

## Disease Resistance in a Changing Climate

### Vocabulary List

**(Fungal) pathogen:** any entity capable of causing disease, such as a microbe, a virus, or a fungus.<sup>1</sup>

**(Tree) breeding:** The application of genetic principles to the genetic improvement and management of forest trees. Specific phenotypes are identified and selected from natural populations of trees and then offspring/seed from trees with those phenotypes are planted in plantations. This is done to increase the occurrence of the desired phenotype by continuing to reproduce trees from those that express the phenotype of interest. Tree breeders are professionals who are involved in this process and are informed by researchers who study forest genomics.<sup>2</sup>

**Allele(s):** A particular version of a gene.<sup>1</sup>

#### **Assisted migration:**

- a) The human-assisted movement of plants or animals to more climatically suitable habitats.<sup>3</sup>
- b) Moving plants/planting seed beyond/outside their current native ranges to facilitate adaptation to a changing climate, e.g. planting seedlings further north (colder climate) outside the range as the current northern portion of a species range becomes warmer.
- c) In a forestry context, moving seed outside of its native range.

**Bioinformatics:** the field of study concerned with managing, analyzing, and interpreting biological information, particularly DNA sequences.<sup>1</sup>

**Candidate genes:** A gene whose chromosomal location is associated with a particular disease or other phenotype. Because of its location, the gene is suspected of causing the disease or other phenotype.<sup>5</sup>

**Conifer:** Tree species that are cone-bearing softwood with needle-like or scale like-leaves, typically evergreen.

**Epidemic(s):** The spread of an infectious disease throughout a population in a short time period.<sup>1</sup>

**Gene expression/Gene pathway(s):** Overall process by which the information encoded in genes is converted into an active product, most commonly a protein. Includes transcription and translation of a gene, and in some cases includes protein activation.<sup>1</sup>

**Gene(s):** A section of DNA (or RNA, for some viruses) that encodes information for building one or more related polypeptides or functional RNA molecules along with regulatory sequences required for its transcription.<sup>1</sup>

**Genetic architecture:** In this context, the overall composition of the genome that has been built using genomics technology.

**Genomics:** The field of study concerned with sequencing, interpreting, and comparing whole genomes from different organisms.<sup>1</sup>

**Hybrid/Hybridize:** The offspring of parents from two different strains, populations, or species.<sup>1</sup>

**Model (Statistical)/Association model:**

- a) A simplified, formal mathematical way to approximate reality and make predictions from this approximation. The statistical model is the mathematical equation that is used. The models include a dependent/response/y-axis variable (the one we want to describe) and independent/predictor/explanatory/x-axis variables (the ones we use to use to describe the dependent variable).<sup>4</sup>
- b) The simplest statistical model is  $y = mx + b$ , where  $y$  is the dependent variable,  $x$  is the independent variable,  $m$  is the slope of the line, and  $b$  is the intercept. Essentially, climate models follow this simple form by using a bunch of independent/predictor/ $x$  variables to explain the output of the dependent/response/ $y$  variable. For example, researchers can use temperature, wind, and precipitation as explanatory variables to model the response of tree growth—this model will tell researchers what height trees grow under different temperature, wind, and precipitation conditions. If the model is good, it can also be used to predict how tall trees will grow in temperature, wind, and precipitation conditions that have not occurred yet, but are likely to occur with climate change.

**Molecular markers:** A marker is a DNA sequence with a known physical location on a chromosome. Markers can help link an inherited disease with the responsible genes. DNA segments close to each other on a chromosome tend to be inherited together. Markers are used to track the inheritance of a nearby gene that has not yet been identified but whose approximate location is known. The marker itself may be a part of a gene or may have no known function.<sup>5</sup>

**Next-generation sequencing:** Also known as high-throughput sequencing, a comprehensive term used to describe technologies that sequence DNA and RNA in a rapid and cost-effective manner.<sup>6</sup>

**Nucleotide sequence data:**

- a) **A/T/G/C nucleotide:** A/T/G/C stands for the four types of bases found in a DNA molecule: adenine (A), cytosine (C), guanine (G), and thymine (T). A DNA molecule consists of two strands wound around each other, with each strand held together by bonds between the bases. Adenine pairs with thymine, and cytosine pairs with guanine. The sequence of bases in a portion of a DNA molecule, called a gene, carries the instructions needed to assemble a protein.<sup>5</sup>
- b) **Nucleotide:** the basic building block of nucleic acids. RNA and DNA are polymers made of long chains of nucleotides. A nucleotide consists of a sugar molecule (either ribose in RNA or deoxyribose in DNA) attached to a phosphate group and a nitrogen-containing base. The bases used in DNA are adenine (A), cytosine (C), guanine (G), and thymine (T). In RNA, the base uracil (U) takes the place of thymine.<sup>5</sup>
- c) **DNA sequence:** The arrangement and order of A/T/C/G nucleotides that make up a specific portion (i.e. sequence) of DNA on the chromosome.

**Phenotype(s):** The detectable physical and physiological traits of an individual, which are determined in its genetic makeup. Also, the specific trait associated with a particular allele.<sup>1</sup>

**Proteomics:** The systematic study of the interactions, localization, functions, regulation, and other features of the full protein set (proteome) in a particular cell type.<sup>1</sup>

**Resistance/Disease resistance:**

- a) In an ecological community; a measure of how much a community is affected by a disturbance.<sup>1</sup>
- b) The ability of an individual and/or population to resist pathogenic infection based on genetic variation within the genome that conveys resistance traits, i.e. the ability of a species to defend itself against disease due to its genetic composition.

**Selecting/Artificial selection:**

- a) Deliberate manipulation by humans of the genetic composition of a population by allowing only individuals with desirable traits to reproduce, as in animal and plant breeding.<sup>1</sup>
- b) Choosing individuals from a population with specific traits to be bred such that the frequency of that trait is increased and/or retained in subsequent generations.

**Transcriptomics:** The study of all the RNA molecules within a cell, otherwise known as the transcriptome. Many studies of the transcriptome focus on messenger (m)RNA molecules only, which reflect the genes that are being actively expressed (as protein products) in a cell or tissue at a given time or in a given situation. However, over 95% of the RNAs in a cell are not translated into a protein, so transcriptomics also includes the study of these non-coding RNAs.<sup>7</sup>

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## References:

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