Introduction

Bacterial vaginosis (B.V) is a polymicrobial disorder characterized by increase in vaginal pH over 4.5, a reduction in or absence of lactobacillus colonization and overgrowth of several facultative and obligatory anaerobic bacteria (*Hay et al 1992, Guise et al., 2001*).

It is the commonest cause of lower genital tract infection among women in childbearing period, although 30-40 % of the cases are asymptomatic (*Hay et al.*, 1992).

It accounts for 36 % of patients attending sexually transmitted diseases clinics & 29 % of patients attending family planning clinics and 10-25 % in obstetric clinics (*Thomason et al.*, 1990).

Bacterial vaginosis is diagnosed in up to 23 % of pregnant women. Although B.V itself is harmless condition, it is linked to pregnancy complications including miscarriage, preterm delivery, preterm premature rupture of membrane, amniotic fluid infection, post partum infection, post C.S. wound sepsis and pelvic infection after child birth. (*Gallagher et al. 2004*).

There is an association between bacterial vaginosis and postoperative infection. 35% of women with clue cells detected in vaginal smear developed vaginal infection or wound infection after abdominal hysterectomy (*larsson et al.*, 1991).

Also clinical trials demonstrated important reduction in many of these adverse events with appropriate screening & appropriate antimicrobial treatment (*Berg and Garham*, 2004).

Organisms associated with bacterial vaginosis have also been recognized as agents of female upper genital tract infection, strong evidence show that bacterial vaginosis may cause pelvic inflammatory disease in non-pregnant women in the absence of gonorrhea and Chlamydia, consequently, bacterial vaginosis could be associated with tubal factor of infertility (*Wilson et al.*, 2002).

Although bacterial vaginosis is not considered a true sexually transmitted infection, yet it is correlated with sexual activities (*Shwebke et al.*, 1999). It has been suggested that the pathogenesis of bacterial vaginosis may be similar to that of urinary tract infections, with the distal intestinal tract and the mouth serving as a reservoir for some bacterial vaginosis- associated flora (*Spiegel*, 1991).

No single microorganism is detected in all women with B.V, though gardnerella vaginalis (G.V.), Bacteroides species and Mycoplasma hominis (M. hominis) were detected in most studies (*Spiegel el al. 1980, Hiller et al., 1990*).

Although bacterial vaginosis is generally believed to be an endogenous condition, a number of behavioral factors are involved, such as the use of contraceptives (*Shoubnikova et al.*, 1997), vaginal douching (*Ness et al.*, 2002) and smoking habits (*Hellberg et al.*, 2000).