Knowledge of rice genetic diversity is necessary to ascertain the germplasm conservation and the development of improved rice genotypes with good quality traits through various breeding programs. Blending of rice with good and poor quality traits by unscrupulous traders to make enormous profits causes a negative impact on the consumer preference and the rice trade. The aim of this study was to determine the physicochemical characterization and the genetic diversity based on gel consistency and alkali digestion among selected Kenyan and Tanzanian *Oryza sativa* genotypes using the SSR markers. In this study physicochemical test were conducted to determine the alkali digestion values and gel consistency of the 12 rice genotypes studied. Genetic diversity based on the gel consistency and alkali digestion using the 8 SSR markers that are tightly linked to the quantitative trait loci's (QTLs) controlling these traits was also determined. Minitab 17.0 software package was used to determine the means and the standard error of means of the gel consistency physicochemical test results while the alkali digestion values were determined based on the standard evaluation system by International Rice Research Institute. PowerMarker version 3.25 was used to determine the major allele frequency, allele number, gene diversity and the polymorphic information content (PIC). GenAlEx version 6.41 was used to determine the principal coordinate analysis (PCoA) and analysis of molecular variance (AMOVA). DARwin 6.0.12 statistical software was used to determine the genetic dissimilarity matrix based on Jaccard's coefficient with 1000 bootstrap values and to draw an unweighted neighbour joining tree. The rice genotypes were classified into various classes based on the existent standard evaluation systems. The number of alleles per locus ranged from 2 to 4 with an average of 2.75 across the 8 markers used. Polymorphic information content (PIC) ranged from 0.5224 (RM577) to 0.1411 (RM85) with an average of 0.3673 observed across all the markers. Gene diversity ranged from 0.5764 (RM577) to 0.1528 (RM85) with an average of 0.4181 with one rare allele was detected using RM577 loci. Pairwise genetic dissimilarity matrix ranged from ranged from 0.9333 to 0.1818 with the least genetic distance being observed between *IR 54* and *BS 370* while the highest, 0.9333 being between *Saro 5* and *IR 2793*. The unweighted neighbour joining tree clustered the rice genotypes into three major clusters and subsequent sub clusters hence effectively differentiating the Kenyan and Tanzanian genotypes based on gel consistency and alkali digestion. These clustering was complemented with the findings in the principal coordinate analysis. These results show that determination of genetic diversity using SSR markers that are tightly linked to the QTLs and physicochemical characterization can be effectively utilized in analysis of diversity in rice germplasm.