterial strains that could improve plant health and growth in specific places. The Argentinian biotech company Bioceres follows a different approach. Guided by metagenomic analyses, the company has isolated multiple bacterial strains from Argentinian soils with the potential of contributing to crops' productivity in different regions of the country. These companies measure microbial products' region-specificity by their capacity to increase yield in particular locations. However, it is not evident how these companies define what constitutes a region when designing these products: are they targeting particular geographies, ecosystems, techno-natures or socially produced "places"? In this paper I analyse how region-specificity is defined in the microbial treatments produced by Bioceres. By following this company's microbial seed treatments from their conception to their materialization, I explore Bioceres' efforts and challenges to create and stabilize this type of plant-microbial associations.

The relevance of this question is linked to the history of the seed industry and its challenges in the age of climate change. Throughout much of the 20th century, the search for plant traits in industrial agriculture was largely guided by Fordist ideals such as plant uniformity, genetic stability, and yield. These plant qualities facilitated the mechanization of agricultural activities and the emergence of a seed industry that could guarantee plant quality from one generation to the other (Kloppenburg 2004, 117–18). In the pursuit of this objective, commercial plant varieties were turned into standard commodities to be planted across different environments. The cultivation of standard plant varieties in different environments was mediated by the expansion of monocrop technonatures. Forests were cleared, undesired plants and insects (weeds and pests) targeted, poor soils chemically fertilized, plant sizes and genetics manipulated, etc. This approach allowed plant breeders, agronomist, and farmers to replace local difference with monocrop uniformity, organizing agricultural fields as Fordist factories (Fitzgerald 2003). In this way, industrial agriculture has encouraged "a one-size-fits-all approach instead of context specific schemes" (Parmentier 2014, 14).

Despite the increasing levels of productivity per-worker that have accompanied this homogenizing approach (Douillet and Girard 2013, 3–4; Mazoyer and Roudart 2009, 12), industrial agriculture has been associated with increasing levels of plant genetic erosion. Plant breeders have prioritized the selection of high-yielding varieties over plants with other qualities (such as disease resistance and tolerance to environmental stress). This process has not only increased the genetic uniformity of crops but it has also made them less resilient in wild environments and more vulnerable to the rapid spread of diseases. Industrial agriculture has therefore been accompanied by a trade-off between crops' productivity and resilience. Novel plant varieties yield more but are generally more dependent on their human caretakers (Warman 2003, 27; Pollan 2016, 19; Hartigan 2017, xx). Moreover, industrial agriculture has been criticized for having a bulldozing effect over local environments and communities (Shiva 1991). As the agricultural frontier becomes smaller, farmers encroach upon highly diverse ecosystems simplifying agricultural landscapes with the tools of industrial monocropping (Schaller 2013, 1).

The increasing frequency and intensity of extreme climate events is changing the underlying conditions that make it acceptable for industrial plant breeders to replace local particularities with monocrop agriculture and to trade plant resilience for productivity. This trade-off is acceptable for industrial farmers insofar as they can compensate for ecosystemic care and protect plants from environmental threat. However, trading plants' resilience for high yields is less desirable when environmental conditions become extreme and industrial strategies to care for crops (such as the use of fossil fuel based agrichemical products) only exacerbate the climate crisis (Schaller 2013, 1). As a result, the seed industry is increasingly questioning the sustainability of the plant productivity/resilience trade-off. Some biotech companies are focusing on finding ways to enhance crops' resilience to extreme climates by paying attention to local particularities.

Aware of the limitations posed by generic techniques of plant breeding, companies such as Indigo AG and Bioceres Crop Solutions have decided to expand their focus beyond seeds and genes. New techniques in microbial research have motivated these companies to turn their efforts to the development of novel agricultural treatments. While plant scientists had been aware of useful plant-microbial interactions for a long time, these interactions were not sufficiently understood. Moreover, microbial research was slow due to the need to culture microorganisms before they could be analysed. The result was that the utility of plant-microbial synergies remained largely limited to the scale of the plot and field, but for the most part could not be scaled up for market commercialization.[1] Metagenomic methods – "a series of experimental and computational approaches that allow a microbial community's composition to be defined by DNA sequencing" (Benezra, DeStefano, and Gordon 2012, 6378) – significantly broke with these limitations. These methods have allowed agricultural scientists to analyse the variation of microbial communities in relation to plant and soil diversity without having to culture its members. These methods have also allowed biotech companies to produce microbial metagenomic libraries and microbial collections that could be potentially useful for the production of "region-specific" agricultural treatments.

Microbial libraries and collections have acquired a new sense of value as computational technologies have opened the door for the development of novel agricultural commodities (Fullilove 2018). Not only do these technologies mediate the transformation of innumerable bacterial strains into novel seed treatments, they also allow exploring interspecies synergies between bacteria, plants, transgenes, and chemical products. For example, the composition of soil microbial diversity can be associated to the cultivation of particular crops or to particular agricultural practices. The power of computational technologies to help humans visualize interspecies synergies is a central variable in the production of new imaginaries of region-specific crops. These technologies highlight the fact that "place" is never an empty space but a web of relations that is co-constructed by organic, inorganic, cultural, and technological relations alike. In so doing, they give agricultural scientists a new tool for imagining useful combinations between these elements, and to establish symbiotic relations between them in particular localities. Thus, while the objective of this article is to unpack what region-specificity means in the production of novel microbial seed treatments, this analysis is based on the observation that novel seed technologies re-create "nature" itself. As novel seed systems combine transgenic, microbial, and computational technologies, they establish dialogues with, and transform entanglements between, local interspecies relations.

The article is organized as follows. I first discuss the emergence of novel microbial treatments in agriculture vis-à-vis the problems of generic plant breeding. I then concentrate on Bioceres' development of new plant-microbial assemblages in Argentina. To do this I use the notions of association and mediation as defined in Actor-Network-Theory. After a short pre-

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[1] The production of microbial inoculants for leguminous plants was an exception that will be discussed later in the article.

sentation of these concepts, the article focuses on three detours faced by Bioceres in its efforts to stabilize plant-microbial associations. These detours were not merely obstacles in a linear process of product development; they had an effect on the way the notion of region-specificity was mobilized in the creation of microbial seed systems.

In the absence of academic studies on the topic, Bioceres had to first produce knowledge about the connection between soil microbial communities and plant growth and health in commercial plant varieties. Then, Bioceres needed to translate this knowledge into commercial products. Non-human mediators (plants, bacteria, soil, chemicals) informed this process, sometimes inspiring human imaginations of plant-bacterial associations and sometimes forcing humans to change their plans. In particular, ideals of replicating plant-microbial relations found in soils and plant roots were quickly abandoned because these relations were considered too complex for humans to replicate. Scientists then concentrated on isolating bacteria that could improve crop performance in bacteria's "native" locations. When these bacteria proved to be useful outside of these areas too, Bioceres' scientists re-defined region-specificity not as a geographical, but as an environmental variable.

The notion of region-specificity can be further problematized when considering the future plans of the company, which are in line with the progress of microbial treatments in the biotech industry. The ideas of preventive medicine are now considered for the development of agricultural products. Soils can be diagnosed and microbial treatments can be customized to "improve" soil microbial compositions in ways that lead to higher yield. In this last strategy, region-specificity becomes increasingly linked to a relational notion of place, where place is not defined by geography or environmental qualities, but by human-plant-microbial-soil relations. I end the article asking if the region-specific logic of novel microbial treatments could be put into dialogue with agroecological principles that promote ecosystemic synergies in agriculture. This dialogue is relevant as the corporate actors of industrial agriculture face significant pressure to diversify their products, while agroecological experts discuss how to scale up their productive systems.

From generic genes to plant-microbial relations

According to the World Food Program: "Climate change is making climate disasters, such as floods and droughts, more frequent and intense, land and water more scarce and difficult to access, and increases in agricultural productivity even harder to achieve" (World Food Program 2015). In fact, as I have shown elsewhere (Silva 2020), Argentinian farmers are beginning to experience the increasing frequency and intensity of droughts. In the past decade, the Argentine agricultural sector suffered three of the most extreme droughts in fifty years (Agrovoz 2018). The last of them took place in the 2017-2018 soy season and led to a decline in soy production of 33 percent with respect to the previous year (Errea and Tassone 2018). Considering that Argentina is the third-largest soy producer in the world, the drought had a significant impact on the national economy. The national Gross Domestic Product (GDP) experienced a decline of around 0.75 percent, without taking into account the indirect effects that the production decline would have on complementary sectors such as transport, commerce, and industry (Errea and Tassone 2018).

One of the strategies that has been pursued around the world to face the agricultural challenges of climate challenge is the development of so-called climate-ready crops—seeds that are tolerant to abiotic stress, such as droughts, soil salinity, frost, and cold. Given the commercial success of first-generation transgenic crops,[2] plant scientists and biotech companies have tried to produce climate-resilient crop varieties through genetic engineering since the early 2000s. However, plant scientists quickly noticed that the creation of transgenic climate-resilient plants responded to a different type of problem than the creation of first generation transgenic crops, such as insecticidal or herbicide tolerant crops. As the CEO of Bioceres explained to me, the capacity of GE plants to kill insects or to tolerate herbicides is a qualitative problem – it happens or it does not happen, the plant kills the insect or it does not.[3] Instead, plants' resilience to climate events such as droughts or floods is a quantitative problem – it can happen in different degrees depending on many variables, such as the intensity of the climate event.

As argued by Passioura (2012, 851), in early experiments, plants modified with climate-resilient traits were able to express tolerance to varied adverse climate conditions under controlled environments. However, these benefits disappeared in field conditions or were accompanied by production decline. This result was largely due to the complexity and variability that is introduced when scaling up a trait of interest from individual plants grown in pots to communal plants grown in fields (Passioura 2012), and also due to poor knowledge of the effects that the variability of climate events (such as the extent, intensity, and frequency of droughts) can have over commercial crops (Chapman et al. 2000, 197). Thus, whereas it was possible to create generic insecticidal or herbicide tolerant crops, Passioura (2012, 851) concluded that "the search for generic drought tolerance using single-gene transformations has been disappointing."

While plant scientists struggled to make use of genetic engineering for the production of generic climate resilient crops, important developments were underway at the intersection of microbial research and epigenetics. This research revealed the potential of plant-microbial associations for the creation of region-specific climate-resilient crops. A landmark study carried out by Turnbaugh et. al. (2006) asked if the microbial communities that live in our gut could make some individuals more prone to obesity than others. Their research was based on the idea that the human metagenome is composed not only by *Homo sapiens* genes but also by the genome of the microorganisms that colonize our bodies, and that these microorganims "encode metabolic capacities that we have not had to evolve wholly on our own" (2006, 1027). The boundaries of the human body were blurred; as suggested by Helmreich (2014), we could rename *homo sapiens* as *homo microbis*.

The importance of Turnbaugh's et. al. (2006) study went beyond this conclusion. Using mice as model animals, the study revealed that colonization of germ-free mice[4] (mice with-

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[2] Around 192 million hectares of land were planted with this type of crops in 2017 with an estimated value of 17 billion dollars (International Service for the Acquisition of Agri-biotech Applications 2018).

[3] Interview with Federico Trucco held on 7 March 2019.

[4] Germ-free mice are bred in isolators which fully block exposure to microorganisms, with the intent of

out a microbiome) with an "obese microbiota" (harvested from genetically obese mice) results in a significantly greater increase in total body fat than colonization with a "lean microbiota" (harvested from lean mice). In other words, obesity is not fully determined by genes. Instead, the microorganisms that mice and humans host in their gut have epigenetic effects on their bodies that could be linked to obesity. The epigenetic effects of gut microorganisms on mice have been further evidenced by Krautkramer et. al. (2016), who showed that shifts in the availability of dietary fiber in mice can lead to changes in gene expression with specific physiological outcomes.[5]

This conclusion was important for agriculture. It allowed imagining new strategies of crop design for conditions of abiotic stress that did not rely on genetic engineering. Iansiti , Toffel, and Snively (2006, 6) describe how Flagship Ventures, a life sciences venture capital firm, became interested in the human microbiome in 2007. Flagship later launched an exploration project in 2012 that was focused on plants and microorganisms and that ultimately led to the development of the agricultural company Indigo AG. The authors also show that in 2013, Monsanto and Novozymes formed a joint venture "focused on developing and commercializing microbial-based biological products" (Iansiti, Toffel, and Snively 2016, 6). The logic behind these investments was straightforward. According to Von Maltzahn, cofounder of Indigo AG:

> *by helping humans, they (microbes) improve their own evolutionary success... If the same is true for plants, which are also full of microbial communities, these microbes might have spent millions of years helping plants survive drought, heat, cold, salt, nutrient stress, and beyond... We concluded that the biology was so special that it might spawn an industry the size of biotech today, potentially $ 50 billion to $ 100 billion of innovative new therapeutics, based on the microbiome.* (Vom Maltzahn in Iansiti, Toffel, and Snively 2016, 6)

In other words, microbial research revealed bacteria as an actant that could be related to plants in ways that would allow imagining promising agricultural effects. In particular, soil bacteria could be central in the process of crops' climate resilience. Diverse microbial combinations could be crucial to unlocking plants' productivity in diverse locations under conditions of climate stress. If these plant-microbial connections could be proven and if useful bacterial communities or bacterial strains could be identified, selected, and added to crops, agricultural companies would have the capacity to create microbial treatments for agricultural climate-resilience. In short, where generic plants had failed, plant-microbial associations could potentially prevail. This was a business opportunity that corporate capital could not ignore.

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keeping them free of detectable bacteria, viruses, and eukaryotic microbes (Kennedy, King, and Baldridge 2018).

[5] See Landecker and Kelty (2019) for a simple explanation of the underlying mechanism.

Region-specific microbes

For more than a decade the Argentinian biotech company Bioceres has been working on the development of a multi-technology and multi-species seed system known as the ECOSeed, where ECO stands for environmentally customized organism. This seed system promises to increase crops' climate resilience by improving their adaptation to different agricultural soils and by helping crops respond differentially to drought variability. The ECOSeed system is composed of carefully selected germplasm, a drought-tolerant transgenic trait, region-specific microbial seed treatments and various digital technologies (such as climate information systems, scout applications to help farmers monitor their fields, and virtual market platforms, among others). Central to the seed systems' differential and region-specific response to droughts are its transgenic and microbial layers. I have explored the mechanism of the ECOSeed's transgenic technology elsewhere (Silva 2020). In this paper I focus on the analysis of the seed systems' region-specific microbial technologies.

Let us travel to the headquarters of Bioceres, where scientists and managers discuss plant-bacterial associations. Bioceres is located in the scientific and technological park of CONICET in the city of Rosario. Inagurated in 2010, the multimillion-dollar building hosts a number of start-up companies, as well as laboratories of genetics, plant improvement, genomics and bioinformatics. In 2019, I negotiated access to the facilities of Bioceres explaining my interest on the company's ECOSeed system. I was given a cubicle on the second floor of the building surrounded by administrative personnel. The cubicle was just a step away from the seed division of the company and one floor above the company's laboratories.

On a particularly sunny day of late September 2019, I had scheduled an interview with Dr. Martín Vazquez. It was an important interview to understand the microbial layer of the ECOSeed system. Dr. Vazquez had led the scientific consortium that discovered useful associations between microbial communities and plant heath and growth, which later motivated Bioceres to invest in the development of microbial seed treatments. In preparation for the interview, I had watched a TEDx talk that Vazquez had given in Rosario (Vazquez 2012). In the presentation, he reflected on the wonders of predictive medicine. He explained how, given the appropriate genome sequencing equipment, we can now predict the probability of an unborn baby to develop a disease in the future. Vazquez recognized the ethical issues that predictive medicine raised as humanity increases its power to decide what type of nature should live or not. Despite the fact that Vazquez did not mention plant organisms in his presentation, it was easy to draw parallels between his conclusions for medical innovations and the future of agriculture. Not only has plant diversity been greatly influenced by plant breeders' decisions about what type of nature is desirable, their power to choose what type of organisms live or die has dramatically increased with the emergence of metagenomic methods.

With the TEDx talk in my mind, I left my cubicle and walked towards Vazquez's office in Bioceres. Sitting behind the glass door of his office he signaled to me to come inside and we were quickly immersed in a discussion about microorganisms and technical devices. Vazquez explained to me that in the early 2000s Bioceres was investing in plant genetic traits with high agricultural potential but that the company lacked the equipment to sequence plant genomes in-house. Despite this, Vazquez knew that the same type of equipment that had given scientists the power to predict genetic diseases could be used to filter plants for useful traits. As a strategic move to increase its bio-prospecting capacity for plant traits, Bioceres decided to lead the creation of a metagenomic and bioinformatics platform, which would become the first one of its kind in Latin America. However, as Vazquez told me, Bioceres could not afford this initiative on its own so it actively sought state funds through research grant proposals. The main project that resulted from these efforts and that allowed Bioceres to create its metagenomic and bioinformatics platform was called "SoilGene." The results of SoilGene motivated Bioceres to create a joint venture with Rizobacter, a local company of microbial inoculants, for the production of region specific seed treatments. The joint venture was called "Semya".

In this section I trace the efforts of SoilGene and Semya to produce knowledge about plant microbial associations and to translate this knowledge into commercial microbial seed treatments. To do this, I use the notions of association and mediation as defined in Actor-Network-Theory (ANT). In ANT, an association is an assemblage of new relations between heterogeneous things and beings that are not necessarily "social" and that were not connected before in the same way (Latour 2005, 5). In the mapping of these associations the analysis of mediation takes precedence over the study of stabilized products. A great deal of mediation or "work-net" (Latour 2005, 132) is necessary to stabilize plant-microbial associations into immutable mobiles (Latour and Woolgar 1986) that behave in predictable ways and that can be therefore traded in the market. Thus, I follow how actors (human or not) mediate the multiple connections created by Bioceres between plants and bacteria. That is, I study how these actors help to define, redefine, stabilize or destabilize microbial seed treatments in uncertain ways. ANT's focus on mediation, serves to highlight the uncertainty that exists on the direction that associations will take before they are stabilized, the agency of mediators in the shaping of results, and the latent prevalence of instability over stability. In ANT, when associations become stable and mediation becomes less uncertain, mediators become intermediaries and the analysis of associations in the making becomes difficult to trace. The ECOSeed's microbial seed treatments, as a product in the making that is still not commercially available, offers a great case for the analysis of human-led plant-microbial mediations.

SoilGene – imagining ideal microbial communities

In 2010, eleven research groups from Bioceres[6], the Universidad de Buenos Aires, the Universidad de Quilmes, and the Universidad de la Plata created the SoilGene consortium. The

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[6] Bioceres was able to finance the creation of its metagenomics and bioinformatics platform mainly through public funds that were channeled to its research branch, the *Instituto de Agrobiotecnologia de Rosario* (INDEAR). INDEAR was created by Bioceres in 2004-2005 in alliance with the pharmaceutical company Bio-Sidus and the state's National Scientific and Research Council (CONICET). In 2009, Bioceres acquired all the shares of INDEAR (Gras and Hernandez 2016, 207), just one year before the creation of the SoilGene consortium. For the sake of clarity, I do not make the distinction between Bioceres and INDEAR in the main

objective of this consortium was to study the soil microbial diversity of the humid areas of the central Argentinian region known as the *Pampas*. The consortium created the largest soil microbial dataset for this region (Rascovan et al. 2013) composed of 19 million DNA sequences, or the equivalent to 3 thousand complete bacterial genomes. Based on the collection of 130 soil samples from five different agricultural and non-agricultural locations in the *Pampas*, the project found DNA sequences that correspond to hundreds of different metabolic routes, many of which could be of agricultural interest (Vazquez, Rascovan, and Carbonetto 2013). Further studies using this dataset showed that there was indeed a relation between microbial communities, plant health, and crop productivity (Rascovan et al. 2016).

Knowledge about the utility of plant-microbial associations in agriculture is not new. Microbial products based on this type of associations have been used for decades, in particular, soil bacteria that can help leguminous plants to transform atmospheric nitrogen into ammonia, which has a fertilizing effect on plants. Despite this, the novelty of the SoilGene project should not be underestimated. While a few bacterial strains had been used in agriculture for many years, efforts to map the genomic sequence of bacterial genomes were very recent, as were initiatives to find correlations between microbial communities and plant health and growth. For Vazquez, there was no question about the novelty of SoilGene: "We are talking about the years 2008–2009, there was no knowledge of this, around the world this was still in the realm of science fiction."[7]

Vazquez explained to me that SoilGene aimed at better understanding Argentinian soils and their microbial diversity under different uses and environmental conditions: agricultural fields vs non-agricultural fields, soils with good agricultural practices and soils with bad agricultural practices, soils that produce high yielding crops with rain and in the absence of rain, among other comparisons. Therefore, a crucial aspect of SoilGene was that it allowed the linking of microbial communities extracted from particular localities to agricultural productivity under conditions of environmental stress. This opened up the prospect of creating region-specific microbial treatments designed from, or that targeted, specific agricultural locations.

This prospect was directly related to Bioceres' plant breeding goals. At the time, Bioceres was investing in a transgenic trait known as HB4 that could improve the tolerance to droughts of commercial crops such as soy and wheat. This second-generation transgenic trait overcomes some of the difficulties of plant breeders' first attempts at producing climate-resilient crops through genetic engineering. It allows plants to respond differentially, not generically, to droughts (Silva 2020). The prospect of adding region-specific microbial treatments to HB4 seeds gave Bioceres the chance of compounding the differential response of HB4 crops to environmental stress. A larger seed system could be created using HB4 and region-specific microbial treatments for the production climate-resilient seeds. Therefore, the pursuit of a genomics and bioinformatics platform for the bioprospection of plant traits led Bioceres

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text of the paper.

[7] Interview with Martín Vazquez held on the 24 September 2019.

to turn its attention to the bioprospection of soil microbia for the production of region-specific microbial treatments.

The idea of turning plant-microbial relations into region-specific microbial treatments is not simple or obvious. What did Bioceres scientists mean when they talked about region-specificity and how did they go about achieving this objective? One floor below Vazquez's office I had the chance to talk to Dr. Mauricio Grisolia, the then head of the genomics and bioinformatics platform of Bioceres.[8] After listening to an incredibly detailed explanation about how the platform was used in the SoilGene project, Dr. Grisolia and I imagined the "ideal" microbial treatment to promote crops' climate resilience. This imaginary product would help plants to replicate in low performing soils the specific plant-microbial associations that are present in high-performing crops. Low performing soils would then acquire the living characteristics of high performing soils through the mediation of bacterial communities and plant roots. The role of bacteria in this imaginary product would be to transfer the characteristics of a good agricultural "place" to the seed, so that plants could grow healthy and yield more in the diverse soils where they would be cultivated.

Grisolia explained to me that devising a product based on microbial communities is nowadays practically impossible. It is already difficult to isolate and prepare a single bacterial strain for agricultural use; it would be much more complex to create products based on the multiple synergic relations of microbial communities. Moreover, the difficulties of such approach are not limited to replicating microbial relations. Soil and plants play a central role in the type of microbial communities that emerge in a given agricultural plot. SoilGene scientists have shown that soils can be widely diverse (acid/basic, humid/dry, compact/porous among other qualities) and their PH can influence soil microbial diversity (Rascovan et al. 2016, 8–9). Moreover different crops (such as soy and wheat) attract different microbial communities to the soil that is closely around and inside their roots (Rascovan et al. 2016, 8). Therefore, the way in which soils, plants and microbia relate would also need to be taken into account for the design of this ideal type of microbial treatment. The difficulty of replicating such interspecies relations made this imaginary product too complex for human manufacturing. Rascovan labelled it "a fiction" in a conversation that I had with him in September 2018.

The alternative to this imaginary product, which was ultimately followed by Bioceres, was to isolate single bacterial strains from local soils. In this alternative, scientists would characterise microbial samples collected from particular regions of the country and then select the bacterial strains that expressed useful qualities for plant growth and health. The selected bacterial strains would become candidates for the production of region-specific microbial treatments for plants. In this case, however, region-specificity had a different meaning. The imaginary product that Grisolia and I discussed in his office used a notion of region-specificity based on a complex set of interspecies relations that were found in certain places and that could not be replicated elsewhere. Instead, as we will see in the next section, the alternative that was followed by Bioceres relied on a hypothesis that linked region-specificity to geography.

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[8] Interview with Mauricio Grisolia held on the 27 September 2019.

Semya – "native" microorganism and their connection to place

Motivated by the findings of SoilGene, Bioceres initiated a joint venture with the neighbouring company Rizobacter, which had positioned itself as one of the most important producers of microbial inoculants in the world.[9] The joint venture was called Semya and it was motivated by the possibility of selecting and culturing bacterial strains that could improve plants' health and growth in particular places. To trace the way in which Semya carried out this task, I had to leave the headquarters of Bioceres in Rosario and travel one hour South to the city of Pergamino, where Rizobacter is located.

Rascovan et. al. (2016) present some of the most important scientific results of Semya. The authors of this publication were, and some continue to be, affiliated to either Rizobacter or Bioceres. From this publication we can infer that the bacterial strains sought by Semya needed to fulfil at least three conditions. First, they needed to offer useful agricultural qualities (fertilizing, fungicidal, or inoculating effects). This explains Semya's focus on bioprospecting for plant growth-promoting microorganisms (PGPM) for wheat and soy. Second, they needed to interact with soils and microorganisms that are closely around and inside roots in ways that allow bacterial strains to successfully colonize plant roots (Rascovan et. al. 2016, 2). In this respect, Semya worked to better understand the microbial composition of Argentinian soils and the ways in which soil properties and crop diversity contribute to soil microbial assemblages. Finally, microbial products needed to survive in local environments, where they are at high risk of being replaced by "indigenous" species. To achieve this purpose Semya worked under the hypothesis that "strains that are naturally adapted to a certain environmental condition would have a better fitness and higher survival rate in that environment" (Rascovan et. al. 2016, 9).

With regards to this last condition, Semya scientists initially went further in this hypothesis, highlighting the importance of microbial "indigenousness". According to Dr. Gustavo Gonzalez Anta, one of the leaders of Semya, "the initial hypothesis was that we were going to find a relation between the microorganisms extracted from a particular region and the performance of plants in that region. We believed that if we moved that microorganism elsewhere its correlation to plant performance was going to be lower that in its region of origin."[10] Thus, the region-specific products that Semya expected to create initially followed a notion of plant-microbial relations that was linked to geography. Microbial seed treatments were expected to contribute to crops' performance the most, in their "native" locations.

Having defined the desired conditions for the production of microbial products for wheat and soy, Semya's scientists needed to collect and culture bacterial samples. Rizobacter's chief PGPM researcher, Marisa Diaz, explained this process to me in a conference room in Rizobacter.[11] Soy and wheat plants were grown in parcels across 11 locations in the country. Microbial samples were collected from soil closely attached to roots and inside roots. The samples were taken to the laboratories of Rizobacter and bacterial communities were iso-

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[9] In 2018, Bioceres became the majority shareholder of Rizobacter.

[10] Interview with Gustavo Gonzalez Anta held on the 5 December 2019.

[11] Interview with Marisa Diaz held on the 15 October 2019.

lated, cultivated in petri dishes and grown into single-species colonies. In total 2533 and 2070 bacterial samples were isolated for wheat and soy respectively. Some strains were lost through manipulation or could not be identified during the process of genomic identification. Others were found to contain the same bacterial strains and repetitions were discarded. In the end, 543 strains from wheat and 683 from soy went through the next phase of biochemical tests, where bacterial strains were filtered for desirable qualities.

A long process of selection was then carried out with the help of growth media. The bacterial strains were put in special substances that allowed to select strains with particular qualities and to discard others without such qualities. For example, when selecting for bacteria than can help plants capture nitrogen, bacteria were grown in a medium without nitrogen. If cultivated bacteria survived and grew in this medium, it was deduced that this bacteria had the capacity to capture nitrogen from the atmosphere and potentially pass it on to plants. Another example is given by an adverse medium where only bacteria expressing the ACC-deaminase enzyme could develop.[12] Roughly speaking, the expression of this enzyme can be used to improve plants' resilience to climate stress (Esquivel-Cote et al. 2013). In a similar way, all the selected samples were filtered in different media for growth promoting, inoculant, and fungicidal characteristics, and only bacteria showing multiple favourable responses were selected. In this way, cultivating media also served as a way of defining certain bacteria according to these traits, which in turn was used to attribute roles to bacteria (as an inoculant, fertilizing, or fungicidal agent).

As mentioned above, the collection of samples in multiple regions of the country followed the hypothesis that native bacteria would have a better fitness and survival rate than alien bacteria. Moreover, it was expected that bacteria would be more useful to plants in the bacteria's region of origin. However, as scientists filtered bacterial strains according to their PGPM qualities and tested their capacity to increase crops' performance in the fields, this last hypothesis was challenged. Dr. Gonzalez Anta told me that among their bacterial candidates for microbial seed treatments, Semya found that some bacterial strains were capable of contributing to plants' performance in many geographical locations with similar environmental conditions. A distinction was therefore drawn between microbial agricultural contributions in particular geographies and their contribution in different environments. In other words, the initial notion of region-specificity guiding Semya's development of microbial seed treatments was transformed. In this new notion, a region is not a geographical location but a set of environmental qualities linked to humidity, heat, rain, soil pH, etc. The transformation in the notion of region-specificity led to the production of a few wide spectrum PGPM bacterial strains for soy and wheat for regions with similar environmental conditions.

From imaginary microbial treatments – based on the idea of replicating plant-microbia-soil relations, we turned to region-specific microbial products – based on the idea that "native" bacteria could help crops adapt better in particular geographical locations. Following Semya's results, we are now forced to take an additional detour linking region-specificity to environmental variables. A crucial aspect behind these detours is the agency of non-hu-

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[12] Interview with Marisa Diaz held on the 15 October 2019.

man mediators. We were forced to give up the relational notion of region-specificity created by plants, microorganisms, and soils, because these relations were too complex for humans to replicate. Now we have to give up the geographical understanding of region-specificity because bacteria, in this particular context, have proven to care little about geographical dislocations.

Microbial diagnostics – a way back to relational thinking

Despite the power of non-humans in our story, there is a large degree of human responsibility in these detours. Semya's geographical hypothesis, linking "native" bacteria to crops' local adaptation, follows what John Hartigan (2017, 58) has referred to as plant racial thinking: a type of thinking that connects geographical places to plant qualities. This type of thinking is so powerful that it has informed projects of ex-situ conservation around the world, which take samples of "native" plants to conserve their qualities in seed banks.

In his book "Care of the Species", Hartigan differentiates racial thinking to what some of his interlocutors in Mexico refer to as *razas* (local plant varieties used for specific purposes given their specific qualities). In a conversation held by Hartigan with a plant scientist called Alfonso, this scientist expresses his frustration with plant conservation initiatives that "only focused on the seed, the seed alone" (Hartigan 2017, 58). Instead, plant *razas* are an aspect of culture because "they are associated with a particular use they're given" (Alfonso in Hartigan 2017, 61). In other words, while racial thinking highlights plant qualities produced by place, without explaining how place and plant qualities are created, *razas* thinking connects plant qualities to human use in particular locations. Through racial thinking plant collectors detach the seed (or the bacteria) from its "native" place and store it in a seed bank (or a microbial library). Instead, in *razas* thinking plant qualities are co-created in particular places by plant-human relations.

In *razas* thinking there is no such thing as plant diversity conservation. "Native" plant qualities cannot be collected and stored because plant qualities will change when plant-human relations are modified. Instead, plants are in a constant process of "improvement" linked to human selection and use in particular places. For example, Virginia Nazarea and Robert Rhoades (2013, 4) argue that plant material stored in genebanks (ex-situ) can deteriorate "due to imperfect conditions and human error" and freeze its evolutionary potential "due to long-term storage, resulting in the inability of germplasm to respond to environmental changes." Similarly, Nazarea and Rhoades argue that in-situ and in-vivo conservation programs rarely yield to any programmatic design. In in-situ and in-vivo conservation plant biodiversity is not conserved. Instead, it flourishes thanks to the messiness and on-going creativity of plants outside the disciplinary infrastructures of seed banks and monocrops.

In the case of microbial treatments, *razas* thinking could be expanded beyond plant-human relations to include plant-microbial relations. While for Alfonso humans select and improve plants for particular uses, Semya scientists have proven that plants can themselves be selectors of microorganisms. They have shown that crops such as wheat and soy attract different type of useful microbial communities to their roots (Rascovan et al. 2016). In fact, recognizing plants as selectors of bacterial qualities is one of the reasons why some agricultural innovators think that some plants have already found the solution to climate change, by attracting microorganisms that "have spent millions of years helping plants survive drought, heat, cold, salt, nutrient stress, and beyond" (Iansiti, Toffel, and Snively 2016, 6). *Razas* thinking, that very localized Mexican concept, can be renamed as relational thinking. In relational thinking, plant, microbial, soil, and even human qualities are the result of relations. Plant or microbial qualities are therefore not the result of being "native" to a place, but the result of the countless human and non-human relations that take place in particular locations. Anthropologists have for a long time been arguing that place is not a geography built on an empty space (Casey 1996) but rather a series of relations (Gupta and Ferguson 1997) that can only be non-exhaustively mapped. Agricultural places are imbued by cultural and biological memory (Nazarea and Rhoades 2013) in ways that cannot be completely de-territolized, redefined as a resource, and re-territorialized in seed banks or in markets (Fullilove 2018, 298).

The conservation of plant qualities linked to particular places is probably best-exemplified through the production of specialized crops that are protected by *appellation d'origine contrôlée,* such as different types of Bordeaux wine or Sicilian Olive oil. Not only are these crops produced through the disciplinary tools of industrial agriculture, producers also have incentives to keep plant qualities as stable as possible from one generation to the next. In this case, specific plant qualities are what constitute the identity of the product. But even in this type of "conservation", place is linked to a series of human and non-human relations that link "geology and climate with culture and craft in the making of food" and that are often referred to as *terroir* or taste of place (Beriss 2019, 62).

Relational thinking helps us to understand why Semya's geographical notion of region-specificity had to be replaced for an environmental notion. It is highly probable that similar types of plant-microbial-soil relations can be found in places with similar environmental conditions to a given bacteria's place of origin. Relational thinking opens up the notion of *terroir* to include a microbial taste of place. Despite this, Semya's turn to environmental explanatory forces behind microbial qualities still hides the relational work that is responsible for the on-going becoming of those environments. From that perspective, bacterial products are thought of as discrete entities able to express useful agricultural qualities in similar environments, as opposed to connected entities capable of modifying the relations that constitute host environments themselves. This explanation might be enough to characterize Bioceres' current microbial products (made of isolated single bacterial strains with PGPM qualities) but is not enough to explain the trajectory of microbial product development in agriculture.

Recall Vazquez explanations in his TEDx talk about predictive medicine. By sequencing the genome of a particular individual, doctors can predict the probability of future illness and target specific changes to prevent undesired outcomes. This approach does not seek to identify and replicate the ideal genetic sequence (yet). Instead, it aims at finding specific harmful mutations that can be corrected through targeted interventions or that can provide information to patients for decision-making. Importing this diagnostic logic into the production of microbial products offers an interesting possibility for agriculture. After examining the microbial diversity of a particular agricultural plot, companies could diagnose the absence of beneficial strains and recommend a targeted microbial treatment (as done by Indigo AG in the US).

Microbial seed treatments of this type do not try to replicate microbial communities in all their complexity, as I had discussed with Grisolia. Also, this type of product is not based on "native" bacteria with particular qualities capable of enhancing plants' performance in native places. Nor is it made of discrete bacteria with agricultural qualities capable of surviving in particular environments. Instead, bacterial products of this type are designed to change the composition of microbial communities by triggering useful relations between plants, microorganisms, and soils. By 2016, this type of relational thinking was already voiced by Semya scientists. Having overcome geographic and environmental hypothesis their objective became to "modulate the composition of root microbiomes to improve crop health and growth" (Rascovan et. al. 2016). This type of approach is already carried out in the US by Indigo AG and Bioceres plans to offer this type of product for Argentina in the future. A first step to achieve this objective is to create a collection of isolated microbial treatments that could be prescribed to farmers to improve the microbial composition of their particular soils. This is where Bioceres efforts are being deployed today.

Conclusion: opening a dialogue between industrial agriculture and agroecology

Focusing on the experience of the Argentinian company Bioceres, this article explored what region-specificity means in the production of microbial seed treatments. It followed scientific imaginations where "ideal" microbial compositions are replicated outside of their places of origin. Since the capacity of plants, soils, and microorganisms to create synergies is too complex to recreate, these imaginations were quickly abandoned by plant scientists, or deemed fictional. Thus, the article traced Bioceres' decision to identify and isolate useful bacterial strains from multiple locations that could be used for the production of microbial seed treatments. This strategy followed a geographical hypothesis: native bacterial strains would have a higher change of surviving and creating synergic interactions with plants in their places of origin. When selected bacterial strains proved to be useful outside of these areas, the geographical notion of region-specificity was replaced by a new notion linking microbial performance to environmental characteristics.

I argued that geographical region-specificity can be linked to what Hartigan (2017) calls racial thinking, a type of thinking that relates plant qualities to particular places without explaining how plant qualities are created in the first place. I confronted racial thinking to the notion of *razas*, which links plant qualities to particular human uses and to the way in which humans select plant varieties based on cultural preferences. When considering microbial treatments, I suggested that *razas* can be expanded to include more-than-human relations. Bioceres scientists have shown that plants can be selectors of microbial life as they co- organize microbial communities in ways that can be useful for plant growth and health. A relational explanation of plant qualities would therefore pay attention to the agency of plants, microorganisms, and other non-humans relations in the production of plant qualities.

The notion of *terroir*, often translated as "taste of place", can therefore be expanded to include the taste of plants and microorganisms.

The environmental understanding of region-specificity that was ultimately adopted by Bioceres is more relational that the previous geographical notion. It points to the particular relations that can emerge under similar environmental conditions. However, I argued that this notion of region-specificity still hides the power of non-human relations in making crops thrive in certain locations. Accrediting and "external environment" for plants and bacterial performance is not the same as arguing that plants and bacteria are enmeshed in an uncountable web of localized relations that help to create those environments. In other words, inter-species relations make plants into highly porous and localized entities (Silva 2020b, 187). Relational thinking is better expressed by current agricultural trends to import the diagnostic logic of preventive medicine into agriculture. This logic seeks to identify existing relations between plants, soils, and microorganisms and to potentiate desired relations through targeted microbial interventions.

An important question emerges from these considerations. Can we see microbial treatments as a move towards agroecological relational principles? From its inception, agroecology has combined ecology and agronomy to analyse the different components of an agroecosystem[13] and the way in which these components interact and are affected by human agricultural management (Wezel et al. 2009, 2). The goal of agroecological knowledge is to produce more sustainable agricultures, giving raise to a wide range of agricultural recommendations that usually focus on the plot or field scale. However, Wezel (2009, 7) argues that while this scalar focus persists up to the present, some researchers have devised a series of productive principles that could help extend agroecological practices to the level of the farm and beyond. Some of these principles prioritize the promotion of multispecies synergies above and below ground "that can sponsor system services like regenerating soil fertility and providing pest management" (Rosset et al. 2011, 163).

While agroecological experts discuss how to scale up agroecological practices by making multispecies alliances above and below ground, this article suggest that agricultural companies are moving in the opposite direction. In this case, the objective is not to scale up practices but to complexify industrial agriculture's homogenizing approach by paying attention to local particularities. It is therefore important to analyse whether or not these oppositional movements are creating trajectories towards each other, and the role of plants, microorganisms and metagenomic technologies in the process.

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[13] Communities of plants and animals interacting with their physical and chemical environments.

References

Agrovoz. 2018. "Por qué la sequía es la 'peor de los últimos 50 años.'" *Agrovoz*, March 29. Accessed November 11, 2020. http://agrovoz. lavoz.com.ar/clima/por-que-la-sequia-es-la-peor-de-los-ultimos-50-anos.

Benezra, Amber, Joseph DeStefano, and Jeffrey I. Gordon. 2012. "Anthropology of Microbes." *Proceedings of the National Academy of Sciences* 109, no. 17: 6378–81. https://doi.org/10.1073/pnas.1200515109.

Beriss, David. 2019. "Food: Location, Location, Location." *Annual Review of Anthropology* 48: 61–75. https://doi.org/10.1146/annurev-anthro-102317-050249.

Casey, Edward. 1996. "How to Get from Space to Place in a Fairly Short Stretch of Time: Phenomenological Prolegomena." In *Senses of Place*, edited by Steven Feld and Keith H. Basso, 1st ed, 13–52. School of American Research Advanced Seminar Series. Santa Fe, N.M. : [Seattle]: School of American Research Press.

Chapman, Scott, Mark Cooper, David Butler, and Robert Henzell. 2000. "Genotype by Environment Interactions Affecting Grain Sorghum. I. Characteristics That Confound Interpretation of Hybrid Yield." *Australian Journal of Agricultural Research* 51, no. 2: 197-208. https://doi.org/10.1071/AR99020.

Douillet, Mathilde, and Pierre Girard. 2013. "Productivité agricole: Des motifs d'inquiétude? (I) Les concepts." *FARM (Foundation pour l'agriculture et la ruralité dans le monde),* 2013 (juillet). Accessed April 19, 2021. https://www.fondation-farm.org/zoe/doc/notefarm7_productivite_juil2013.pdf.

Esquivel-Cote, Rosalba, Marina Gavilanes-Ruiz, Rocío Cruz-Ortega, and Pilar Huante. 2013. "Importancia agrobiotecnológica de la enzima ACC desaminasa en rizobacterias, Una revisión." *Revista Fitotecnia Mexicana* 36: 251–58.

Errea, Damian, and Paola Tassone. 2018. "El Impacto de La Sequía En La Actividad Será Transitorio Y Concentrado En El Segundo Trimestre de 2018." *Ideas de Peso.* Banco Central de La República Argentina. Accessed July 6, 2020. https://ideasdepeso.com/2018/06/04/el impacto-de-la-sequia-en-la-actividad-sera-transitorio-y-concentrado-en-el-segundo-trimestre-de-2018/.

Fitzgerald, Deborah. 2003. *Every Farm a Factory*. New Haven: Yale University Press.

Fullilove, Courtney. 2018. "Microbiology and the Imperatives of Capital in International Agro-Biodiversity Preservation." *Osiris* 33, no. 1: 294–318. https://doi.org/10.1086/699993

Gras, Carla, and Valéria A. Hernandez. 2016. *Radiografía del nuevo campo argentino: Del terrateniente al empresario transnacional*. México, DF: Siglo Veintiuno.

Gupta, Akhil, and James Ferguson, eds. 1997. *Culture, Power, Place: Explorations in Critical Anthropology*. Durham, N.C: Duke University Press.

Hartigan, John. 2017. *Care of the Species: Races of Corn and the Science of Plant Biodiversity*. Minneapolis: University of Minnesota Press.

Helmreich, Stefan. 2014. "Homo Microbis: The Human Microbiome, Figural, Literal, Political." *Thresholds* (November), 52–59. https://doi.org/10.1162/thld_a_00076.

Iansiti, Marco, Michael Toffel, and Christine Snively. 2016. "Indigo Agriculture." *Harvard Business School Case,* Case No: 617 020.

International Service for the Acquisition of Agri-biotech Applications. 2018. "Global Status of Commercialized Biotech/GM Crops." Brief 54. Accessed February 14, 2021. https://www.isaaa.org/resources/publications/briefs/54/default.asp.

Kennedy, Elizabeth A., Katherine Y. King, and Megan T. Baldridge. 2018. "Mouse Microbiota Models: Comparing Germ-Free Mice and Antibiotics Treatment as Tools for Modifying Gut Bacteria." *Frontiers in Physiology* 9 (October): 1534. https://doi.org/10.3389/fphys.2018.01534

Kloppenburg, Jack Ralph. 2004. *First the Seed: The Political Economy of Plant Biotechnology*. Madison: University of Wisconsin Press.

Krautkramer, Kimberly A., Julia H. Kreznar, Kymberleigh A. Romano, Eugenio I. Vivas, Gregory A. Barrett-Wilt, Mary E. Rabaglia, Mark P. Keller, Alan D. Attie, Federico E. Rey, and John M. Denu. 2016. "Diet-Microbiota Interactions Mediate Global Epigenetic Programming in Multiple Host Tissues." *Molecular Cell* 64, no. 5: 982–92. https://doi.org/10.1016/j.molcel.2016.10.025.

Landecker, Hannah, and Chris Kelty. 2019. "Outside In: Microbiomes, Epigenomes, Visceral Sensing, and Metabolic Ethics." In *After Practice: Thinking through Matter(s) and Meaning Relationally*, edited by Laboratory: Anthropology of Environment / Human Relations, 53–65.

Latour, Bruno. 2005. *Reassembling the Social: An Introduction to Actor-Network-Theory*. Oxford : Oxford University Press.

Latour, Bruno, and Steve Woolgar. 1986. *Laboratory Life: The Construction of Scientific Facts*. Princeton: Princeton University Press.

Mazoyer, Marcel, and Laurence Roudart. 2009. "Des agricultures manuelles à la motorisation lourde : Des écarts de productivité considérables." *Grain de Sel* 48: 12. Accessed April 19, 2021. https://www.inter-reseaux.org/wp-content/uploads/pdf_GDS48_p12_Mazoyer_Roudart.pdf.

Nazarea, Virginia D, and Robert E. Rhoades. 2013. "Conservation Beyond Design: An Introduction." In *Seeds of Resistance, Seeds of Hope: Place and Agency in the Conservation of Biodiversity*, edited by Virginia D. Nazarea, Robert E. Rhoades, and Jenna Andrews-Swann, 3–18. Tucson: University of Arizona Press.

Parmentier, Stéphane. 2014. *Scaling-up Agroecological Approaches: What, Why and How?* Belgium: Oxfam-Solidarité. Accessed April 19, 2021. http://www.fao.org/fileadmin/templates/agphome/scpi/Agroecology/Agroecology_Scaling-up_agroecology_what_why_and_how_-OxfamSol-FINAL.pdf.

Passioura, John B. 2012. "Phenotyping for Drought Tolerance in Grain Crops: When Is It Useful to Breeders?" *Functional Plant Biology* 39, no. 11: 851. https://doi.org/10.1071/FP12079.

Pollan, Michael. 2016. *The Omnivore's Dilemma: A Natural History of Four Meals*. New York, NY: Penguin Books.

Rascovan, Nicolás, Belén Carbonetto, Diego Perrig, Marisa Díaz, Wilter Canciani, Matías Abalo, Julieta Alloati, Gustavo González-Anta, and Martín P. Vazquez. 2016. "Integrated Analysis of Root Microbiomes of Soybean and Wheat from Agricultural Fields." *Scientific Reports* 6, no. 28084. https://doi.org/10.1038/srep28084.

Rascovan, Nicolás, Belén Carbonetto, Santiago Revale, Marina D Reinert, Roberto Alvarez, Alicia M Godeas, Roxana Colombo. 2013. "The PAMPA Datasets: A Metagenomic Survey of Microbial Communities in Argentinean Pampean Soils." *Microbiome* 1, no. 21 (online). https://doi.org/10.1186/2049-2618-1-21.

Rosset, Peter Michael, Braulio Machín Sosa, Adilén María Roque Jaime, and Dana Rocío Ávila Lozano. 2011. "The Campesino to Campesino Agroecology Movement of ANAP in Cuba: Social Process Methodology in the Construction of Sustainable Peasant Agriculture and Food Sovereignty." *Journal of Peasant Studies* 38, no. 11: 161–91. https://doi.org/10.1080/03066150.2010.538584.

Schaller, Noémie. 2013. "L'agroécologie : Des *définitions* variées, des principes communs." Analyse 59 (Juillet): 1–4. *Centre d'études et des prospective*. Ministère de l'agriculture de l'agroalimentaire et de la forêt. https://agriculture.gouv.fr/lagroecologie-des-definitions-variees-des-principes-communs-analyse-ndeg59.

Shiva, Vandana. 1991. *The Violence of the Green Revolution: Third World Agriculture, Ecology, and Politics*. London: Atlantic Highlands, N.J., USA: Penang, Malaysia: Zed Books; Third World Network.

Silva, Diego. 2020. "Keep Calm and Carry On: Climate Ready Crops and the Genetic Codification of Climate Ignorance." *Science Technology & Human Values*. https://doi.org/10.1177/0162243920974092.

Silva Diego. 2020b. Argentinean Agribusiness and the Porous Agricultural Company. *Tapuya:*

Latin American Science, Technology and Society 3, no. 1: 170–189.

Turnbaugh, Peter J., Ruth E. Ley, Michael A. Mahowald, Vincent Magrini, Elaine R. Mardis, and Jeffrey I. Gordon. 2006. "An Obesity-Associated Gut Microbiome with Increased Capacity for Energy Harvest." *Nature* 444 (7122): 1027–1031.

Vazquez, Martín P. 2012. "Compartiendo Nuestro Genoma En Una Red Social." Presented at the TEDx Rosario, Rosario Argentina, February 1. Accessed April 19, 2021. https://www.youtube.com/watch?v=Si9CCjfBEzY&ab_channel=TEDx-Talks.

Vazquez, Martín P, Nicolás Rascovan, and Belén Carbonetto. 2013. "Una nueva herramienta para estudiar la biodiversidad del suelo." *Ciencia con voz propia* (blog). October 29, 2013. Accessed April 19, 2021. https://www.conicet.gov.ar/una-nueva-herramienta-para-estudiar-la-biodiversidad-del-suelo/.

Warman, Arturo. 2003. *Corn & Capitalism: How a Botanical Bastard Grew to Global Dominance*. Chapel Hill: University of North Carolina Press.

Wezel, A., S. Bellon, T. Doré, C. Francis, D. Vallod, and C. David. 2009. "Agroecology as a Science, a Movement and a Practice. A Review." *Agronomy for Sustainable Development* 29, no. 4: 503–15. https://doi.org/10.1051/agro/2009004.

World Food Program. 2015. "Two Minutes on Climate Change and Hunger. A Zero Hunger World Needs Climate Resilience." *Climate and Disaster Risk Reduction Programmes*. Unit World Food Program. Accessed April 19, 2021. https://docs.wfp.org/api/documents/WFP-0000009143/download/?_ga=2.38064035.1224722245.1594650392-719131962.1594650392.

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