NEWS AND VIEWS

PERSPECTIVE

A microarray’s view of life in the desert: adding a powerful evolutionary genomics tool to the packrat’s midden

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Identifying the genetic architecture of adaptive traits is fundamental to understanding how organisms respond to their environment, over both ecological and evolutionary timeframes. Microarray technology that allows us to capture the simultaneous expression of thousands of genes provides unparalleled insight into how organisms cope with their environment at the transcriptional level. Recent studies in Molecular Ecology demonstrate how microarrays can rapidly identify which genes and pathways allow organisms to face some of the most fundamental physiological challenges posed by the environment, including compensation for the hypoxic and thermal stress of high-altitudes (Cheviron et al. 2008) and, in this issue, the biotransformation of toxic plant secondary compounds by mammals (Magnanou et al. 2009).

Microarrays (Ekins et al. 1989; Fodor et al. 1991) are glass slides affixed with hundreds to thousands of oligonucleotide or cDNA sequences (probes). Messenger RNA transcripts (typically reverse transcribed to cDNA) are isolated from a tissue/sample of interest and hybridized to the array. Binding to specific probes indicates that a particular gene was transcriptionally active at or near the time of sampling and thus provides a potentially comprehensive measure of gene expression. Although a tremendously powerful tool, commercially produced oligonucleotide arrays are only available for a handful of model organisms. Nonetheless, evolutionary ecologists have exploited this resource by using a cross-species hybridization approach (e.g. Saetre et al. 2004), that is, hybridizing a model organism array with a nonmodel sample (Bar-Or et al. 2007). Magnanou et al. (2009) present a novel example of using a model muroid microarray (Agilent Technologies, Rattus) to study physiological response in a wild, nonmodel muroid, Neotoma.

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Members of the genus Neotoma range throughout Central and North America (Hall 1981). Referred to as packrats or woodrats (Fig. 1a), these animals are known for their prolific den-building capabilities where they gather vegetation from the surrounding environment to build elaborate, multichambered houses. These houses or middens (Fig. 1b) are conspicuous parts of many communities and contribute to the maintenance of local biodiversity by providing relatively stable internal microclimates utilized by a range of organisms (Reichman 1988; Cranford 1982; Verts & Carraway 2002). Many chambers hold leaves and other plant materials collected in the environment suggesting that woodrats may actively manage their caches to allow natural breakdown of toxic secondary compounds before ingestion (Dearing 1997; Morton & Pereyra

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Fig. 1 (a) Adult Neotoma lepida. (b) Neotoma lepida house at the base of a Juniper tree. Photos courtesy of D. Dearing.
phylogenetically closely related populations of Neotoma lepida that face distinct plant toxins in their current foraging environments. One population is found in a creosote bush (Larrea tridentata) dominated habitat of the Mojave Desert while the other occupies a region in the Great Basin Desert dominated by juniper (Juniperus osteosperma), far north of the current and historic range of creosote. Juniper and creosote produce different plant secondary compounds and, thus, present distinct metabolic challenges to herbivores. In the laboratory, Magnanou et al. (2009) fed wild-caught adult woodrats from each population either their native or non-native diet, and quantified gene expression in the liver. The authors find that creosote and juniper diets induce distinctive biotransformation pathways no matter the native diet of the test population. However, both populations up-regulated more genes in common (49%) on the juniper diet than on one of creosote (21%). Both species ingested similar amounts of juniper-laden chow and, in response, up-regulated 26–27 genes (half of which were the same loci). Despite this relatively similar response, neither population maintained positive mass balance on a juniper diet, suggesting that this plant represents a significant challenge to these animals. In contrast, the native-creosote feeders from the Mojave ate 30% more creosote-laden chow than their Great Basin (creosote-native) counterparts, up-regulated 30 genes vs. 14, and maintained positive mass balance while the Great Basin animals lost mass. Despite a broad range of plasticity exhibited by these populations, meeting the challenge of creosote appears beyond the scope of response available to Great Basin animals, suggesting Mojave animals have either adapted or developmentally acclimated to this potent diet through some combination of genes and pathways described by the authors. Furthermore, although not able to maintain positive mass balance on juniper, the response presented by Mojave animals to this plant may be the result of retained ancestral biotransformation capabilities, as suggested by the authors, and/or the result of recent gene flow with N. lepida populations that inhabit juniper-dominated elevations throughout southwestern Utah and other portions of the Mojave Desert. Overall, the breadth of response during a short acclimation period suggests that woodrats may have the capacity to rapidly deploy alternate biotransformation pathways to meet new challenges and opportunities in their foraging environment. Importantly, a detailed 40,000-year record of vegetational shifts has been preserved in packrat middens along with the remains (faecal pellets, teeth and bones) of the packrats that occupied these various communities through time (Betancourt et al. 1990). Once we fully develop the ability to obtain genetic profiles from these packrat remains, this system will reveal a nearly unparalleled view of mammalian response to climate change.

As is appropriate in cross-species hybridization analyses, the authors call for caution in the interpretation of their results. Cross-species hybridization analyses are subject to probe-matching errors that could either over- or under-represent true expression patterns (Bar-Or et al. 2007). Nonetheless, supplementation of microarray results with follow-up quantitative polymerase chain reaction, as presented in the current study, and/or functional assays, provide critical additional support in the identification of key genes and pathways. Likewise, several ‘pre-analysis’ probe filtration steps can be taken to a priori eliminate probes that are unlikely to provide accurate data. For example, hybridizing whole genomic DNA from a nonmodel organism to the model microarray can identify which probes have too many mismatches to be included in an experiment (Hammond et al. 2005). In short, although still in the early stages of development, many pre- and post-supplementary analyses to cross-species hybridizations can dramatically increase the biologically meaningful conclusions that can be drawn from these data-rich analyses.

Pioneering efforts such as that of Magnanou et al. (2009) form a bridge between the natural selective environment in which these organisms find themselves and the powerful genomics infrastructure that exists for relatively few model organisms. We will quickly be in a position when, no matter the organism of interest, species-specific microarrays will be readily available. Nonetheless, in the interim, innovation of analyses and experimental design with the tools currently in hand is establishing the foundation of our functional genomics framework and its application to our understanding of how organisms interact with their environment.

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References

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