How might similarities and differences in genetic codes, or the proteins built as a result of this codes, be used to determine how closely related different species are?

It seems that the person who sent this question confuse the terms genetic code and genome sequence. The genetic code is the set of rules by which information encoded within genetic material (DNA or mRNA sequences) is translated into proteins. To produce a protein, a cell must first make working copies of the gene that encodes it. These copies, called messenger RNA (mRNA), consist of a specific string of words, or codons. Each codon represents one of the 20 different amino acids cells use to assemble proteins (codon of mRNA (nucleotide triplet) – word of genetic code – specify amino acid). The meaning of each codon is the same in most known organisms (genetic code is "universal")—a strong argument that life on earth evolved only once. However, the genetic code has been found to differ for a few codons in many mitochondria, in ciliated protozoans, and in Acetabularia, a single-celled plant. Most of these changes involve reading of normal stop codons as amino acids, not an exchange of one amino acid for another. These exceptions to the general code probably were later evolutionary developments; that is, at no single time was the code immutably fixed, although massive changes were not tolerated once a general code began to function early in evolution.

Concerning to genome sequences they differ among species significantly. The closer two species are the less differences are observed between their genomes sequences. The number of differences between the species can indicate the level of their relation. The relative species usually appear at the same time and have the common ancestor. The species with low level of differences in genome are likely to appear at the same time and come from the same ancestor while species with high level of differences must have different ancestors. As far as proteins are encoded by DNA, the same thing can be applied to protein sequencing. However, with some limitations because introns are excised when RNA becomes mature.