

CLIMATE CHANGE

Sex-specific responses

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WILL PETRY

Different sexes often exhibit distinct phenotypes, including varied responses to the environment, which raises an intriguing question — do plants respond to climate change in a sex-specific manner? Studying the dioecious plant *Valeriana edulis*, William K. Petry, at the University of California, USA and colleagues report a rapid sex-specific response to increasing water scarcity.

V. edulis grows in the Rocky Mountains, where water availability increases with elevation. A survey of sex ratios in 31 populations across the species's elevation range showed that male frequency declined as aridity decreased, resulting in female-biased populations at higher elevations.

Data across four decades for nine populations showed that males became more frequent across the species's elevation range with the decrease of precipitation and soil moisture over time. This provides evidence that climate change is driving an upslope shift of male frequency at a rate of 175 metres per decade, a magnitude higher than the hitherto reported rate of species's range shift. The sex-specific climate response is likely to arise from sex-specific reproductive life span and water use efficiency.

The change in male frequency at high elevations elevates seed set and female fitness by increasing pollen availability. Lower down, however, where females are already pollen saturated, the female frequency decrease could lead to widespread effects at multiple levels of ecological organization — such as arthropod communities, which rely more on female than male *V. edulis* plants. JL

ETHNOECOLOGY

Losing traditional knowledge

J. Ethnobiol. 36, 412–432 (2016)

Wild plants and fungi are an important economic resource in the temperate forests of Chile, and for traditional societies worldwide. Their use is contingent on knowledge embedded in stories and memories passed down from generation to generation — but the transmission of this knowledge is grinding to a halt.

Antonia Barreau of the University of British Columbia, Canada and colleagues conducted participant observation, free-listing exercises and interviews with a multi-generational group of the Mapuche people of the Andes. They recorded the most frequently

used and recognized local wild plants and fungi, and found that the extensive knowledge of wild plants displayed by adult women and elders was not shared by younger generations.

An important route for transmission of ecological knowledge is experience. Children used to accompany their elders on foraging trips and learn about wild plants *in situ*, but now more children attend boarding schools in cities, private ownership limits access to the forest, and deforestation destroys the habitats of the wild foods. Recognition that ecological knowledge is reliant on specific places and memories passed down through generations, and integrated conservation of intangible and ecological heritage, could arrest this trend. LNE

AGRICULTURAL GENETICS

Rapid gene mining

Nature Genet. <http://doi.org/bmjnp> (2016)

Next-generation sequencing greatly facilitates the application of genome-wide association studies (GWAS) in identifying agronomically important genes. However, population stratification and long linkage disequilibrium (LD) still impede the effective implementation of GWAS. To improve the power of GWAS, Kenji Yano, at Nagoya University, Japan and colleagues have developed a new method for agronomic gene identification.

The researchers carefully selected a panel of 176 *japonica* rice varieties with low structure and the typically long LD of rice populations. GWAS analysis using a linear mixed model detected 26 loci associated with heading date.

For five of the loci, the candidate region was estimated using pair-wise LD correlations. 'Large-effect' polymorphisms that are non-synonymous or disrupt splicing junctions were then specifically analysed to rapidly narrow down candidate alleles. This strategy allowed the authors to identify one gene in four of the five loci, whose role in heading date control was previously known or validated by transgenic experiments by the authors. Another gene, *NALI*, which controls panicle number, was also discovered in a similar manner.

This approach failed to demonstrate statistical significance for the *Hd1* gene underlying the fifth heading-date locus, which the researchers attributed to allelic heterogeneity. Nevertheless, gene-based association analysis could be a solution for allelic heterogeneity through mapping multi-allelic genes. JL

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STOMATAL DEVELOPMENT

Grasses vs *Arabidopsis* Proc. Natl Acad. Sci. USA <http://doi.org/bmjn> (2016)

Soon after plants colonized the land half a billion years ago, they developed stomata to facilitate gas exchange with their new environment. Much later, grasses branched out and successfully adapted to different environments. Grass stomata are unique: linearly aligned, with dumbbell-shaped guard cells, and more efficient. Raissig, Abrash and colleagues from Stanford University, USA, focused on the transcription factors involved in stomatal development in the model grass *Brachypodium distachyon*, and compared them with their better-known *Arabidopsis* orthologues.

Using an unbiased forward genetic screen to identify mutants lacking stomata, and reverse genetics with CRISPR-induced mutations, the authors identify and characterize a series of transcription factors involved in stomatal development in *Brachypodium*. Curiously, *Arabidopsis* and *Brachypodium* use orthologues in the same general developmental processes, but they are differently 'wired', with distinct functions and post-translational regulation.

Stomatal development has become a model for studying postembryonic lineage, asymmetric divisions and cell fate in plants. The accumulated knowledge of this gene regulatory network, central to the evolutionary success of grasses, could now be used for targeted approaches to increase crop productivity through more efficient stomata. GT