acids per second) (*5*). In addition, these studies provided the first direct observation of translation initiation frequency in cells, occurring every 30 to 40 s on an actively translated mRNA; this is suggested to be the rate-limiting step for most protein production (*6*) (see the figure, panel B).

These averaged features agreed well with bulk biochemical measurements, but single-molecule analyses can also reveal how translation is variable among mRNAs. It has been widely accepted that mRNAs continually bind initiation factors through their 5′ cap and recruit ribosomes. By tracking a single mRNA over several hours, Yan *et al*. and Wu *et al*. revealed fluctuations between nontranslating and translating states of mRNA. The time scale for switching translation on and off ranged from 15 min (seen as "bursts") to 3 hours across different cell types and reporters. Although the cause of the fast translation bursts remains unknown, they may be coupled with the localization of mRNAs, or reflect cycles of mRNA decapping and cytoplasmic recapping (*7*).

Translation kinetics vary widely between genes, depending on the mRNA sequence and RNA binding proteins bound to the transcript, and are subject to dynamic control (*8*). Wang *et al*. shed new light on the classic translation regulation pathway triggered by the response to oxidative stress and by the unfolded protein response in endoplasmic reticulum. These stress responses induce phosphorylation of the eukaryotic translation initiation factor eIF2α, generally reducing overall initiation while activating a subset of mRNAs, including the transcript encoding the stress-induced transcription factor activating transcription factor 4 (Atf4). Surprisingly, this translation activation is transient, only lasting ~150 s, despite the sustained increase in the amount of Atf4 protein seen during stress.

Locally controlled translation can restrict protein production to a specific place within the cytoplasm and thereby plays many roles in the internal spatial organization of the cell (*9*). For example, regulated protein synthesis at specific neuronal synapses is required for long-term potentiation of those synaptic connections, and thus for learning and memory. Wu *et al*. and Wang *et al*. directly visualized translation occurring within dendrites, the branched projections of neurons. Dendritic mRNAs are thought to be transported from the cell body to the synapses in a translationally repressed state. The authors observed a trend of higher translation efficiency toward the proximal end of dendrites, and lower efficiency at the distal end. Intriguingly, translation is not completely silenced during transport; ~20% of mRNAs are actively translated while exhibiting rapid (~2 μm/s) and directional movement along dendrites.

An mRNA being actively translated by a number of ribosomes forms a complex known as a polysome. Polysome mobility varied between subcellular compartments and between individual mRNAs in both neurons and less elaborated cells. Most cytosolic polysomes showed freely diffusive movement, although some showed constrained, "subdiffusive" movement, and a rare few were actively transported.

The protein encoded by the mRNA also influenced polysome mobility—longer reading frames produce larger, slower-moving polysomes at steady state. Nascent actin protein being synthesized by the ribosome yielded subdiffusive polysome movement, perhaps mediated by actin protein-protein interactions. Secreted proteins undergoing cotranslational membrane insertion restrained polysome movement even more.

Such nascent protein interactions might also explain why, although the majority of polysomes behaved independently, a detectable fraction (~5%) of polysomes from two distinct mRNAs encoding the same protein comigrated in cytoplasm. This compartmentalized "dipolysome" may be explained by the cotranslational assembly of a protein complex, as observed in bacteria (*10*).

Although these studies relied on exogenous reporters to detect translation, tagging endogenous loci by genome editing could illuminate translation in a yet more physiological context. Indeed, following in the footsteps of single-molecule mRNA tracking, measurement of translation in diverse tissues and developmental conditions will uncover critical information on the dynamics of translation and its regulation in time and space. ■

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ECOLOGY

Soil immune responses

Soil microbiomes may be harnessed for plant health

By **Jos M. Raaijmakers**[1,2] *and* **Mark Mazzola**[3]

Soil microorganisms are central to the provision of food, feed, fiber, and medicine. Engineering of soil microbiomes may promote plant growth and plant health, thus contributing to food security and agricultural sustainability (*1*, *2*). However, little is known about most soil microorganisms and their impact on plant health. Disease-suppressive soils offer microbiome-mediated protection of crop plants against infections by soil-borne pathogens. Understanding of the microbial consortia and mechanisms involved in disease suppression may help to better manage plants while reducing fertilizer and pesticide inputs.

There are two types of disease suppression in soils. General suppression is based on competitive activities of the overall micro- and macroflora and is universal to all soils.

> ***"The complexity of soil microbiome–plant interactions argues for [taking] a community perspective."***

Specific suppression is attributed to the enrichment of specific subsets of soil microorganisms. Specific suppression has been reported for plant pathogenic fungi, fungal-like oomycetes, bacteria, nematodes, and parasitic weeds. It is eliminated by soil pasteurization or biocides and can be transferred to conducive soils, in which only general suppression is operative, via soil transplantations. When Henry first reported transplantation of disease-suppressive soils 85 years ago, he elegantly showed that specific suppression of *Helminthosporium* foot rot of wheat was most likely

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caused by the combined action of soil bacteria and fungi (*3*).

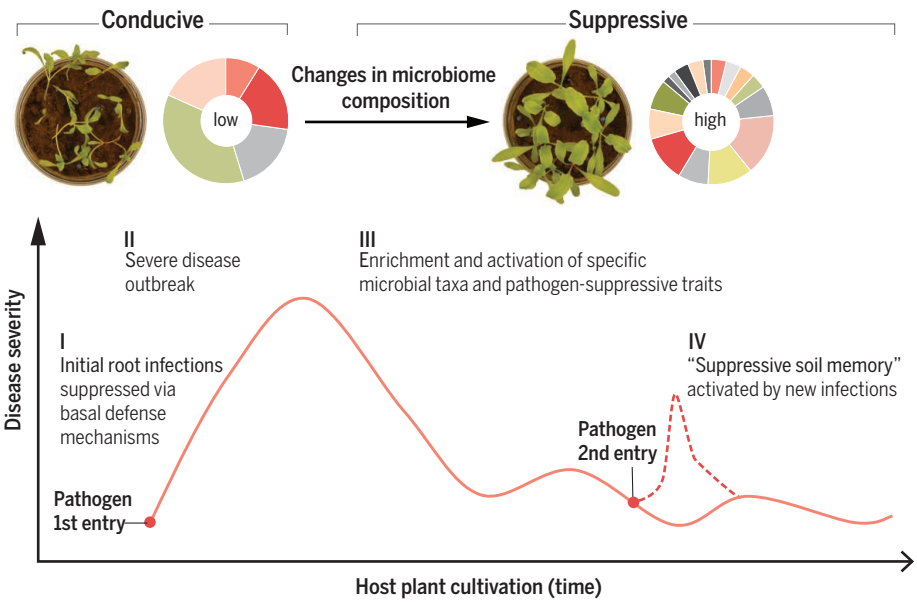
Specific suppression of various fungal root pathogens is typically induced by a disease outbreak that occurs in field soils during continuous cultivation of a susceptible host plant. Once established, specific suppression can dissipate if nonhost plants are grown or other root diseases emerge. It is rapidly regained in the presence of the original host plant and inducing pathogen (see the figure).

The characteristics of general and specific suppression of soils are comparable to those described for innate and adaptive immunity in animals. Both general suppression of soils and innate immunity in animals provide a fast, nonspecific line of defense against an invading pathogen. Both specific suppression of soils and the adaptive immune response in animals require time to react to the invading pathogen, are specific to the pathogen, and have a memory of the previously encountered pathogen (see the figure).

Specific suppression is mechanistically complex, requiring enrichment and activation of select microbial consortia and antagonistic traits that interfere with the infection cycle. Eliciting specific suppression requires multilateral interactions between pathogen, host plant, and soil microbiome. The initial interaction between pathogen and plant, leading to a disease outbreak, may cause the release of metabolites from the pathogen and the plant, which in turn enrich and activate pathogen-suppressive microbes (*4*).

Specific suppression of several fungal root pathogens has been attributed, in part, to the production of antifungal metabolites by different bacterial genera (*5*, *6*) and to carbon competition and induced systemic resistance by nonpathogenic fungi (*7*, *8*). Kinkel *et al.* have implicated *Streptomyces* species in suppression of scab, a bacterial disease of potato (*9*). Olatinwo *et al.* have proposed parasitism by the fungus *Dactylella oviparasitica* as a key mechanism in suppression of a plant pathogenic nematode (*10*). Although the interactions in soils suppressive to a specific pathogen are biologically complex, the mechanisms appear to be the same in different soils from geographically distinct regions (*11*). This functional similarity across many agroecosystems suggests that it may be possible to develop a universal approach to engineer disease-suppressive soil microbiomes.

Molecular and chemical technologies now allow identification of differences in microbiome composition between suppressive and conducive soils beyond the description of select microbial genera. They further enable comprehensive analyses of the temporal changes in microbiome activities as the soil shifts from the conducive to the disease-suppressive state. This knowledge also allows elucidation of the mechanisms that lead to the onset of specific disease suppression.



Lines of defense. If a pathogen can circumvent the basal defenses in both soil and plant, a severe disease outbreak may occur. This disease outbreak can last for years but will ultimately enrich for specific microbial consortia and pathogen-suppressive traits in the soil and plant microbiome. This specific suppression can dissipate but is rapidly regained in the presence of the original host plant and inducing pathogen. The images show plants exposed to a fungal pathogen in disease-conducive and -suppressive soils. In the conducive soil with a low abundance of antagonistic microbial consortia, the fungal pathogen causes disease (left), whereas in the suppressive soil with a high abundance of antagonistic microbial consortia, most seedlings remain healthy (right).

Studies of disease-suppressive soils have not yet yielded far-reaching solutions to soil-borne disease management and enhancing crop productivity. Rather, the main outcome has been the isolation of single microbial species subsequently applied to soil or plant seeds as biological agents for pathogen control. Many of these microbial strains fail to establish or survive in soil or on plant roots because of competition with the indigenous soil microbiome. As a result, this approach has met with limited success in large-scale agriculture. The complexity of soil microbiome–plant interactions argues for new strategies that go beyond "one-microbe-at-a-time" approaches and take a community perspective. This includes the design and application of mixtures of different microbial species, referred to as synthetic communities or syncoms (*12*). A second strategy involves augmenting indigenous disease-suppressive consortia native to the soil ecosystem. Engineering such indigenous microbial consortia could yield a more stable soil memory that limits pathogen infestations.

Practical means to attain this outcome in sustainable disease management include selection of or breeding for plant genotypes with specific root traits that recruit or activate pathogen-suppressive microbial populations (*12*, *13*). Agricultural production system inputs, including soil amendments such as compost and seed meal, can also be used, like prebiotics in humans, to selectively drive the microbiome to a composition and active state that limits proliferation of soil-borne pathogens (*14*). To this end, fundamental knowledge of coevolutionary trajectories in plant-pathogen-microbiome interactions is needed (*10*). Mechanistic understanding of specific plant metabolites and pathogen effectors that trigger, like vaccines in animals, the adaptive immune response of soils may provide practical means to engineer the indigenous soil microbiome for enhancing plant health and securing future crop yields. ■

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