The study was conducted at Taj Al-Nahrain station in Al-Qadisiyah governorate, which is 200 km from the center of Thi Qar governorate, for the period from 10/15/2021 to 4/15/2021. 85 Holstein cows imported from Germany were used in this experiment, and they were selected from among 700 cows. At the station, all of them were in the third production cycle, in addition to the laboratory part that was conducted in the laboratories of the Department of Life Sciences at the College of Science / Thi Qar University for the purpose of separating the genetic material (DNA), conducting the polymerase chain reaction, electrophoresis and identifying genetic mutations in the studied genetic piece on the prolactin gene, The following are the most important results obtained: 1- From the results of the nucleotide sequencing study on the 156 base pair gene segment, the presence of four important point mutations was detected in the non-coding region (intron 3) of the prolactin gene in the studied cow sample. 2- Obtaining four mutations, the first of which is G79C, which has two genetic structures only (GG and GC), and it is of the silent type (silent), as there was no change in the amino acid Leucine, and the second is C83T. This mutation appeared as in the previous one with two genetic structures, namely wild CC and hybrid CT But it differed from it that it was a missense mutation, which led to a change in the resulting amino acid code to be Tyrosine instead of Histidine, and the third mutation A92T showed that this mutation at site 92 of the studied genetic segment of the prolactin gene appeared with two genetic structures: AA and AT It was a missense mutation by changing the code that produces the amino acid Threonine to Serine. The last mutation G168C changed the code that produces the amino acid arginine to the code that produces the amino acid Proline, which indicates that it is a Missense type mutation, and it was also found that it appeared with only two genetic structures (GG and GC). 3- The C79G mutation did not show any significant effect between the characteristics of the studied milk components, as although the wild formula GG: 70% was mathematically superior to the hybrid GC: 30% and 3.43% compared to 3.42%, respectively, a highly significant superiority is noted (P ≤0.01) For the frequency of the G allele compared to the C allele, it b was not proven that there is a significant effect of this mutation in its wild and hybrid compositions on all studied milk production traits despite the mathematical superiority of GC genotype in most of these traits in Holstein cows. 4- The C83T mutation showed an 80% superiority for the CC genotype over the CT genotype (20%) and significantly (P≤0.01). It was an average of 14.04 kg/day, and the C83T mutation had no significant effect on the characteristics of milk components. 5- The results showed that the A92T mutation was observed in the majority of the studied cows carrying the AA genotype, by 84%, compared to the minority who carried the AT genotype, and by 16%, which reflects the significant superiority (P≤0.01) of the AA genotype compared to AT, as well as the prevalence of the A allele. (92%) on the T allele (8%), and there was no significant effect between genotypes AA and AT in all studied traits. 6- The G168C mutation shows a high moral superiority (P≤0.01) of the GG genotype (82%) over the GC genotype (18%) and the prevalence of the G allele over the C allele by 91 and 9%, respectively, and the superiority of cows with the GC genotype over the same The genotype (GG) was significantly (P≤0.05)) in the trait of persistence in production at rates of 1.5 and 1.4%, respectively, while the cows carrying the wild formula (GG) were significantly (P≤0.05) superior in the trait of length of the production season by 303 days compared to At 301 days in cows carrying the GC genotype, as for the rest of the milk production traits, the genotype of the mutation did not show any significant effect on them, and on the characteristics of the milk components, the percentage of protein was uniquely affected by the significant (P≤0.05) of the genotype of the G168C mutation in the prolactin gene, with the superiority of the composition GG genotype (P≤0.05) increased by 2.66% compared to 2.55% for GC genotype. While we did not notice a significant effect of the above mutation on the other characteristics of milk components, which included each of the percentage of fat, non-fat solids, density, protein percentage and degree of freezing. 7- Most of the averages of the studied traits appeared at rates higher than their counterparts in other previous studies, and most of the simple correlations between these traits were high and significant