A genetic marker is an easily identifiable piece of genetic material, usually DNA, that can be used in the laboratory to tell apart cells, individuals, populations, or species. The use of genetic markers begins with extracting proteins or chemicals (for biochemical markers) or DNA (for molecular markers) from tissues of the plant (for example, seeds, foliage, pollen, sometimes woody tissues). Laboratory protocols (often well developed, but may need adjustments for certain species) are then applied, resulting typically in visual representations from staining or tagging techniques, which are then converted into data — usually allele types and frequencies, or presence/absence data. Genetic markers thus allow us to characterize genetic diversity.

[a genetic marker is used to tell apart cells, individuals, populations, or species]

Defining, measuring, and interpreting genetic diversity are largely overlapping pursuits. To begin, one can categorize genetic variation as being neutral, detrimental, or adaptive. These values are relative to the organism in which the genetic variation resides (and so may change category from one species to another) and also to a specific time and place (as, for example, alleles that might confer resistance to a disease in one situation may be detrimental when the pathogen is absent).

Another approach is to categorize genetic diversity on the basis of underlying genetic complexity: whether the particular trait of interest is the result of one or many genes acting in concert. If the former, the trait is often simple in its expression — perhaps either present or absent. If there are several or many genes responsible for the trait, there may be many more types or values for that trait. Generally, the more genes, the more 'continuous' the range of expression for that trait. Height is a good example of the latter.

Two general approaches to studying genetic diversity reflect these categories. Genetic markers (biochemical markers such as allozymes, and more recently, molecular markers such as microsatellites) are traditionally involved in measuring neutral genetic diversity at single loci, often randomly sampled in a genome. Quantitative genetics is a field that describes both the experimental designs and statistical analyses for studying the more complex situations of multiple genes acting to produce traits with detrimental or adaptive values. Obviously, these categories are not mutually exclusive: for example, some adaptive or detrimental traits may be the result of single genes. And these two approaches are becoming more closely aligned as technological advances allow the detection of genes — one, few, or many — responsible for various traits. In this Volume, the focus is on single genes or sequences of DNA, presumed neutral (that is, not influenced by selection), and described and measured with 'genetic markers'. More information on quantitative genetics can be found in Volume 6.

The choice of the most appropriate genetic marker for a

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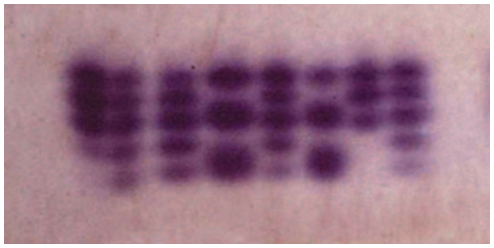
study will depend on the characteristics of that marker, species characteristics (generation time, information already available for the species, tissue types available, existing protocol development for markers for that species, and so on), and genome characteristics (for example, which genome is most appropriate — cpDNA, mtDNA, nuclear DNA?) Among the defining and distinguishing characteristics of the various genetic markers are:

Variability (and resolution) that can be detected by the marker. This will often depend on how much protocol development there has been for that species (for example, the number of 'probes' developed to sample the genome), as well as the cost. This difference between potential to detect variability, and that often available in practice is reflected in the table to the right.



species (phylogenetic) relationships, gene flow, hybridization, fingerprinting, genetic structure of populations, and other objectives. Allozymes, however, are mixed in their utility — often assumed to measure neutral genetic diversity (and therefore suitable for similar studies as molecular markers) but also including some enzymes that are known to be influenced by selection. So there are some instances in which allozymes can be useful in studying certain types of adaptive genetic variation. Also, some markers are specific to, or better developed for, certain genomes (e.g., mtDNA or nuclear DNA). In addition, different genomes and even different sections of DNA within the genome are known to reflect different mutation rates, and thus the information derived from them is interpreted differently, as reflecting different time dimensions of the population's or species' genetic history.

Criterion	AFLP	RAPD	Microsatellites	nRFLP	Allozymes
Number of possible loci detected	Many	Many	Many	Many	Perhaps 10-20
Replicability	High	Variable	High	High	High
Resolution	High	Moderate	High	High	Moderate
Nature of markers	Dominant	Dominant	Codominant	Codominant	Codominant
Lab time, ease of assay	Short, moderate to difficult	Short, easy to moderate	Moderate, easy to moderate	Long, difficult	Short, easy to moderate

Table. Characteristics of genetic markers. AFLP: Amplified Fragment Length Polymorphism; RAPD: Random Amplified Polymorphic DNA; Microsatellites (also known as Simple Sequence Repeats, SSRs); nRFLP (Restriction Fragment Length Polymorphism, from the nuclear genome).

Dominance or codominance (that is, whether the marker reports on diversity at both (codominant) or only one (dominant) allele for any particular gene or 'locus').

Cost of the analysis.

Time required from data collection through analysis to results.

Expertise or technology needed at all stages from sampling through analysis.

Replicability or how consistent the test results are when repeated in the same or different laboratories.

The objectives best served by the markers. For example, molecular markers are generally considered to measure neutral DNA variation and consequently are useful in studies of

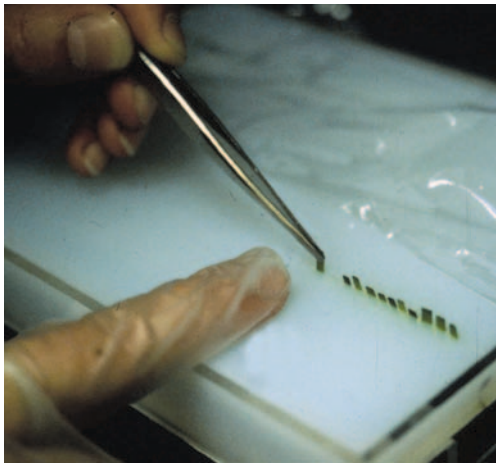


Photo credits: Deborah Rogers. Allozyme analysis: (upper right) Loading a Gel, (upper left) Stained Isozymes.

In summary, no single genetic marker is inherently 'good' or 'bad': markers vary in attributes and in their most appropriate application. Many of these features may change over time. For example, costs may go down as the technological tools are better developed, automated, or otherwise become more cost effective. In concert with this trend, less expertise or time may be required for the procedures. New markers may be developed in the future, making some of the current markers less attractive. Finally, DNA sequencing is increasingly common and as this advances for various species, there may be less need to use markers that give insights based on just a small sample of the genome. ■