The present microbiota in the gastrointestinal tract, is a complex ecosystem composed by several hundreds of species of microorganisms, the majority of they bacteria, which they have adapted to the life in the mucous surfaces of the alimentary canal or in the light of the intestine. The establishment and diversity of the intestinal microbiota in the newborn is a complex process influenced so much by internal factors as such external factors as the age gestational, the type of childbirth, the hospitalization, geographical differences, the administration of antibiotics, and fundamentally, the type of infantile supply (Fanaro and Cabbage., 2003). This microbiota, though it has important benefits on the human health can behave, under such certain circumstances as the physical or structural alteration of the intestinal barrier, since potentially pathogenic given the capacity of these microorganisms to invade the guest and to originate different infections and diseases (Guarner and Malagelada, 2003).

In the fecal flora of newborn healthy, between the bacilli gramnegativos that colonize the intestinal tract, and concretely between them belonging to the family *Enterobacteriaceae*, *Escherichia coli* is in the habit of being the predominant species, though other species can be isolated as *Klebsiella spp., Enterobacter spp., Citrobacter spp., Proteus spp*. etc, (Adlerberth and col., 1991).

Therefore, this study was carried out by the aim to know the profile of settling for Enterobacteriaceae from the birth up to an approximate period of three months, to observe the possible influence of the supply, as well as to study different characteristics of *E. coli.* This was possible thanks to the accomplishment of a clinical, double blind test, randomized and controlled in a group of healthy newborn children for vaginal childbirth. The duration of the study was of approximately 3 months and during this period 4 controls were programmed: to 11-17, 26-29, 47-51 and 86-91 days of age respectively.

The intestinal colonization of microorganisms in the newborn infants during the birth. After 12 or 15 days following birth, first stage of this sampling, the percentage of colonization by gram-negative bacilli (GNB) was 97%.The percentages of colonization caused by GNB, from which approximately 99% were Enterobacteriaceae. This result was obtained in the group of the newborn infants following different feeding patterns. Meanwhile the percentage was slightly higher for those infants fed with the standard formula.

From all the species of *Enterobacteriaceae* found in the gut flora, *E. coli* was the predominant isolated species. At the end of this research, approximately three months later, the percentage of infants colonized by this species was higher than the previous one found in the first period of sampling, after 12 or 15 days following birth.

Making a difference in the feeding of the three groups of the newborn infants, it can be appreciated that the percentages of colonization by *E. coli* in the milk-fed group and supplemented formula-fed were very similar and at the same time lower than those obtained from the standard formula. At the end of this period the percentages of colonization by *E. coli* were about 100%.

In the gut flora of the newborns infants colonized by *E. coli* this species was isolated as the only flora or as a flora found with other Enterobacteriaceae. From all these it is mentioned *K. pneumoniae* as the second intestinal colonizing species more frequent in the newborn infants.

The average of gram-negative bacilli, mostly Enterobacteriaceae, was around $10^{8.5}$ ufc/g.

When the count of GNB was analysed and also that of *E. coli* depending on their feeding, there were significant differences between the group of standard formula, the milk-fed group and those artificial formula groups. After the analysis it was observed that in every period the group of infants fed with the standard formula obtained the higher count.

The dynamics of intestinal colonization by strains of *E. coli* revealed that the most of these strains, around 81% were at least three weeks in the gut flora and therefore the most of them were classified as resident strains.

Focusing on the fact that the different feeding could modify the distribution of resident and transitory strains in the gut flora, it was observed that those infants fed with the standard formula offered a very similar percentage of resident and transitory *E. coli* strains.

From the four different phylogenetic groups in which *E. coli* strains can be classified, B2 was the predominant phylogenetic group. Even differentiating the strains into resident and transitory ones, B2 was the most frequent group. The same happened when the *E. coli* strains were differentiated according to the infant feeding.

Among the genes of virulence found in the total of *E. coli* strains, the most predominant gene was the *sfa/foc.* The percentage of strains in which two or more genes of virulence were found was around 30%. This percentage was representative of Extraintestinal Pathogenic *Escherichia coli* (ExPEC) strains. The phylogenetic distribution of these strains was represented mostly by that phylogroup of B2, followed by the group D.

If we focus on the type of feeding, the highest percentage of ExPEC strains was detected in the group of infants fed with the standard formula. Then, it was followed by the infants fed with the supplemented formula and finally the breastfeeding group with the lowest percentage of strains.

Finally, on the research of antibiotic sensitivity of *E. coli* strains, it was detected a significant percentage of resistance to ampicillin and quinolones. The percentage of strains carrying the betalactamases extended spectrum (BLEEs) was 3%. By chance these strains were isolated from breastfeeding infants.

The results of this study suggest that from the first days of life up to the final period, the percentages of colonization for Enterobacteriaceae in the intestinal flora of the children are high. *E. coli* is the predominant species, and studying his characteristics to emphasize that, the majority phylogoup to which these vine-stocks belong is the B2, and that together with the phylogroup D, are those who present major number of factors of virulence. Observing the influence of the factor supply to say that, the formula suplemented exercises an effect similar to the mother lactation on the intestinal studied microbiota, regarding percentages of intestinal colonization for Enterobacteriaceae (and concretely for *E. coli*), inventories, dynamics of colonization of the vine-stocks of *E. coli*, and of characteristics of phylogroup and factors of virulence. Though we it cannot underline firmly due to the enormous variability inter-subjects of the test.