discipline is in most cases insufficient to answer students' curiosity. When such a theme is assigned to a Biology teacher, probably the most important obstacle is that teachers often lack appropriate knowledge about the social side of the issue.

PL-5 PLANT RESPONSE TO ABIOTIC STRESS

D. Bar-Zvi

Ben-Gurion University, Beer-Sheva, Israel

Being sessile organisms that cannot relocate, plants are continuously exposed to the everchanging environment. To accommodate to these changes, plants evolved intensive molecular, biochemical and physiological mechanisms to respond to hostile environments. These changes include a global change in the transcriptome and proteome. I will discuss three molecular examples for plant response to drought and salt stress: (a) Salt stress impairs chloroplast structure and affects this organelle's gene expression and genome copy number. (b) Transcription factors are key players in reaching new steady states in transcript levels. The stress hormone, abscisic acid, regulated ABI4 transcription factor plays central role in root biology under stress and non-stress conditions. ABI4 modulates the activity of the Na⁺ transporter HKT1;1 and controls lateral root formation. (c) The Ubiquitin-Proteasome System (UPS) is a major pathway for controlled protein degradation in all eukaryotes, including plants. Proteins descended for degradation are covalently marked by a short ubiquitin chain, by a three step pathway. The third step, is catalyzed by a large family of substrate specific ubiquitin-ligases, is believed to be the modulated step in the decision of protein fate. We have identified new ubiquitin-ligases involved in plant response to abiotic stress, and study their role in plant response to the environment.

PL-6 ANALYSES OF MORPHOLOGY, PHYSIOLOGY, AND MICROBIAL DIVERSITY AFTER A RECENT DIETARY SWITCH IN A LIZARD

A. Herrel

UMR 7179 C.N.R.S/M.N.H.N., Département d'Ecologie et de Gestion de la Biodiversité, Paris, France

Although evolution is commonly considered a slow process, recent evidence has shown that organisms can show dramatic and measurable phenotypic responses after introductions to novel environments in relatively short time spans. We have previously shown how lizards ($Podarcis\ sicula$) have rapidly evolved differences in head morphology, bite strength, and digestive tract structure after experimental introduction onto a small island in the Adriatic Sea, Croatia. Despite the short time scale (36 years) since this introduction, the introduced lizards became omnivores and evolved caecal valves in the hindgut, a structure rarely observed in lizards. These changes in morphology and performance parallel those typically documented among species and even families of lizards in both the type and extent of their specialization. Here, we present novel data on 1) the morphology of the cranium and its muscles using μ CT scanning and 3D geometric morphometric approaches, 2) the digestive physiology of the two populations, and 3) the diversity of the microbiomes in the hindgut using metagenomic sequencing approaches.