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Isolation and Identification of *Shigella* Isolated from Diarrheal Cases and Investigation of its Genetic Variance Using Random Amplified Polymorphic DNA

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ABSTRACT

Current study has rewarded attention to analyze genetic variation and genetic characterization among 10 Shigella isolates from unknown sources to detect the genetic distance between them by use Randomly Amplified Polymorphic DNA (RAPD) technique was performed, a technique based on PCR interaction.

In this study, 6 random primers were used (OPF-16, OPD-20, OPA-06, OPE-20, OPX-01, OPY-03) in RAPD technique, the results revealed that the primers (OPA-06, OPD-20, OPF-16, OPE-20, OPX-01) showed bands differed in numbers and locations between the studied isolates those were varied with the unique bands or in the absence of specific main band ,while the primer (OPY-03) didn't gave any multiplication result, the differences in molecular weight between the volumes and the difference in the number of these band were recorded, the primer (OPX-01) gave the largest number of band (73bands) and the primer (OPD-20) gave the lowest number of band (30 bands), while the rest of the primers were gave different numbers of band approximated between (30-73).

The genetic distance values of the 10 isolates were ranged from 0.88891-0.28742. If the genetic material matches any two studied species, it indicates that the genetic distance between them should be equal to zero, and the genetic similarity ratio is equal to 1. The genetic distance values among the ten isolates have been invested in finding the genetic relationship that binds them all to Clusters, where the Shigella species are divided into two main groups: The first group included two groups, the first included two subgroups, one of which included isolate No. 1 and the other included tow isolaties No.2 and 3, the second was included two subgroups, the first subgroup included two categories, one of which included the isolates 4 and 7 and the other included isolate No. 5, while the other one was included the isolate No. 6. The second main group included two categories, one of which included the isolates No 8 and 9 and the other included isolate No. 10 and all the branches in the tree are types of follow-up to the genus of Shigella.