

ENVIRONMENTAL SCIENCE

Renewable Benefits

Few would doubt the proposition that wind and solar power provide health and environmental benefits by reducing emissions of carbon dioxide and other air pollutants, although few have considered in depth how the advantages of those renewable energy technologies might differ regionally. The variability of the advantages of renewable power is largely a function of the type of power generation that it displaces. Siler-Evans *et al.* look at how existing power generation facilities are distributed across the United States and analyze the impacts of replacing those facilities with wind or solar installations. They find uneven but significant—and in some regions, very large—social and environmental benefits resulting from the adoption of those technologies. They also discuss the value of the Production Tax Credit Subsidy for wind energy generation, how its effectiveness could be improved by regional differentiation of the policy, and how the large-scale adoption of wind or solar energy production might affect their more site-specific analysis. — HJS

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EVOLUTION

Open to Change

Changes in the regulation of gene expression can result in changes in organismal phenotypes. Nakagawa *et al.* have used phylogenetic analysis and biochemical measurement to study DNA binding specificity changes in the forkhead box (Fox) family of transcription factors. This family is present in a wide range of species and is one of the largest classes of transcription factors in humans. They used phylogenetic inference methods to examine the relationship of Fox domain sequences spanning 623 genes from 65 species, and they characterized binding specificity *in vitro* for 21 Fox proteins and combined this with published binding data for 9 proteins. They found that changes in specificity from canonical forkhead primary (FkhP) and forkhead secondary (FkhS) motifs to alternative DNA sequences have occurred separately in three different Fox subfamily lineages. In fungal Fox3 proteins, two specificities have arisen, FHL-3 and FVH, but only FVH binding involves the mutation of residues involved in DNA recognition. In the metazoan FoxM subfamily, proteins retain specificity for FkhP and FkhS but are also able to bind an FHL motif, whereas in the holozoan FoxN subfamily, some proteins exhibit a similar bispecificity, yet others have lost the ability to bind the

canonical sites and only bind FHL-N. Fox domains that display bispecific binding are probably able to switch between two conformations with distinct DNA binding specificities. Such bispecificity may be central in the evolution of transcriptional regulatory networks. — VV

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MICROBIOLOGY

Hide and Seek

Plants and their fungal pathogens are at war. Plant surface receptors, which contain lysin motifs (LysMs), sense fungal chitin oligomers, which are basic components of fungal cell walls, and



thereby trigger immune defenses against the fungus. The fungi, in turn, have evolved molecular countermeasures. Sanchez-Vallet *et al.* report

structural studies of a fungal effector protein, Ecp6, which is secreted by the leaf mold *Cladosporium fulvum* and provides a means for the pathogen to hide from the host. Ecp6 also contains LysM, but unlike the plant's receptors, the fungal motifs dimerize in the presence of its own chitin to form a deeply buried groove that binds chitin with high affinity and keeps it out of sight of the plant's immune responses. LysM seems to be ubiquitous among fungi and may represent a common mechanism by which such pathogens can evade host defenses. It is interesting that two evolutionarily distant organisms have converged on the ability to recognize the same molecule via the same motif that resides in divergent proteins and with antagonistic effect. — CA

eLife **2**, e00790 (2013).

PLANT SCIENCE

Location and Timing

In plants, the circadian network coordinates physiological processes with the daily rhythms of light and dark. The protein GIGANTEA (GI) is found in both nuclear and cytoplasmic compartments of the plant cell and regulates different partners in the two locations. Using *Arabidopsis*, Kim *et al.* constructed plants with disrupted subcellular localizations of GI. Their modeling analyses of the