Water is a necessity for all living beings, without it there would be no life. Life originated in water and the ultimate basis of it, the protoplasm, is a colloidal solution of complex organic molecules in a watery medium (70 to 90% of water). Most of the biological phenomena take place in water medium. Moreover, wherever water exists in nature it always holds life. So the study of a water body is the study of life as well. Water is essential at all levels of life, cellular to ecosystem and it stands as the key substance for the existence and continuity of life through different cyclic processes in nature; it plays the central role in mediating global scale ecosystem processes, linking atmosphere, lithosphere, and biosphere, by moving substances among them, and enabling chemical reactions to occur. Humans depend on this resource for all their needs of existence and survival. Nature has an innate mechanism to maintain its purity after every natural use, but unables to do so at the rate at which humans add dirt to it. Nature does not know how to deal with several toxins and pollutants that are flowing from industrial and other wastes. Therefore, humans are bound to monitor the impact of this activity on natural freshwaters continuously.

The study on Bacterial diversity of Dal lake with particular reference to Pathogenic bacteria was carried out from April 2010 to March 2012. The study area
(Dal lake; latitude 34° 07’ N, longitude 74° 52’ E, altitude 1583 m) selected for this work is a multi-basined lake with many inlets and outlets, so an extensive network of sixteen sites with different altitudes and geographical co-ordinates viz., Hazratbal open, Hazratbal littoral, Nigeen open, Nigeen littoral, Gagribal open, Gagribal littoral, Nishat open, Near Centeur, Boathall nallah-I, Boathall nallah-II, Tailbal nallah-I, Tailbal nallah-II, Dal lock Gate-I, Dal lock gate-II, Pokhribal nallah-I and Pokhribal nallah-II were selected. Among the selected sites eight (8) sites were selected in the four basins, four (4) were selected from two inlets and four (4) were selected from two outlets. These sites selected included microhabitats from both littoral zones as well as limnetic zones. The water samples collected from sixteen sites were selected randomly from different basins, outlets and inlets of the lake, under consideration for exploring the bacterial diversity and were collected on seasonal basis in poly ethylene (PET) bottles, which were previously carefully cleaned and rinsed three to four times with distilled water. All the samples were collected from the surface and subsurface of lake water by plunging the open end of each sterile bottle before turning it upright to fill. During collection of samples, extreme care was exercised to avoid contamination of the parts of bottle and collected samples were processed for the analysis of bacterial community using the standard methodology. The glassware used and media prepared for the work was carefully sterilized using different standard techniques. The techniques used for the isolation of bacteria from the water samples included spread plate technique, pour plate technique and streak plate technique. The data on bacteriological analysis was analysed to measure the degree of contamination of water samples in Dal lake on seasonal basis from sixteen different microhabitats by plating the different dilutions on culture media that included general (Nutrient agar) as well as selective media like Eosin methylene blue agar, Cetrimide agar, etc. After incubation, the cultured bacterial colonies were enumerated in order to assess bacterial load in terms of colony forming unit (CFU/ml). The colonies were further characterized on the basis of macroscopic as well as microscopic character. The isolated colonies showed marked variation in their features and on these differences, a representative sample colony of each was coded as SMB-1 to SMB-45. The coded colonies were streaked on selective media to obtain pure cultures and then for biochemical analysis, using Hi-media biochemical test strips, for further
identification. The biochemically identified bacteria (Bergey’s manual specification) were subjected to molecular analysis by 16S rRNA gene using polymerase chain reaction which was carried out by means of universal bacterial primers 8F and 1492R which provides an accurate means to identify bacterial diversity and thereby studying the phylogenetic relationship between them. The sequences so obtained were confirmed and compared to known 16S rRNA sequences in gene bank (NCBI, Pune) by using BLAST algorithm and found to be 69% to 100% similar to the sequences of 16S rRNA gene of bacteria. Tests for the presence of total coliforms were carried out by multiple tube fermentation technique, which revealed higher level of total coliforms with their value ranging from 3 MPN/100ml. The highest number of these indicator organisms were observed at site 15 and 16 (Pokhribal outlet) in summer season and minimum at site 5 an 13 (inlet) in winter season. The category wise distribution of coliform count showed that 57.81% water samples lie in the category III followed by 39.07% in category II, 3.1% in category IV and 0% samples in category I. The perusal of data considers the water unfit for drinking purpose however, fit for recreational purposes. In order to gain insight into bacterial load, the culturable bacterial colonies were counted by Quebec colony counter and observed in terms of colony forming unit (CFU/ml) which reveals substantial number of heterotrophic bacteria. Total bacterial count ranged between 0.2×10⁴ to 28.7×10⁴ cfu/ml and the highest count was found at site 16 (Pokhrial outlet) in summer season and lowest count in winter season at site 6 (Boathall nallah). Out of 5941 colonies, 3123 colonies (52.56% occurrence) were isolated in summer season followed by 1502 colonies (25.28% occurrence) in autumn, 844 (14.87% occurrence) in spring and 432 (7.27% occurrence) in winter. The Gram’s reaction revealed that out of 5941 colonies, 4146 (69.78%) were Gram negative and 1795 (30.21%) was Gram positive bacteria. Among 4146 Gram negative colonies, 4116 (69.33%) were bacilli and 30 (0.45%) were cocco- bacilli whereas among 1795 Gram positive colonies, 698 (11.72%) were bacilli and 1097 (18.49%) were cocci. The species identified biochemically belonged to family *Enterobacteriaceae* (23 spp.), *Bacillaceae* (5 spp.), *Enterococaceae* (5 spp.), *Vibrionaceae* (3 spp.), *Pseudomonadaceae* (2 spp.), *Micrococccaceae* (2 spp.), *Aeromonadaceae* (2 spp.), *Staphylococaceae* (1 spp.), *Moraxellaceae* (1 spp.) and *Alcaligenaceae* (1 spp.). The site wise abundance distribution and species
composition of different bacterial genera indicated that maximum number of species were isolated from family *Enterobacteriaceae* followed by *Bacillaceae* and *Enterococaceae*. The forty five (45) bacterial species were isolated during the course of study. The highest number of bacterial species occurred at site 1, 2, 9, 15 and 16 whereas lowest number of species (29) at site 6. The highest bacterial species were observed in summer months and lowest in winter month showing influence of temperature on bacterial colonies. Analysis of variance (ANOVA) showed that the observed distribution of the bacterial colonies in different seasons is statistically significant. Therefore, seasonal variation in occurrence of bacterial colonies was observed between different study sites of the lake. The bacterial flora in the lake consisted of diverse life forms ranging from Proteobacteria to Firmicutes and Actinobacteria which belonged to different selected micro habitats across the lake. The bacterial population showed a diverse seasonal and temporal variation on the basis of occurrence in different sites which were categorized into four groups named as open, littoral, outlet and inlet sites. *E.coli* was found to dominate different habitats of lake in all the seasons of the year. The ANOVA carried out between different sites for bacterial species isolated from different microhabitats showed that 71% results were statistically significant with 7% as highly significant (p < 0.01) and 27% as non significant (p < 0.05). The Bray Curtis cluster analysis of the study sites developed on the basis of presence and absence of a species at the respective sites showed similarity ranged from 31 to 87% with the least similarity of 31% between site 1 and 7 and maximum similarity of 87% between site 3 and 4. From the value of different indices computed for 16 sites for the occurrence of different bacterial species, the Shannon wiener index was highest at site 16 (3.68) and lowest at site 8 (3.26). The analysis of variance showed that highly dominance and diversity patterns varied significantly with highly even distribution of bacterial species in microhabitats of the lake. The data of correlation analysis between the pH and bacterial load at sixteen sites indicated that there was a negative correlation of pH with the bacterial load and positive correlation of temperature with bacterial load and the results were found to be statistically significant. For the purpose to study the impact of pathogenic bacteria isolated from Dal lake on humans, a random survey of the 20% of population i.e., 384 individuals (64 families) out of 1920 individuals (320 families) who were engaged in
one or the other activity related to lake water was carried out through questionnaire. The data of which reveals that the disease was more prevalent in males than in females under the age group of 20 years followed by age group of 21 to 40 years and then by above 40 years. The symptoms of gastrointestinal diseases were reported in 26 cases (6.77%) and other symptoms like high fever, chills, rigors, sweating and body aches in 17 cases (4.42%). The prevalence as per the source of water being used revealed that disease symptoms were more prevalent in individuals consuming lake water as compared to tap water. The results were statistically found to be significant. The most of the bacteria isolated were recognized as human pathogens, capable of initiating water borne infections, thus potentially water transmitted. The obtained data in the study reflect the importance of microbiological monitoring especially related to pathogenic bacteria.