Literature Review
The order Chiroptera consists of approximately 1116 species, classified under two sub orders Megachiroptera and Microchiroptera with 202 genera under 18 families (Wilson & Reeder 2005). The evolutionary origin of bats is not well understood, due to the lack of fossil records. The earliest fossil bat *lacronycteris index* (Jepsen 1966; 1970) resembles extant species, giving no indication of the ancestral form. Bats may be derived from arboreal insectivores (Jepsen 1970; Yalden & Morris 1975) or share a common ancestor with the Dermaptera (Novacek & Wyss 1986; Padian 1987; Simmons 1995). However the discovery of similarities in the visual pathways of the brain between the Megachiroptera and primates may suggest separate origins of the two chiropteran sub orders (Pettigrew et al.1989). If so, flight evolved twice within mammals, with microbats appearing as early as the mid Cretaceous and megabats evolving later from primitive primates (Hill & Smith 1984; Pettigrew et al.1989).

Bats constitute the second largest and the most diverse mammalian order. Based on their taxonomy it is further divided in to two suborders – Megachiroptera and Microchiroptera. More than 900 species are recognized and depending on their morphology and it inhabit both tropical and temperate zones (Jones et al. 2002). Its roosting sites include caves, rocks, crevices, mines, tree bark, tree trunks, unused buildings and also in man-made structures like mines and underground tunnels (Altringam 1996). The Megachiropterans feed on flowers, fruit, nectar and pollen and are confined to Old World tropics. Although considerable variation in their size occurs within the suborder (from 10 g to 1.5 kg), as a group they tend to be larger than the Microchiropterans (Nowak 1994). The Microchiropterans, as the name implies, are
much smaller in size (from 2 g to 196 g), but they far exceed the Megachiropterans in number and distribution. Its dentition is well developed to feed on insects and small vertebrates like fish, frog, lizard and bats. The most striking difference between Megachiropterans and Microchiropterans is that the former orient primarily by vision and olfaction and latter by echolocation. Only a few megabat species belongs to the genus *Rousettus*, produce tongue-clicking for orientation.

The principal mechanism enabling navigation and foraging in the dark for the most of Microchiroptera species is echolocation (Griffin 1958) which involves emitting high frequency sounds through the nose or mouth and enabling the bat to locate and catch the prey (Fenton 1984). The frequency, intensity and structure of echolocation calls vary greatly among species (Fenton 1984; Hill & Smith 1984) and even within species (Masters et al. 1991; Fenton 1984; Obrist 1995) and are closely linked to different foraging niches and foraging strategies (Neuweiler 1989). Through the evolutionary process, bats have effectively partitioned food resources through variations in their food preference and foraging strategies (Neuweiler 1989; Fenton 1990). Species from a few Microchiroptera families have diverged upon the strategies of gleaning, i.e. capture prey from surfaces rather than capture prey in aerial pursuit, may not rely upon echolocation. Gleaning bats *Macroderma gigas* (Guppy & Coles 1983), *Nycteris grandis* and *Nycteris thebaica* (Fenton et al. 1983), *Megaderma lyra* (Fiedler 1979; Marimuthu & Neuweiler 1987; Marimuthu et al. 1995), the gleaning bats apparently use echolocation for general orientation, but not locate prey. They did not increase their pulse emission rate prior to prey capture, suggesting that they were not actively scanning prey; instead they rely on prey-generated sounds for localization (Marimuthu & Neuweiler 1987). These prey-generated sounds are typically well below the frequencies
used in echolocation. Gleaning requires highly maneuverable flight and the ability to hover (Norberg & Rayner 1987); their broad and short wings contribute to maneuverability (Aldridge 1986).

To detect and localize these low-frequency sounds many of these bats have evolved with relatively large pinnae to collect long wavelength acoustic energy more effectively (Brown et al. 1978; Guppy & Coles 1988; Rubsamen et al. 1988; Bruns et al. 1989). However, a few studies suggest that vision is used predominantly when adequate illumination is available and at such situation, the bats switch off their echolocation (Bell 1985; Heffner & Heffner 1992). Sound cues help to direct their best vision to the source of sound during localization (Koay et al. 1998). Silent foragers are less likely to attract their attention of their own predator or conspecifics that compete for food resource. The ability of gleaners to employ a variety of sensory cues confers a number of advantages over other echolocating bats. Many insects’ ears are sensitive to echolocation calls of aerial insectivorous bats and respond with negative phonotaxis or evasive flight maneuvers (Millers 1983). The ability to use other sensory cues particularly prey generated sound in addition to echolocation enables bats to search for prey using both active and passive detection systems. In this way broaden their available prey base to include both aerial and surface moving insects and expand their ecological niches. In general Chiroptera is a highly gregarious order (Bradbury 1977), Cardioderma cor is a carnivorous species roost year-around (McWilliam 1987), most species form diurnal groups or ‘colonies’ during atleast a part of their life cycle (Bradbury 1977). At this extreme, aggregations of millions of individuals have been recorded in Tadarida brasiliensis (Hill & Smith 1984). Colony formation facilitates mating (Dwyer 1970), information transfer (Wilkinson 1992; Brooke 1997), food sharing (Wilkinson 1984),

Population study is an important behavioural study to estimate immigration, dispersal and foraging (Alcock 1989). Since 1966 (Hubby & Lewontin 1966) genetic markers have become a major tool to study population biology, paternity (McCracken & Bradbury 1977; 1981; Bruke et al. 1989), kinship (Packer et al. 1991; De Ruiter & Geffen 1998) and gene flow among group (Plumbi & Baker 1994). There are several traditional techniques applied to study natural population. Mark and recapture (Raghiuram et al. 2006), survey of roosting sites (Lewis 1995), and direct observation of individuals or population (Burland & Wilmer 2001) provided the data which failed to give accurate information about population status. At that moment, protein electrophoresis (Murphy et al. 1996) was the predominant technique employed to study the natural population. But the results produced by this technique were not considered as satisfactory. Later on DNA genetic markers were established which could be the most effective tool to study natural population when combined with ecological and behavioural studies (Hillis et al. 1996). Earlier studies were focused on multiple and single locus DNA finger printing.

Polymerase Chain Reaction (PCR) based Randomly Amplified Polymorphic DNA (RAPD) techniques first described by Williams et al. (1990) are attractive complement to conventional fingerprinting (Williams et al. 1990). Nanogram amount of genomic DNA is subjected to PCR using short synthetic oligonucleotide of random
sequence. The technique scans a genome for this small inverted base repeats and amplifies intervening DNA segments of variable length. The amplification products are resolved on agarose gels as dominant genetic markers, which are inherited in a Mendelian fashion (Williams et al. 1990; Carlson et al. 1991). It is widely used in biology to distinguish species (Arnold et al. 1991; Wilkerson et al. 1993), strain identification (Williams & St Clair 1993), paternity analysis (Petri et al. 1997; Marcela et al. 1998; McCracken et al. 1999) and to study genetic variations within and between populations (Haig et al. 1996; Zhivotovsky & Vavilov 1999). RAPD technique was used as molecular marker to analyze the genetic diversity of *Megaderma lyra* which instigate that the conservation of this species is essential (Rajan & Marimuthu 2006).

Microsatellite DNA and Mitochondrial DNA (mtDNA) analyses are commonly used to understand the social organization of mammals (Girman et al. 1997). Microsatellites have been found to be variable even in populations which have low levels of allozyme and mitochondrial variation (Estoup et al. 1995a, 1995b, 1996; Paetkau & Strobeck 1994). Microsatellites are the short tandem repeats consists of 2-6 bp present in both coding and non-coding regions of prokaryotic and eukaryotic genomes. Microsatellite possesses high mutation rate and more polymorphic nature than allozyme (Hancock 1999). The available genome data indicates that the distribution of microsatellites in genome is ubiquitous and non-random (Metzgar et al. 2000; Toth et al. 2000; Katti et al. 2001; Li et al. 2002; Subramanian et al. 2003; Zhang et al. 2004; Cruz et al. 2005; La Rota et al. 2005; Lawson & Zhang 2006; Grover et al. 2007; Kim et al. 2008). Some microsatellites have influence on genome by regulating the expression of genes (Li et al. 2002; Kashi & King 2006). Likewise a dinucleotide repeat present in the genome of voles seems to affect its mating behaviour (Hammock & Young 2005).
The timing and frequency of the reproductive cycle is primarily influenced by environmental conditions in many mammals. Reproductive strategies within Chiroptera have been reviewed by Racey (1982). Species exploiting various food supplies over the season time increase their reproductive periodicity (Racey 1982) ensuring energetically
expensive activities, such as lactation, coincide with food abundance (Lavia frons, Vaughan & Vaughan 1986). Reproductive timings are most diverse among tropical species (Bradbury 1977; Racey 1982). The pattern of reproduction is classified into four broad categories, such as seasonal and aseasonal monoestry, bimodal polyestry, seasonal and aseasonal polyestry. Species such as Megaderma spasma reproduce once in a year, are categorized as seasonal monoestry (Ramakrishna 1951), Pipistrellus nanus (O’Shea 1980). In bimodal polyestry, bat exhibits a restricted breeding season with two pregnancies occur in quick succession. This pattern is seen in small pteropodids such as Rousettus leschenaulti (Gopalakrishna 1964) and Cynopterus sphinx (Krishna & Dominic 1984). In most of the cases, polyestry is facilitated by the occurrence of a postpartum estrus (Myers 1977). Seasonal polyestry is characterized by continuous breeding most of the year with a brief reproductive quiescence; it has been reported in Pipistrellus mimus (Krishna 1985) and Myotis nigricans (Wilson 1973). Aseasonal polyestry has been reported in vampire bat Desmodus rotundus (Turner 1975), Pipistrellus dormeri (Madhavan 1978) and Eonycteris spelaea (Beck & Lim 1973).

In mammalian reproduction lactation is energetically costlier (Millar 1977; Oftedal 1985; Gittleman & Oftedal 1987) and it provides essential nutrients required for the rapid growth of offspring immediately after birth (Hayssen 1993; Lee 1997) and influences the reproductive success (Smith 1977; Pond 1977; Daly 1979). There are several researches focused mainly on the energetic cost of lactation (Boyd 1998). Since previous reports on empirical studies confirmed that lactation induce physiological stress to the mothers, reduced survival rate and future reproductive success (Loudon et al. 1983; Clutton-Brock et al. 1989). In order to cope up with this, a special type of parental care called as allonursing is developed in few bat species (McCracken 1984; Eales et al.
1988; Wilkinson 1992), which share roosts and reproduce communally but it appear to be low in many mammals (Packer et al. 1992). Alloparental care facilitates the development of parenting skills, cohesion of groups and social organization (McKenna 1981; Kunz et al. 1994a). Early observations suggest that female suckled young ones indiscriminately in *Tadarida brasiliensis* (Davis et al. 1962), *Miniopterus australis* and *Miniopterus schreibersii* (Brosset 1962). Further studies proved that female bats suckle their own infants in *Antrozous pallidus* (Brown 1976), *Desmodus rotundus* (Schmidt 1972), *Eptesicus fuscus* (Davis et al. 1968), and *Myotis velifer* (Kunz 1973) except in cases of mistaken identity in *Tadarida brasiliensis* (McCracken 1984), due to high maternal mortality in *Pipistrellus pipistrellus* (Eales et al. 1988) and high reciprocity in *Nycticeius brasiliensis* (McCracken 1984) and milk stealing by young ones observed in *Tadarida brasiliensis* (McCracken 1984) and milk stealing by young ones observed in *Tadarida brasiliensis* (McCracken & Gustin 1991). In some species like *Nycticeius humeralis*, milk dumping appears to be common due to the absence of auditory and olfactory cue essential for mother-infant recognition (Watkins & Shump 1981).

Allonursing provides high immune response and develop resistance against pathogens and parasites to the young ones (Roulin 2002). There are several hypotheses proposed on the purpose of nursing alien offspring. According to misdirected parental care hypothesis the female unintentionally nurse alien offspring and the maternal care was misdirected. The female give milk without noticing whether it is her own baby or other and hence leads to stealing of milk (Packer et al. 1992; Cameron et al. 1999). In *Tadarida brasiliensis mexicana* and *Nycticeius humeralis* females selectively nurse their offspring over others (McCracken 1984; Wilkinson 1992). In reciprocity hypothesis, the level of fitness is similar in females nursing each other’s offspring than when they do not share milk (Pusey & Packer 1994). This type of nursing is important for the females want to be temporarily relieved from maternal duties (Riedman 1982; Perry 1996) and to
act as alternative source when her mammary glands are momentarily depleted of milk at different times (Roulin & Heeb 1999). The kin selection hypothesis states that females prefer to nurse closely related than unrelated offspring (Packer et al. 1992). In milk evacuation hypothesis the mothers nurse alien offspring if she has surplus milk which was not consumed by its own offspring completely (Wilkinson 1992). This hypothesis is not applicable when a female nurses alien offspring while her own offspring is feeling hungry and attempt to suckle foster mothers. The parenting hypothesis states that female nurse alien offspring in order to improve their maternal skills, and hence allonursing should be performed mainly by inexperienced females.

Furthermore, host-parasite interaction is an important and interesting part in social organization of bats. The parasite develops specific mechanisms to increase their fitness by exploiting resources from host. Host inturn increase their own fitness by minimizing negative effects of parasite infestation. This leads to a co-evolutionary arms race between the parasite and the host (Van valen1973; Lively 1996). Most of the studies on host-parasite relationship assumes host as a habitat for the parasite which provides the array of environmental stimuli that shape its behaviour and ecology. The nature and specificity of parasitic association is strongly influenced by the ecology and behaviour of both host and parasite (Brooks & McLennan 1993; Hart 1992; Marshall 1982; Mayr 1957; Poulin 1998a). Bat flies (Diptera: Streblidae and Nycteribiidae) are the most conspicuous ectoparasites of bats (Mammalia: Chiroptera). Highly specialized blood feeders, parasitize only on bats, host-specific, live in the fur and wing membrane. It usually spends their entire life on the body of the host except during larviposition (Ching & Marshall 1968; Overal 1980b; Marshall 1981; Dick & Patterson 2008). The role of ectoparasites in their host is to increase the costs of reproduction (Møller 1993;
Bize et al. 2004), cause energetic costs (Giorgi et al. 2001), evoke the risk of disease transmission (Durden et al. 2004; Bowman et al. 1997) and negatively influences the growth and development (Fitze et al. 2004). Streblids are obligate bat parasites, whose distributions are related to ecological factors that are associated with colonial cave-dwelling bats (Webb & Loomis 1977; ter Hofstede & Fenton 2005). They are winged, move from one bat to another within a roost, host specific and do not seem capable of surviving long off the host (Wenzel et al. 1966). The females of these flies undergo pupation and deposit larvae on the wall of the host’s roosts and imagoes emerge after metamorphosis only with the presence of potential host (Ryberg 1947; Marshall 1971). The difference in parasite load on males and females depends on the bats social behaviour and their roost fidelity (Zahn & Rupp 2004; Lučan 2006; Reckardt & Kerth 2006; Wohland 2000). Usually males showed high roost fidelity compared to females, the recorded low parasite load on males possibly due to high grooming behaviour, immunocompetence and sex hormones (Christe et al. 2000; Lučan 2006). The biology and ecology of several species of Trichobius was reported earlier (Ross 1961; Kunz 1976). Following that the relationship of ectoparasite and its host on Atribius jamaicensis, and Carollia perspicillata was studied (Overal 1980a). Later on studies describe about ectoparasites density and host specificity on neotropical bat Myotis myotis (Giorgi et al. 2004; ter Hofstede & Fenton 2005), reproductive success of bat fly Basilia nana and its host Myotis bechsteinii roosting behaviour, selection of host based on sex (Reckardt & Kerth 2006; Christe et al. 2007; Sharifi et al. 2008) was documented. Possible co-evolutionary interactions of host-parasite are studied by their behaviour/life cycle (Reckardt & Kerth 2006), immunocompetence (Christe et al. 2000), transposable elements (Yoshiyama et al. 2001) and genome-wide analysis (Liu et al. 2006).
The survey of *Mariner*-like elements in parasitoid wasps and its host moth shows 97.6% nucleotide sequence identity. The occurrence of horizontal transfer of *Mariner*-like elements is generally accepted but the mechanism remains unclear (Hartl et al. 1997). It was doubted that some intermediates might be involved in horizontal transfer, since transposable elements are not capable of moving from one species to another directly. It was further confirmed that the viruses acts as shuttles to transport the transposable elements to enable horizontal transfer (Miller & Miller 1982; Fraser 1986). According to Yoshiyama et al. (2001) the horizontal transfer was facilitated by the intimacy of host-parasite relationship. In addition, the genome of blood-feeding bug *Rhodnius prolixus* carries four distinct transposon families in its genome which shows 98% sequence identity and cluster phylogenetically with those of the opossum and squirrel monkey, considered as its preferred mammalian hosts in South America and the transposons present in the pond snail *Lymnaea stagnalis*, a cosmopolitan vector of trematodes infecting diverse vertebrates, whose ancestral sequence is nearly identical and clusters with those found in Old World mammals. These data provide a strong evidence of horizontal transfer among animals and the large amount of DNA generated by the amplification of horizontally transferred transposons supports the idea that the exchange of genetic material between hosts and parasites influences their genome evolution (Gilbert et al. 2010).

SINEs (Short Interspersed Nuclear Elements) are 80 to 400 bp repetitive DNA sequences, non-autonomous, non-LTR retrotransposon lack open reading frame, encode LINEs to mobilize and transcribed via RNA polymerase III, and are ubiquitous in eukaryotes (Okada 1991; Ohshima et al. 1996; Batzer & Deininger 2002; Deininger et al. 2003; Ohshima & Okada 2005; Kajikawa & Okada 2002; Dewannieux et al. 2003).
SINEs are derived from either 7SL RNA or from other tRNA genes, characterized in diverse genomes (Ullu & Tschudi 1984; Daniels & Deininger 1985; Sakamoto & Okada 1985). However, eukaryotes like *Drosophila melanogaster* and *C. elegans* shows the absence of SINEs in their genome (Eickbush & Furano 2002). Its evolution, function and structural organization remain ambiguous in many organisms (Kramerov et al. 1999). It proliferates via transcription followed by reverse transcription (Okada 1991; Deininger & Batzer 2002). Parallel insertion of mobile elements in individuals in different genome, free of homoplasy, with known ancestral state and high stability once inserted in to the genome. Insertions are identical by descent all such characteristics make mobile element a novel source of genetic variation for phylogenetic and population genetic studies (Batzer & Deininger 2002). They are widely distributed in genome as many copies, small size and its character make them to use effectively in population structure, conservation genetics, phylogeny, genomic diversity, regulate function of gene and its expression and host-parasite evolution (Ray 2007; Nikaido et al. 1999, Laha et al. 2007; Deininger 1989; Shedlock & Okada 2000). Earlier study reported that SINE families from mammals are transcribed by RNA polymerase III (Fuhrman et al. 1981; Slagel & Deininger 1989). Since SINEs do not possess any open reading frames, the L3-like LINE element may help to generate a cDNA copy, which could be inserted at a region containing a double strand break in the genome. These SINEs are mobilized by LINE like element; LINEs were active in most mammals including bats (Cantrell et al. 2008). Theoretically, secondary structure can be used to identify the homologous region and utilized as an additional data to infer the phylogenetic relationship (Billoud et al. 2000). Mobile elements are repetitive DNA sequences have unique ability to move, make copies of them and occupied 40% to 90% of a genome and easily amplified even from low quantity of DNA. Its nature of distribution in genome as many copies, small
size and its character make them to use effectively in population structure, conservation genetics, phylogeny and host-parasite evolution (Ray 2007; Nikaido et al. 1999; Laha et al. 2007). Different types of SINEs were isolated from different genomes include plant and animal taxa and named accordingly like Mg SINE from rice blast fungus Magnaporthe grisea (Kachroo et al. 1995), SINE isolated from pink salmon was designated as Sma-1 (Takasaki et al. 1997), two novel 7SL RNA derived SINE families TuI and Tu II and a novel tRNA derived SINE family Tu II from tree shrew (Nishihara et al. 2002). The Rhin-I and Das-I was identified from the genome of horse shoe bat Rhinolophus ferrumequinum and nine banded armadillo (Borodulina & Kramerov 2005). Four new types of SINE were identified from Megachiropterans two of them are MEG-RS and MEG-RL descend from cellular RNA, MEG-T2, tRNA derived SINE and MEG-TR, hybrid tRNA/5S rRNA which are neither found in microbats not in other mammals (Gogolevsky et al. 2009).