Introduction

Infection are still one of the most common cause of hospitalization and mortality in children and neonates, sepsis represents the most important cause of neonatal morbidity and mortality after congenital malformations **(Stoll. 2004).**

Clinical diagnosis of sepsis is not easy, because symptoms and signs are not specific and moreover a dramatic deterioration of clinical conditions can supervene very rapidly, even in asymptomatic newborn infants. Because the preliminary report of blood culture is not available before 48-72 h, it is customary to start treatment at birth in all neonates with risk factors for early sepsis and / or with alterations of some laboratory tests (i.e white cell count, total neutrophil count, immature/total (I / T) ratio, CRP). However, the sensitivity and specificity of each laboratory test are far from 100% **(Manucha et al., 2005)**, so that a large proportion of neonates not really infected are treated with broad spectrum antibiotics. The possibility of having a 100% sensitive and specific method for the identification of bacteria in blood, with results available in a short period of time, could allow the onset of treatment only in neonates with infection, thus reducing the use of broad-spectrum antibiotics **(Stoll. 2004).**

Molecular biology techniques such as Polymerase chain reaction (PCR) have been used as a specific and sensitive method for diagnosis of different bacteria, viral and protozoal infections **(Stoker. 1990).**

DNA sequences presents in all bacteria, such as portions of DNA encoding the 16S ribosomal RNA, have been used to define organisms as bacteria,

those sequences have been amplified with PCR using an automated method allowing detection of even small amounts of bacteria and diagnosis of sepsis **(Andrade et al., 2008).**