them experimentally for more than forty years (141). This means that the boundaries said to define human races have been culturally imposed in shifting and unstable clusters of alleles (Marks 1995, 117).

It turns out that genetic variation in human populations is mostly a matter of differences in the relative proportions of the same sets of alleles. In fact, the distribution of particular phenotypes shifts gradually from place to place across populations as the frequencies of some alleles increase, whereas those of others decrease or stay the same. Moreover, the distributions of some traits (like skin color) do not match the distributions of other traits (like hair type). Such a pattern of gradually shifting frequency of a phenotypic trait from population to population across geographic space is called a **cline**. Clines can be represented on maps such as that presented later in Figure 5.4, which shows the gradually shifting distribution of differences in human skin color from the equator to the poles.

Phenotypic contrasts are greatest when people from very different places are brought together and compared, while ignoring the populations that connect them (Marks 1995, 161). This is what happened when Europeans arrived in the New World, conquered the indigenous peoples, and imported slaves from Africa to work on their plantations. But if you were to walk from Stockholm, Sweden, to Cape Town, South Africa (or from Singapore to Beijing, China), you would perceive gradual changes in average skin color as you moved from north to south (or vice versa). Evolutionary biologists argue that skin pigmentation is distributed in this way as a consequence of natural selection: individuals in tropical populations with darker skin pigmentation had a selective advantage in equatorial habitats over individuals with light pigmentation. By contrast, populations farther away from the equator faced less intense selection pressure for darkly pigmented skin and perhaps even selective pressures in favor of lighter skins. But *different* selection pressures would have been at work on other traits, such as stature or hair type, within the same population, which is why the geographical distributions of these traits do *not* match up neatly with the distribution of skin pigmentation. To make things even more complex, different genes may be involved in the production of similar phenotypic traits in different populations: for example, although different ancestral populations of humans living near the equator have dark skin, the identity and the number of alleles involved in the production of this phenotypic trait may be different in different populations.

cline A pattern of gradually shifting frequency of a phenotypic trait from population to population across geographic space.

Evidence for this gradual geographical intergradation of human phenotypes led biological anthropologist Frank Livingstone (1964) to declare more than 40 years ago that "There are no races, there are only clines" (279). Clinal variation explains why people searching for "races" have never been able to agree on how many there are or how they can be identified. *Clines are not groups.* The only group involved in clinal mapping is the entire human species. Each cline is a map of the distribution of a *single* trait. Why not, therefore, superimpose a grid over a particular geographical region, and then sample individuals randomly from the grid squares? As Peter Wade and his colleagues point out, "Starting with a grid tends to produce gradients or clines of gradual variation and reduces the impression of located genetic populations; the absence of boundaries suggests the continuous movement and biological mixture of peoples between populations" (2014, 23). Although many people may think that human population movement and mixture is relatively recent, studies of ancient DNA are now suggesting that human populations have been moving and mixing with one another for hundreds of thousands of years, if not longer (Bolnick et al. 2016, 328). And modern clinal mapping reveals similar patterns of movement and mixture.

Biologists might compare the clinal maps of trait A and trait B to see if they overlap and, if so, by how much. But the more clines they superimpose, the more obvious it becomes that the trait distributions they map *do not coincide* in ways that neatly subdivide into distinct human subpopulations; that is, clinal distributions are *not concordant.* Since the biological concept of "race" predicts exactly such overlap, or concordance, it cannot be correct. In other words, *clinal analysis tests the biological concept of "race" and finds nothing in nature to match it.* And if biological races cannot be found, then the so-called races identified over the years can only be symbolic constructs, based on cultural elaboration of a few superficial phenotypic differences—skin color, hair type and quantity, skin folds, lip shape, and the like. In short, early race theorists "weren't extracting races from their set of data, they were imposing races upon it" (Marks 1995, 132).

The Molecularization of Race?

During the 1960s and 1970s, anthropologists and others explained that there was no biological basis for race; in other words, all humans are part of a single species. Although there is internal variation within the species, it does not easily fall into the cultural categories of "race" as they had developed in the United States. In the past thirty years, however, we have witnessed in the United States and elsewhere a resurgence of attempts to explain