R. C. Patel Educational Trust's
R. C. Patel Arts, Commerce and Science College
Shirpur-425405, Karvand Naka, Dist.- Dhule (Maharashtra)
E-mail - principal@rcpasc.ac.in

Affiliated to: K. B. C. North Maharashtra University, Jalgaon-425001

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R. C. Patel Educational Trust's
R. C. Patel Arts, Commerce and Science College
Karvand Naka, Shirpur 425405, Dist - Dhule, Maharashtra
☎: (02563) 299328
E-mail: principal@rcpasc.ac.in

President
Hon. Bhupeshbhai Patel

Principal
Dr. D. R. Patil

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Dr. Sandip P. Patil
IQAC Co-ordinator
IQAC Coordinator
R. C. Patel Educational Trust's
R. C. Patel Arts, Commerce and Science College
Shirpur, Dist.-Dhule (M.S.) 425405

R. C. Patel Arts, Commerce and Science College Shirpur ★ R. C. Patel Educational Trust's

Dr. D. R. Patil
IQAC Chairman & Principal
PRINCIPAL
R. C. Patel Educational Trust's
R. C. Patel Arts, Commerce and Science College
Shirpur, Dist.-Dhule (M.S.) 425405

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Gut, oral and skin microbiome of Indian patrilineal families reveal perceptible association with age

Diptaraj S. Chaudhari[1,3,7], Dhiraj P. Dhotre[1,7*], Dhiraj M. Agarwal[2], Akshay H. Gaike[1,2], Devika Bhalerao[2], Parmeshwar Jadhav[2], Dattatray Mongad[1], Himangi Lubree[2], Vilas P. Sinkar[1], Ulhas K. Patil[3,6], Sundeep Salvi[4], Ashish Bavdekar[5], Sanjay K. Juvekar[2] & Yogesh S. Shouche[1*]

The human microbiome plays a key role in maintaining host homeostasis and is influenced by age, geography, diet, and other factors. Traditionally, India has an established convention of extended family arrangements wherein three or more generations, bound by genetic relatedness, stay in the same household. In the present study, we have utilized this unique family arrangement to understand the association of age with the microbiome. We characterized stool, oral and skin microbiome of 54 healthy individuals from six joint families by 16S rRNA gene-based metagenomics. In total, 69 (1.03%), 293 (2.68%) and 190 (8.66%) differentially abundant OTUs were detected across three generations in the gut, skin and oral microbiome, respectively. Age-associated changes in the gut and oral microbiome of patrilineal families showed positive correlations in the abundance of phyla Proteobacteria and Fusobacteria, respectively. Genera *Treponema* and *Fusobacterium* showed a positive correlation with age while *Granulicatella* and *Streptococcus* showed a negative correlation with age in the oral microbiome. Members of genus *Prevotella* illustrated high abundance and prevalence as a core OTUs in the gut and oral microbiome. In conclusion, this study highlights that precise and perceptible association of age with microbiome can be drawn when other causal factors are kept constant.

Aging is an extremely complex, perpetual, progressive and multifactorial process resulting in decreased physiologic functions of all the organ systems[1]. Studies have reported that the human microbiome, the latest discovered organ, is also significantly influenced by increasing age[2–4]. Studies have suggested that the complex and diverse communities of microbes that inhabit the gut vary through different stages of an individual's life[5]. Many of these alterations are harmless and natural, while some of the alterations can have an important effect on overall homeostasis[6]. Importantly, notable changes in the human microbiome occur when the immune system is relatively weak, i.e., at the start of life and during aged life[7]. Many of the fluctuations in the microbiome are harmless and natural; nonetheless, studies have shown that some disturbances in the gut microbiome can have important effects on health and disease[6]. Earlier studies on human microbiome analyses have discovered an increased abundance of *Bacteroides* species in the elderly population[8]. An enriched abundance of Proteobacteria a bacterial group containing 'pathobionts' known for causing impairment in a susceptible host, i.e., in centenarian's[2–4]. But the populations used for these studies were either from different geographical locations or with different diets[2–4]. In agreement with the studies on the human gut microbiome, in older micro-pigs[9] also decreased abundance of beneficial microbes including probiotic bacteria and short-chain fatty acid-producers was recorded while *Bacteroides* were increased with the increasing age[9].

Several studies have shown age-associated effects in the experimental animals wherein, transfer of an aged microbiome into germ-free mice leads to systemic inflammation[10,11], on the contrary replacement of microbiome of the aged mice with the microbiome of younger mice boosts the local germinal center reactions[1]. Researchers

[1]National Centre for Microbial Resource, National Centre for Cell Science, Central Tower, Sai Trinity Building Garware Circle, Sutarwadi, Pashan, Pune, India. [2]Vadu Rural Health Program, KEM Hospital Research Centre, Pune, India. [3]R. C. Patel ASC College, Shirpur, Dhule, India. [4]Chest Research Foundation, Marigold Premises, Survey no 15, Kalyaninagar, Pune, India. [5]KEM Hospital, Pediatrics Department, KEM Hospital, Rasta Peth, Pune, India. [6]Department of Microbiology, Government Institute of Science, Aurangabad, India. [7]These authors contributed equally: Diptaraj S. Chaudhari and Dhiraj P. Dhotre. *email: dhiraj@nccs.res.in; yogesh@nccs.res.in

noted that the aged mice's germinal center reaction was stronger following fecal transplantation from the younger mice[1]. Moreover, remodeling of the gut microbiome has shown to increase the lifespan in diverse organisms, including *Drosophila melanogaster*[12,13], killifish[14], mice[15], etc.

Coevolved with the host and its ancestors for millions of years, the microbiome plays a key role in the maintenance of host health and wellbeing by performing various functions ranging from digestion, protection against pathogen colonization to host immunity and regulation of central nervous[16–21]. Also, the microbiome is responsive to a variety of confounding factors such as host ethnicity[22,23], age[24,25], diet[26,27] and geographic location[24,28]. Hence, it is imperative to study the same population longitudinally for the exploration of a precise association of age and microbiome. Studying the microbiome of genetically linked individuals of multiple generation families having similar diet, ethnicity and staying in the same geographic regions can help in estimating the perseverance of microbiota obtained in early years and its progression with age. Traditionally, India has an established convention of the joint family system, which is an extended family arrangement consisting of three or more generations living in the same household structure bound by genetic relatedness[29,30]. Especially in rural and semi-urban joint families in India, family members live in the same house structure and have similar dietary and sanitary habits. Hence, the Indian population provides a unique opportunity to understand age-related changes in the human microbiome. Studies relating to the influence of FUT2 and birth mode variants on microbiome[31], diabetes-associated microbiome[32], obesity-related microbiome[33], the microbiome of celiac disease patients[34], an association of microbiome with ayurvedic Prakriti types[35], microbiome structure of rural, urban[36] and tribal[37] populations were carried out in the Indian populations. However, age-related changes in the human microbiome across different body habitats are unknown. The majority of studies understanding the age and human microbiome correlations have been focused on the gut microbiome, while changes in oral and skin microbiome in the aging process have been relatively less studied.

In the present study, we provide a comprehensive analysis of the human microbiome from the gut, oral and skin ecosystems from 54 healthy subjects belonging to six different patrilineally related three generation families staying together in rural Indian settings. The study population has harmonized dietary, social habits, hygiene and sanitation habits, economic status and geographic position. Predominantly, other microbiome contributing factors were harmonized and age was the only distinguishing factor. 16S rRNA gene amplicon sequencing-based microbiome analysis performed to investigate the age-related changes in the gut, skin and oral microbiome of Endogamous Agriculturist Indian (EAI) sub-population.

Results

Gut, oral and skin microbiome profile of EAI population. Overall, a total of 9,566,497 sequences were generated, out of which 8,048,975 (File S1) were taxonomically assigned, resulting in 6,708 OTUs for the gut microbiome. Four samples (St.D1004, St.D301, St.S610 and St.S612) were removed from further analysis due to lower sequencing depth. Bacterial phyla such as Bacteroidetes (49.3%), Firmicutes (41.6%), Proteobacteria (5.7%), Actinobacteria (2.18%) and Tenericutes (0.4%) were highly dominant and constituted ~99% of the total gut microbiome. Presence of 174 different bacterial genera was noted, wherein *Prevotella* (50%), *Dialister* (12%), *Bacteroides* (9%), *Megamonas* (3%), and *Succinivibrio* (3%) were among the dominant taxa contributing to a total of 77% of the gut microbiome (Fig. S1a). Although, genus *Prevotella* was observed to have varying relative abundance ranging from 2% to 77% across the study population, its dominance was evident from the fact that 62% (n = 31) of the study subjects had an abundance in a range of 33% to 77% of the total gut microbiome (Table S1).

In the oral microbiome, 7,568,649 good quality sequences (File S1) clustered into 2,167 OTUs. Analysis based on the taxonomic assignment of these reads revealed a higher abundance of bacterial phyla such as Proteobacteria (34%), Bacteroidetes (32%), Firmicutes (24%), Fusobacteria (6%) and Actinobacteria (2%) constituting 96% of the oral microbiome. Genera *Neisseria* (20%), *Streptococcus* (15%), *Prevotella* (14%), *Porphyromonas* (10%), and *Haemophilus* (10%) were found to be the five most dominant genera totaling up to 69% of the oral microbiome (Fig. S1b). The relative abundance of genus *Prevotella* was observed to be more than 10% in half of the population (Table S2).

The skin microbiome data comprised of 10,951,175 good quality sequences (File S1) clustered into 10,920 OTUs. Skin microbiome analysis showed a higher abundance of phyla Firmicutes (49%), Proteobacteria (26%), Actinobacteria (12%) and Bacteroidetes (8%) collectively on 11 different body sites including dry, moist and sebaceous regions. Only one percent of OTUs were assigned to phylum Cyanobacteria. The skin microbiome showed the highest number of OTUs (n = 10,920) compared to oral and stool samples. *Corynebacterium* (10%) *Alloiococcus* (9%), *Staphylococcus* (8%), *Streptococcus* (7%) and *Anaerococcus* (6%) were the most dominant and diverse bacterial genera detected in the skin microbiome (Fig. S1c). Alpha diversity analysis measures, i.e., observed species (OTUs), Chao1, Shannon and Inverse Simpson revealed no significant differences in the gut and skin microbiome when compared between the three age groups (Fig. 1), family structure and dietary habits (Table 1). However, significant differences were observed in the oral microbiome between the age groups (ANOVA, $p < 0.05$ with Benjamini-Hochberg FDR corrections) (see Fig. 1B).

Contribution of core taxa in the gut, oral and skin microbiome of patrilineal families. Bacterial genera prevalent in 95% of the study population with more than 0.1% abundance were considered as a part of the core microbiome. Estimation of core microbiome was performed for individual families (n = 6 families) and the overall EAI study population. Amongst the 171 total bacterial genera detected in the gut microbiome, only three genera, namely *Prevotella, Ruminococcus* and *Faecalibacterium*, were recorded as a part of core microbiome across all the families (Fig. 2a, Table S3). These core taxa represented 23% to 91% gut microbiome composition of the participants (Fig. S2). With the aforementioned detection threshold few bacterial genera were explicitly detected in particular family as core taxa wherein, *Parabacteroides* was detected in family D3, *Haemophilus* and *Roseburia* in family D8, *Streptococcus* and *Dorea* in family D10 (Fig. S3, Table S3).

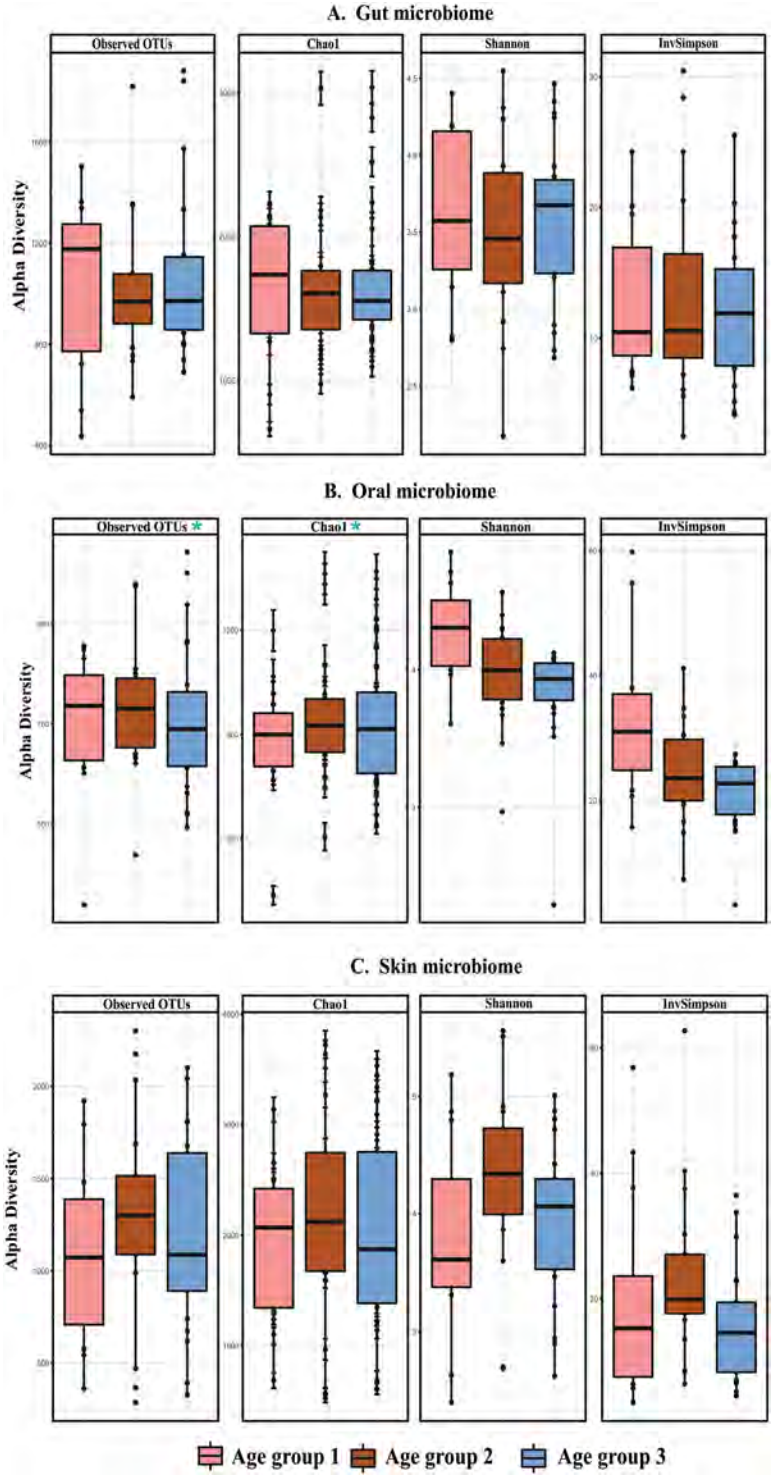

Figure 1. Boxplot of alpha diversity measures across the three generations (age groups) in the gut (**A**) oral (**B**) and (**C**) skin samples. The boxes denote interquartile ranges (IQR) with the median as a black line.

The core microbiome of oral samples represented presence of 13 (6.7%) bacterial genera amongst the 192 total genera. These genera include *Neisseria, Streptococcus, Prevotella, Porphyromonas, Haemophilus, Fusobacterium, Granulicatella, Veillonella, Capnocytophaga, Rothia, Aggregatibacter, Gemella* and *Lautropia* (Fig. 2b). Overall, these core taxa estimated 79% to 96% of the total microbiome composition (Fig. S2).

In the skin microbiome samples, *Corynebacterium* and *Streptococcus* were the only bacterial genera detected as core taxa across all the families (Fig. 2c, Table S5). Similar to the gut microbiome, family-specific bacterial genera were also detected in the skin microbiome. These genera include *Novosphingobium* in family D8, *Enhydrobacter, Salinicoccus* and *Butyrivibrio* in family D10, and *Haemophilus* and *Gemella* in family S6 (Fig. S5, Table S5). These

Sample Type	Description	Samples Nos.	Chao1 (Average)	Goods coverage (Average)	Observed species (Average)	PD whole tree (Average)	Shannon (Average)	Simpson (Average)
Human gut	Age group 1	11	2020.02 ± 466.57	0.996 ± 0.996	1314.73 ± 1314.73	64.92 ± 64.92	5.29 ± 5.29	0.91 ± 0.91
	Age group 2	18	1907.05 ± 635.75	0.996 ± 0.003	1228.89 ± 426.12	61.11 ± 17.02	4.88 ± 1.05	0.86 ± 0.13
	Age group 3	23	2123.67 ± 539.53	0.996 ± 0.001	1378 ± 368.18	66.93 ± 15.07	5.17 ± 0.74	0.9 ± 0.9
Human skin	Age group 1	12	2883.26 ± 1038.83	0.99 ± 0.007	1853.25 ± 831.07	107.51 ± 35.29	5.47 ± 1.3	0.91 ± 0.07
	Age group 2	17	3293.69 ± 1147.45	0.992 ± 0.007	2310.47 ± 880.29	122.83 ± 34.75	6.2 ± 1.15	0.95 ± 0.03
	Age group 3	23	3054.99 ± 1398.22	0.977 ± 0.078	2135.13 ± 1098.27	113.52 ± 46.59	5.7 ± 0.97	0.91 ± 0.05
Human oral	Age group 1	12	**736.55 ± 141.25***	0.999 ± 0.001	**607.67 ± 116.94***	32.33 ± 4.74	6.11 ± 0.57	0.96 ± 0.02
	Age group 2	18	**800.83 ± 160.61***	0.999 ± 0	**629.61 ± 109.04***	33.84 ± 7.94	5.81 ± 0.47	0.96 ± 0.02
	Age group 3	24	**809.69 ± 200.33***	0.999 ± 0	**611.5 ± 140.96***	33.52 ± 9.85	5.64 ± 0.54	0.95 ± 0.06

Table 1. The table illustrates the diversity indices calculated for the gut, oral and skin samples. *Statistically significant differences across the generations.

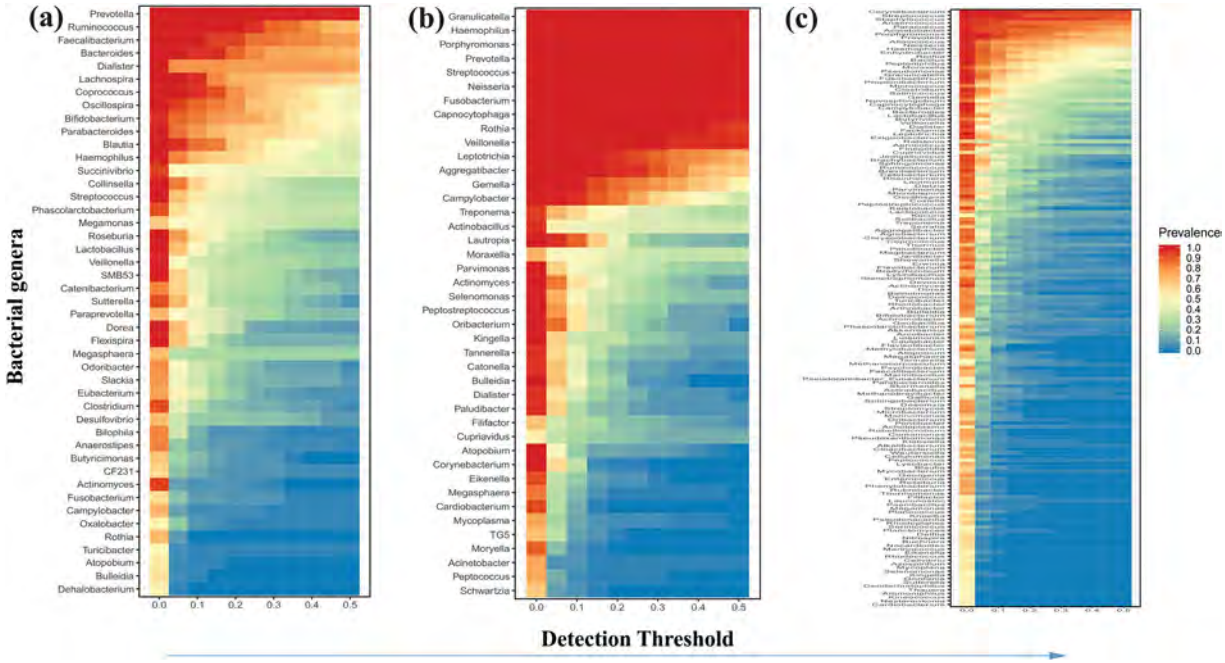

Figure 2. Heatmap representing the core bacterial genera detected across the gut (**a**), oral (**b**) and skin (**c**) microbiome samples of the EAI population.

core taxa represented 37% to 94% of the total microbiome (Fig. S2). Largely, the contribution of core taxa in the gut, oral and skin microbiome of all the patrilineal families was identical.

Influence of diet on the gut microbiome. Detailed dietary information of the study population was collected using the food frequency questionnaire (FFQ). With the help of a nutritionist, the dietary information was subsequently converted into the daily intake of carbohydrates, proteins, fats, lipids, fibers and calories (Table S6). Investigation revealed that average carbohydrates consumption in the first, second and third-generation members was 166, 396 and 339 grams, providing 74%, 81% and 80% of daily calories in the respective generations. Overall the type and amount of dietary components were similar across the population, except for family D3, which has relatively lesser consumption of these components. Canonical correspondence analysis (CCA) based on the abundance of bacterial genera, amount of dietary components and samples metadata showed that all the samples were scattered across the ordination plot and no clear clustering of the samples was observed based on age group or gender (Fig. 3). The variation explained by the ordination plot was also non-significant, reporting 7.5% for the gut, 10.6% for the oral and 6.9% for the skin microbiome (Fig. 3). Also, correlation analysis between the relative abundance of bacterial taxa and routine consumption of dietary components showed no significant association (Fig. 4).

Association of age and microbiome. Microbiome community structure of gut, oral and skin samples was investigated across three generations (age groups). Amongst the prevalent bacterial genera of the gut microbiome, *Succinivibrio* and *Ruminococcus* were highly abundant in the age group 1, *Dialister, Megamonas,*

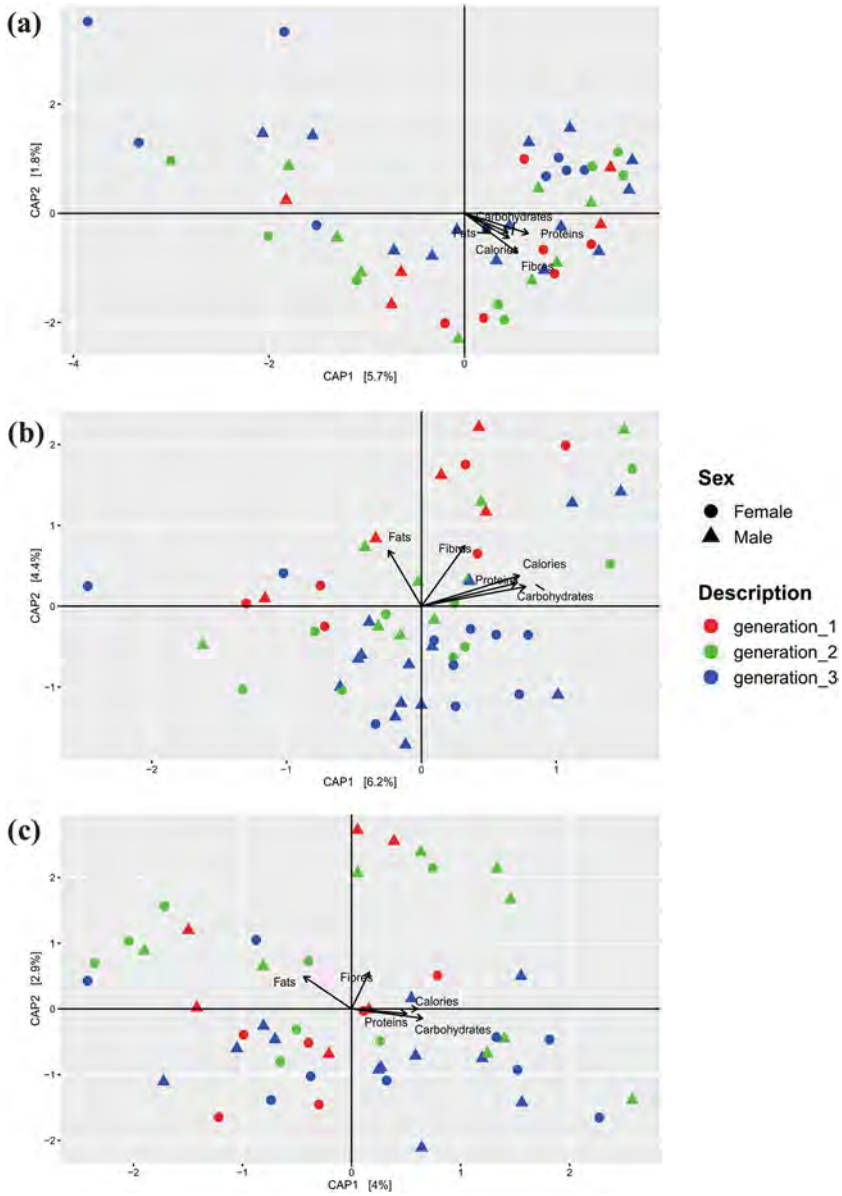

Figure 3. Canonical correspondence analysis (CCA) plot of bacterial genera and age group relationship calculated for gut (**a**) oral (**b**) and skin (**c**) microbiome of the endogamous agriculturist Indian subpopulation.

Phascolarctobacterium, Megasphaera and *Faecalibacterium* in the age group 2 and *Prevotella, Bacteroides* and *Bifidobacterium* were in the age group 3 (Table S7a). Likewise, in the oral microbiome *Prevotella, Fusobacterium, Veillonella, Capnocytophaga, Rothia* and *Aggregatibacter* were highly abundant in the age group 1, genus *Haemophilus* in age group 2 while *Neisseria, Streptococcus, Porphyromonas* and *Granulicatella* in the age group 3 (Table S7b). High abundance of few bacterial taxa was recorded in particular age groups in the skin microbiome samples also, wherein *Corynebacterium, Alloiococcus, Peptoniphilus, Haemophilus, Acinetobacter* and *Clostridium* were highly abundant in age group 1, *Anaerococcus, Porphyromonas* and *Campylobacter* in age group 2 and *Staphylococcus, Streptococcus, Novosphingobium, Paracoccus, Moraxella* and *Prevotella* in age group 3 (Table S7c). Primarily, age-associated changes were observed in the microbiome structure of three-generation members and to strengthen these observations; statistical analysis was also completed. Comparative microbiome analysis in three age groups showed no significant differential abundance of bacterial genera in the gut and skin microbiome. However, the oral microbiome showed significant variations in the abundance of genera *Dialister*, *Fusobacterium, Streptococcus, Selenomonas, Filifactor* and *Treponema* (Fig. 5D) (ANOVA, $p < 0.05$ with Benjamini-Hochberg FDR corrections). We confirmed our observations using qPCR analysis for quantifying the absolute proportion of genus *Prevotella* in the total human gut bacteria (Fig. 5E).

Beta diversity analysis using non-metric multidimensional scaling (NMDS) plots based on Bray-Curtis metrics showed no clear clustering in the samples based on the age groups of the study population (Fig. S6). Age-associated changes in the microbiome were further analyzed based on differentially abundant OTUs

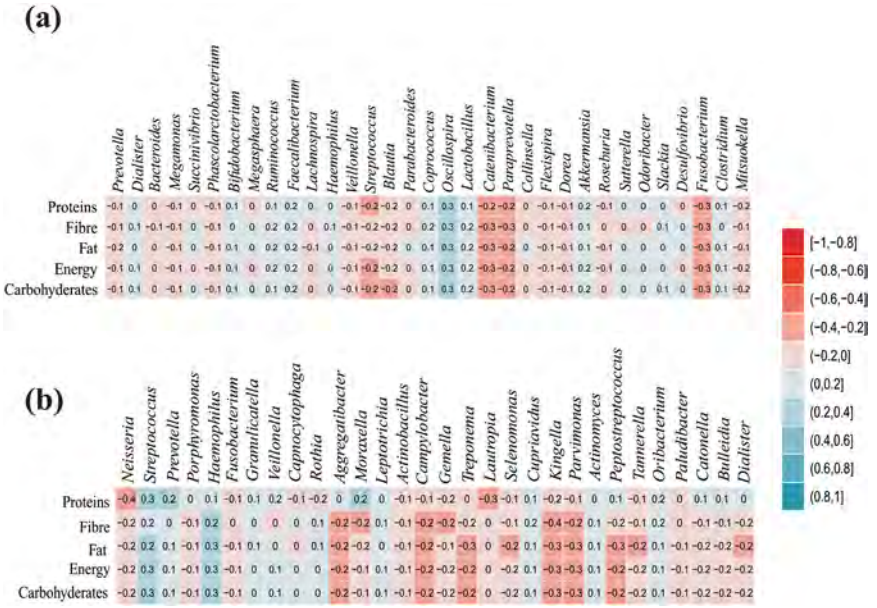

Figure 4. Correlation analysis of microbiome (genus levels) and dietary consumption of carbohydrates, proteins, fats, fibers and calories for the human gut (**a**) and oral (**b**) microbiome.

(ANOVA, $p < 0.05$ with Benjamini-Hochberg FDR corrections). Investigation revealed the presence of 69 (1.03%) differentially abundant OTUs across three age groups in the gut microbiome. Similarly, 190 (8.66%) and 293 (2.68%) differentially abundant OTUs were observed in human oral and skin microbiome, respectively. A high number of differentially abundant OTUs were present in the oral samples. Beta diversity analysis using these differentially abundant OTUs showed clustering of samples based on the age groups in the gut, oral and skin samples (Fig. 5A–C).

We further performed a correlation analysis of gut, oral and skin microbiome with age. Linear regression analysis using the nonparametric Spearman correlation revealed a higher abundance of phylum *Proteobacteria* with increasing age in the gut microbiome ($p < 0.05$) (Fig. 6A). While, in the oral microbiome of the population, a higher abundance of phylum *Fusobacteria* was observed with the increasing age ($p < 0.05$) (Fig. 6B). However, no such age-based correlations were observed in the skin microbiome.

Amidst the total 171 bacterial genera in the gut microbiome, only genus *Bacteroides* showed age-associated changes. Decreased abundance *Bacteroides* was recorded with the increasing age (nonparametric Spearman correlation ($p < 0.05$) (Fig. 6B). Whereas, in the oral microbiome of the population, bacterial genera *Treponema* and *Fusobacterium* showed a positive correlation (Fig. 6D,E) while genera *Granulicatella* and *Streptococcus* showed a negative correlation with the age ($p < 0.05$) (Fig. 6F,G). However, in the skin microbiome, no such statistically significant correlations were noted.

Discussion

Indian patrilineal extended family structure provides a unique opportunity to study the underlying effects of age, diet, and genetics influencing the human microbiome. Such family structure is a widely seen residential unit comprising of 2–4 patrilineally related generations living together, particularly in rural and semi-urban settings[29,30]. In the present study, we analyzed gut, oral and skin microbiome from 54 healthy subjects belonging to six different families from a single biogeographic region (Dongargaon: 18.6199° N, 74.0807° E and Shikrapur: 18.6924° N, 74.1323° E).

In the gut and oral microbiome, we found a high prevalence of *Prevotella* (Fig. 2a,b; Tables S1 and S2), a bacterial genus known to be associated with degradation of complex plant polysaccharides[38,39]. Indian diet is rich in plant-based carbohydrates, and our observations are consistent with earlier reports where a high prevalence of *Prevotella* in the gut microbiome of the Indian population was observed[39,40]. Prevalence of *Prevotella* has also been reported in the African population consuming a diet rich in carbohydrates and fibers[41].

Understanding the confounding factors that shape and define the oral microbiome is crucial for understanding the broader systemic health[42], as oral microbiome has long been known to be a reservoir for infection at other body sites[43]. In our analysis, high abundance of bacterial genera *Neisseria*, *Streptococcus*, and *Prevotella* were observed (Fig. S1b). Genus *Neisseria* is aerobic and primary colonizers of the oral cavity, *Streptococcus* is a facultative anaerobe while *Prevotella* is the obligate anaerobic bacteria. The high abundance of aerobic, facultative anaerobic and obligate anaerobic bacteria suggests the role of oxygen sensitivity in structuring the composition of bacterial diversity associated with the oral cavity. This diverse microbiome can perform versatile metabolic functions crucial for the healthy oral cavity. Earlier, these bacterial genera reported being common residents of the oral cavity in different populations in the healthy state[44–47].

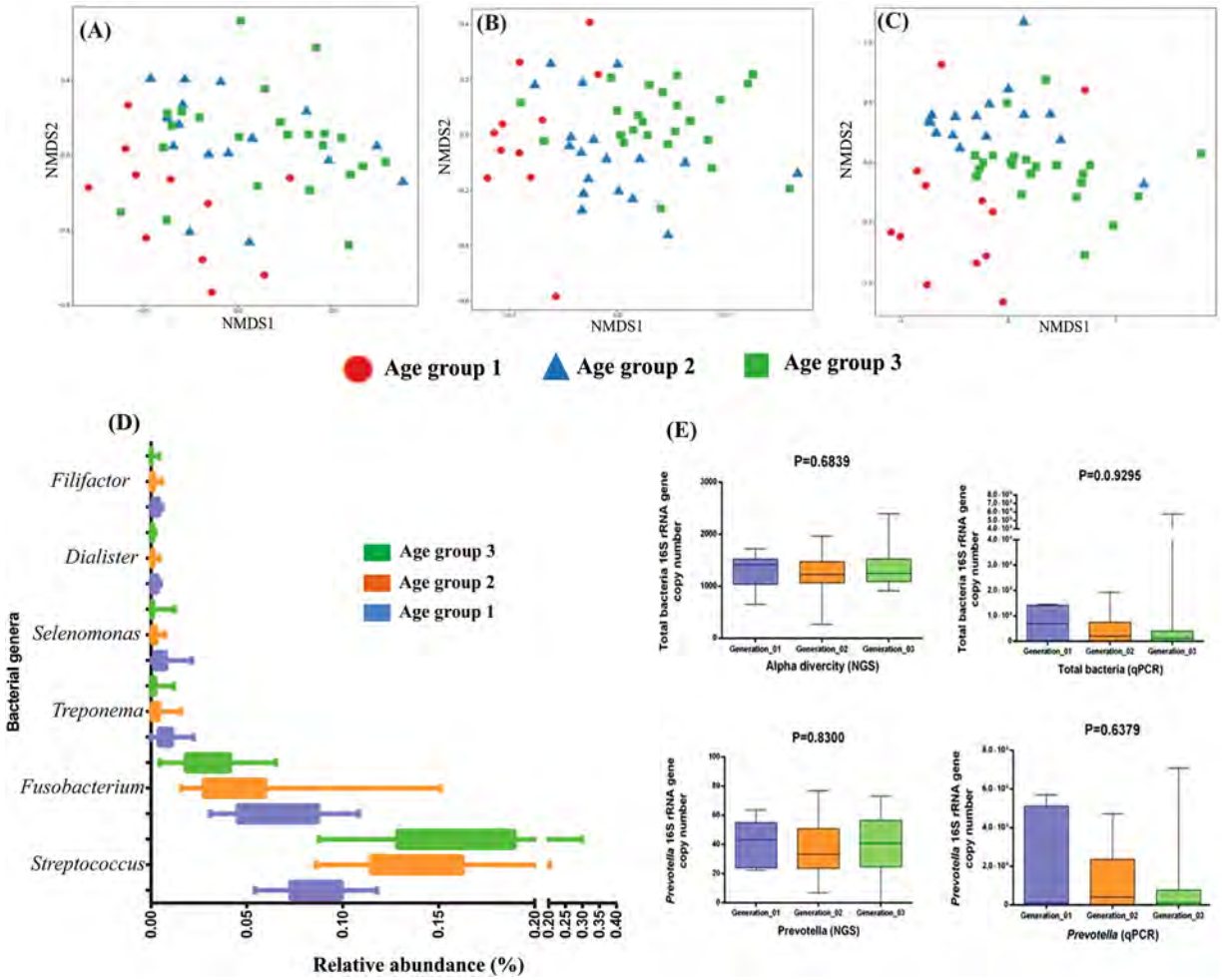

Figure 5. Nonmetric Multidimensional Scaling (NMDS) ordination displaying microbiome communities across the three generations in the gut (**A**), oral (**B**) and skin (**C**) microbiome. (**D**) Box plot showing differentially abundant genera in the human oral microbiome across the members from the three age groups. (**E**) Next-generation sequencing and qPCR results showing the abundance of *Prevotella* and total bacteria in the human gut microbiome across three age groups.

Investigating influencing factors is important to determine homeostatic forces that contribute to a healthy skin microbial community[48]. In the skin microbiome, *Corynebacterium*, *Alloiococcus*, and *Staphylococcus* were found to be the most abundant genera (Fig. S1c). These observations are in agreement with those reported by earlier studies in diverse ethnic groups, globally[49]. In contrast with an earlier study that reported Actinobacteria as the most dominant phylum of the skin microbiome[50], we observed dominance of Firmicutes followed by Proteobacteria and then Actinobacteria. These differences in skin microbiome of EAI sub-population could be associated with unique genetics, ethnicity and environmental conditions.

Further, different regions of the human skin like dry, moist and sebaceous are known to harbor different microbial community[51]. These differences could not be ascertained in our study since skin samples collected from 11 different body sites were pooled together before sequencing. The skin of healthy individuals generally harbors low microbial biomass and it requires sufficient starting material[52]. Hence DNA from all the 11 body locations of the participants were extracted separately and eventually pooled together before sequencing to avoid sequence artifacts associated with low biomass samples[52].

Microbial diversity, which contributes to the core microbiome, can provide a snapshot of homeostasis in the population and deviations from this core can be associated with different physiological states[53]. Presence of three, 13 and two core genera were observed in the gut, oral, and skin microbiome, respectively (Fig. 2). Genus *Dialister* was also amongst the highly abundant core taxa of the gut microbiome in all the families of the EAI population (Figs. 2, S3). An earlier study has reported that microbial enzymatic repertoire is known for the conversion of dietary fibers into short-chain fatty acids (SCFA)[54]. Our observations of a higher abundance of *Dialister* in Indian sub-population along with high consumption of dietary fiber suggests a need to test this possible association, as these bacteria are previously reported for SCFA production (propionate)[55]. Gut and oral microbiome showed a high proportion of core microbiome compared to the skin microbiome. Amongst the core taxa in oral microbiome, *Porphyromonas* are known for the expression of the *fimA* gene, which encodes for the surface protein important for attachment to other oral bacteria[56]. The oral microbial flora comprises diverse human-associated

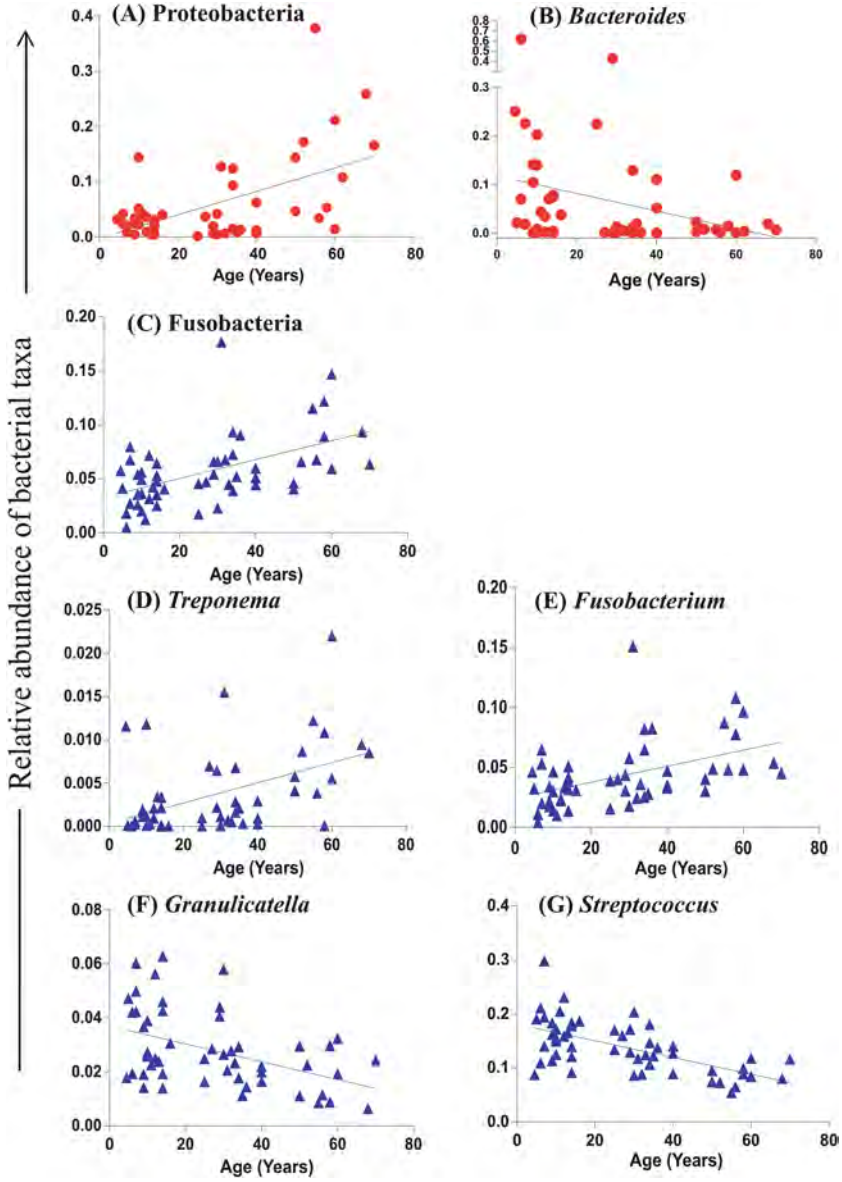

Figure 6. Correlation analysis of bacterial abundance with age, Phylum *Proteobacteria* (**A**) and Genus *Bacteroides* (**B**) of gut microbiome; Phylum *Fusobacteria* (**C**), genera *Treponema* (**D**), *Fusobacterium* (**E**), *Granulicatella* (**F**) and *Streptococcus* (**G**) of oral microbiome ($p =< 0.05$, $r^2 > 0.2$ for all the correlation).

biofilms, which are influenced by oral *streptococci*, the main group of early colonizers[57]. *Fusobacterium* was also prevalent taxa in the oral microbiome. In the complex ecosystems like oral cavity microbial co-aggregations like *Fusobacterium* and *Streptococcus*, which mediates a variety of cooperative metabolic functions[57]. Skin is the largest organ and represents the primary physical barrier between the host and the external environment. The overall representation of the core microbiome was only 15%, presumably due to oil, moist and sebaceous site-specific bacterial community structure and transient nature of the skin microbiome. Due to the acidic pH of the skin (4.4 to 5), despite the transient nature of skin microbiome, only mutualistic skin bacteria like *Streptococcus*, *Staphylococcus* and *Corynebacterium* can grow and detected as core taxa. Unique combination of taxa such as *Dialister, Prevotella, Bacteroides, Megamonas, Succinivibrio* in gut, *Streptococcus, Fusobateria Neisseria, Prevotella, Porphyromonas* in oral and *Corynebacterium, Alloiococcus, Staphylococcus, Streptococcus, Anaerococcus* and *Peptoniphilus* in skin were observed in EAI subpopulation emphasizing the effect of diet, host genetics and environmental factors on microbiome. Overall the core microbiome structure of the EAI population was similar across all the families which can be associated with similar dietary patterns, socioeconomic status, ethnicity, and agriculture-based lifestyle. Few low abundant bacterial taxa were exclusively detected as core taxa of specific families (Tables S3–S5). However, no relatable information was observed for the distinctive presence of these taxa.

Dietary information of the study population was collected using the food frequency questionnaire (FFQ) and this information is subsequently translated into the daily intake of carbohydrates, proteins, fats, lipids, fibers and calories with the help of a nutritionist. Detailed analysis showed that carbohydrates provide about 74%, 81% and

80% calories in the first, second and third generation members, respectively (Table S6) and overall, the consumption of other dietary constituents was comparable across the three generations. Correlation analysis of bacterial genera and routine dietary consumption of carbohydrates, proteins, fats, lipids, fibers and calories showed that there is no statistically significant correlation suggesting the relatively similar structure of microbiome and overall dietary pattern (Fig. 4). This observation is further strengthened by limited variation observed in the CCA analysis and no specific clustering was observed based on the generation (age groups) or the gender of the study participants (Fig. 3). A balanced diet helps in maintaining human health and the changes in the diet are responsible for the associated alterations in the microbiome. Singh *et al*., have shown that dietary alterations can induce microbiome associated changes in 24 hours, which can be alternating and yet reproducible[58]. Patrilineal families in this study follow the typical diet for several generations, and generally, all members of the family eat the same food irrespective of their age. The routine diet of the study populations comprises majorly of wheat and/or pearl millet bread, rice, vegetables and millets. The correlation analysis on this population revealed no statistically significant differences in the microbiome and the diet. This emphasizes the fact that overall homogeneity in the diet helps in maintaining the microbial state. Other confounding factors, including birth mode (cesarean section delivery and normal delivery), monozygotic or dizygotic twins had no effect on the microbiome as all the participants recruited in the study have the same normal delivery birth mode and none of the participants were twins.

A substantial number of studies have reported the association between age and the human microbiome[59,60], but the majority of these studies were among unrelated individuals who lacked constant causal contributing factors. Participants from three generations belonging to patrilineal families and living in the same household were recruited in this study to understand the perceptible effect of age on the microbiome. This sampling strategy allowed us to have a minimum impact of other confounding factors on the microbiome. Human microbiome dynamics changes with the time as the 'holobiont' integrates and responds to signals from the environment[61]. A direct causal relation between age-specific microbial communities and host aging has also been explored in laboratory model organisms, including flies, fish and mice[1,12–16], etc. Microbiome community structure of gut, oral and skin samples illustrated differences in the abundance of bacterial genera in three age groups. Here, *Succinivibrio* known for higher fiber degrading potential[62] and *Ruminococcus* were highly abundant in first-generation members (Table S7a). The specific reason for the higher abundance of these taxa is not known and it demands further investigation. Bacterial taxa known for healthier metabolism were abundant in the gut microbiome of the second generation members such as *Dialister* and *Phascolarctobacterium* the SCFA producers[63,64], *Megasphaera* the key carbohydrate metabolizing bacteria of Indian population known for having diverse and unique sets of Carbohydrate-Active enzymes (CAZymes)[65], *Faecalibacterium* is also the most abundant and important commensal bacteria of the human gut microbiota[8]. In addition to *Prevotella, Bifidobacterium*, the early gut colonizers and *Bacteroides* were higher in the third generation members (Table S7a). In the skin microbiome also age-related changes in the abundance of bacterial taxa were recorded. Genus *Corynebacterium* was highly abundant in first-generation members (Table S7c). Recent study understanding the extrinsic and intrinsic host factors influencing skin microbiome composition suggested that *Corynebacterium* OTUs were associated with skin aging[66], specifically with the hyperpigmented spots and wrinkles[66]. With the increasing age, physiological changes occur in the skin structure explains the association of key bacterial taxa in the members of the respective age groups. In our study, only 1.03% OTUs were found to be differentially abundant across three age groups, suggesting a nominal but profound effect of age on the gut microbiome. With the increasing age, the high abundance of Proteobacteria was detected (Fig. 6A). A higher abundance of this bacterial phylum was reported to be associated with the altered gut microbiome and dysbiosis[67,68]. Studies have shown an increase in the abundance of Proteobacteria with age correlating with the weaker immune response to the opportunistic pathogens, thereby leading to a decrease in the commensal microflora[69,70]. Proteobacteria have been suggested as the potential diagnostic criteria for dysbiotic conditions[7].

Similarly, in the oral microbiome, *Fusobacteria* was found to increase with increasing age (Fig. 6C). Few genera of this phylum are known opportunistic pathogens[71]; however, studies on the association of members of this phylum longitudinally with age can give more insights into their mutualistic or pathogenic role. Further, we observed a negative correlation in the abundance of Bacteroides with age (Fig. 6B); this is in contrast to previous studies demonstrating the higher abundance of genus *Bacteroides* with increasing age[72,73]. With the increasing age, physiological changes occur in the oral cavity like thinning of oral mucosa, smooth and loosened stippling aspect, narrowing and alteration of the gingival epithelium, modification of epithelial-connective interface and decreasing of keratinization[74]. Here, *Granulicatella* and *Streptococcus* abundance decreased with age (Fig. 6D,E) while *Treponema* and *Fusobacterium* abundance increased with age (Fig. 6F,G). *Granulicatella* is the component of normal oral flora and *Streptococcus* is also normal flora and early colonizers of the oral microbial community. On the contrary, few members of the genera *Treponema* and *Fusobacterium* are opportunistic pathogens. These age-related changes could be associated with the physiological changes in the oral cavity with the increasing age.

This study expressly describes the age-related changes in the microbiome. However, analysis of hematological and biochemical parameters of blood may have further provided an opportunity to understand its association with the microbiome, the clear picture on age-related changes in the overall metabolism and health and disease status. Further studies with additional samples and multoimics approach can help strengthen these findings.

In conclusion, this study particularly highlights the precise and perceptible association of age with the microbiome. Our finding suggests that the age-related changes are very specific and bacterial phylum Proteobacteria needs to be investigated in detail to understand its specific physiological role in gut microbiome. Similarly, bacterial taxa, including *Treponema*, *Fusobacterium*, *Granulicatella* and *Streptococcus* the member of the human oral microbiome, can be explored for their importance in the oral microbiome. Also, the findings suggest that core taxa constitute more than 75% of the gut and oral microbiome, while only 67% of the skin microbiome, indicating a larger variability of the microbiome present on the skin. We present baseline data of the human microbiome from a healthy Indian sub-population, which could be used as a reference for further studies, including diabetes[75–77] obesity and inflammatory diseases.

Methods

Ethical clearance declaration. The study was approved by the ethics committees of the National Centre for Cell Science (NCCS), Pune and King Edward's Memorial Hospital Research Centre (KEMHRC), Pune. Written informed consent from the study subjects or their parents wherever applicable were taken, as per the guidelines of the institutional ethics committee and Indian Council of Medical Research (ICMR), India. We confirm that all the experiments were performed as per the approved guidelines.

Recruitment of subjects. Subjects were recruited from the Vadu Health and Demographic Surveillance System (Vadu HDSS) area of the Vadu Rural Health Program, KEM Hospital Research Centre, Pune (VRHP, KEMHRC, Pune). The Vadu study population comprises of about 170,000 individuals that reside in 22 villages. The objective of Vadu HDSS is to create a longitudinal database of demographic information, including fertility, mortality, migration and marital status, of the Vadu area. Two villages, namely Dongargaon (Latitude: 18.7442326, Longitude: 73.4504317) and Shikrapur (Latitude: 18.687639, Longitude: 74.125671) were selected out of the total Vadu HDSS region.

The recruitment was done based on the following criteria.

1. Minimum three generations (I- age >50 years, II- age between 25 to 40 years and III- age between 3 to 15 years) with at least two members per generation must be living together in the same house structure.
2. Self-declared healthy individuals.
3. Families with individuals having a history of consumption of alcohol, tobacco and recent (last 3 months) use of antibiotics were excluded from the study.

Among the 30 families screened, six families comprising of 54 individuals fulfilled the required criteria and were included in the study.

Metadata and sample collection. A Food Frequency Questionnaire (FFQ), along with 48 hrs dietary recall was administered before sample collection. Detailed information on the consumption of the food item and quantity for each meal of the day were recorded. With the help of nutritionists, this information then translated into the daily consumption of carbohydrates, proteins, lipids, fibers and calories. Additional metadata about the use of antibiotics and medicines, hygiene and sanitary practices, lifestyle, socioeconomic status, social habits, health and diseases (self-reported with or without medical records based on standard questionnaire) and other demographic characteristics were recorded. Separate health status questionnaires for adults and children were administered for the selection of healthy adults for the study (Tables S8 and S9).

Detailed information on routine dietary consumption of different food nutriments, their frequency and quantity were collected and recorded from the study participants. This information was recorded for three important meals, i.e., breakfast, lunch, and dinner. Also, the data on routine consumption of any additional specific food nutriment besides these three meals was recorded. The information on routine dietary consumption was then used for calculating the routine consumption of carbohydrates, proteins, lipids, fibers, and calories.

Gut, oral, and skin samples from the recruited subjects were collected in triplicates (with an interval of one week). Freshly voided, early morning fecal sample was collected in a sterile container. Early morning oral washing (before brushing or gargling) was collected using freshly prepared sterile 1X PBS (pH 7.4) in a sterile container. Skin samples from 11 different body sites per individual (belonging to three different regions, i.e., moist, oily and sebaceous region) were collected as described in Fig. S7. All samples were stored at −80 °C until further processing.

Microbiome profiling. DNA extraction from fecal (representative of the gut), oral and skin samples was done using QIAamp stool DNA mini kit, QIAamp DNA mini kit, and QIAamp blood and tissue DNA extraction kit, respectively (Qiagen, USA). The DNA extraction was performed according to the manufacturer's instruction with the inclusion of bead beating and freeze-thaw treatment at −80 °C and 90 °C for 10 minutes alternatively. Metagenomic sequencing of the V3-V4 region of the 16S rRNA gene was done using Illumina Miseq platform, paired-end (2 × 300 bp) sequencing, as described earlier[78].

Bioinformatics and statistical analysis. Assembly of paired-end reads for each sample was carried out using FLASH (Fast Length Adjustment of SHort reads). Low-quality sequences were removed during the assembly with low overlapping regions (less than 20 nucleotides)[79]. Microbial diversity analysis was done using standard QIIME (v1.8.0) pipeline[80]. Closed reference-based OTU picking approach was used to cluster reads into Operational Taxonomic Units (OTUs) at 97% sequence similarity using UCLUST algorithm[81] and Greengenes database (13.8) and representative sequences from each OTU were selected for taxonomic assignment. Beta diversity and other statistical analysis was performed using Phyloseq[82], corrplot[83], vegan[84] and Microbiome[85] packages in R. Additional statistical analysis were performed using STAMP[86] and GraphPad Prism (GraphPad Software, La Jolla California USA). A web-based tool InteractiVenn was used for the analysis of shared and unique bacterial genera[87].

Quantification of genus *Prevotella* in study population. Quantitation of genus *Prevotella* and total bacteria from fecal samples was carried out using qPCR as described previously[88]. Briefly, for quantifying 16S rRNA gene for total bacteria and *Prevotella*, 10 µl reactions in triplicate were set containing a suitable pair of primers[88] (Table 2), 50 ng of Metagenomic DNA and SYBR green master mix (Applied Biosystems Inc. USA), using 7300 Real-time PCR system (Applied Biosystems Inc. USA). Following PCR conditions: initial denaturation at 95 °C for 10 min, followed by 40 cycles at 95 °C for 10 s, 60 °C for 1 min was used. Group-specific standard curves

Sr. No	Bacterial taxa	Primers	Sequence (5′-3′)	Amplicon size (bp)
1	Total bacteria	341F	CCTACGGGAGGCAGCAG	177
		518R	ATTACCGCGGCTGCTGG	
2	Prevotella	PrevF	CACCAAGGCGACGATCA	283
		PrevR	GGATAACGCCYGGACCT	

Table 2. Details for the qPCR primers and their amplicon size.

were generated from serial dilutions of a known concentration of respective PCR products. Additionally, melting curve analysis was performed at the end of qPCR cycles to check the amplification specificity. Average values of the triplicate were used for enumerations of tested gene copy numbers for each group using standard curves.

Data availability

The sequence data is available at NCBI SRA submission with accession number SRP116277 (Bioproject ID: PRJNA399246) for gut microbiome, SRP135853 (Bioproject ID: PRJNA438584) for skin microbiome and SRP135913 (Bioproject ID: PRJNA438728) for oral microbiome.

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Author contributions

S.K.J., S.S., A.B., D. P. D. and Y.S.S. conceived the study. D.S.C., D.P.D., D.M.A., S.S., A.B., S.K.J. and Y.S.S. designed the study. D.M.A., D.B., P.J., A.H.G. and S.K.J. provided the samples. D.S.C. performed the experiments. A.H.G., D.B. and P.J assisted in the experiments. Y.S.S., S.J., V.P.S. and U.K.P. provided guidance with the experiments. D.S.C. and D.P.D. performed the bioinformatics and statistical analyses. D.M. helped in that data analysis. H.L. guided in analysis of routine diet of the study subjects. D.S.C. and D.P.D. drafted the manuscript with input from V.P.S., Y.S.S. and S.K.J. All authors contributed to manuscript revisions, have read and approved the final version of the manuscript.

Competing interests

The authors declare no competing interests.

Additional information

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Correspondence and requests for materials should be addressed to D.P.D. or Y.S.S.

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Understanding the association between the human gut, oral and skin microbiome and the Ayurvedic concept of *prakriti*

Diptaraj Chaudhari[1,3], Dhiraj Dhotre[1]*, Dhiraj Agarwal[2], Arun Gondhali[2], Anand Nagarkar[2], Vikas Lad[2], Ulhas Patil[3,4], Sanjay Juvekar[2], Vilas Sinkar[1] and Yogesh Shouche[1]*

[1]*National Centre for Microbial Resource, National Centre for Cell Science, Central Tower, Sai Trinity Building Garware Circle, Sutarwadi, Pashan, Pune, India*

[2]*Vadu Rural Health Program, KEM Hospital Research Centre, Pune, India*

[3]*R. C. Patel ASC College, Shirpur, Dhule, India*

[4]*Department of Microbiology, Government Institute of Science, Aurangabad 431 004, India*

**Corresponding author (Emails, dhiraj@nccs.res.in; yogesh@ncs.res.in)*

Ayurveda is one of the ancient systems of medicine which is widely practised as a personalized scientific approach towards the general wellness. Ayurvedic *prakriti* is broadly defined as the phenotypes which are determined on the basis of physical, psychological and physiological traits irrespective of their social, ethnic, dietary and geographical stature. *Prakriti* is the constitution of a person, which comprises *vata, pitta,* and *kapha* and is a key determinant of how one individual is different from the other. Human microbiome is considered the 'latest discovered' human organ and microbiome research reiterates the fundamental principles of Ayurveda for creating a healthy gut environment by maintaining the individual-specific microbiome. Hence, it is important to understand the association of human microbiome with the Ayurvedic *prakriti* of an individual. Here, we provide a comprehensive analysis of human microbiome from the gut, oral and skin samples of healthy individuals (n=18) by 16S rRNA gene-based metagenomics using standard QIIME pipeline. In the three different *prakriti* samples differential abundance of *Bacteroides, Desulfovibrio, Parabacteroides, Slackia,* and *Succinivibrio* was observed in the gut microbiome. Analysis also revealed *prakriti*-specific presence of *Mogibacterium, Propionibacterium, Pyramidobacter, Rhodococcus* in the *kapha prakriti* individuals *Planomicrobium, Hyphomicrobium, Novosphingobium* in the *pitta prakriti* individuals and *Carnobacterium, Robiginitalea, Cetobacterium, Psychrobacter* in the *vata prakriti* individuals. Similarly, the oral and skin microbiome also revealed presence of *prakriti*-specific differential abundance of diverse bacterial genera. *Prakriti*-specific presence of bacterial taxa was recorded and only 42% microbiome in the oral samples and 52% microbiome in the skin samples were shared. Bacteria known for preventing gut inflammation by digesting the resistant starch were abundant in the *pitta prakriti* individuals, who are more prone to develop gut-inflammation-related disorders. In summary, human gut, oral and skin microbiome showed presence or high abundance of few bacterial taxa across three *prakriti* types, suggesting their specific physiological importance.

Keywords. Ayurvedic *prakriti*; human microbiome; 16S rRNA gene; next generation sequencing

1. Introduction

The human microbiota consists of the 10–100 trillion symbiotic microbial cells harboured by each person, which possess ~10 times more bacterial cells than the number of human cells (Ley *et al.* 2006). Microbiome represents over 100 times the amount of genomic content compared to human genome (Qin *et al.* 2010). Human microbiome is emerging as a key player in maintaining human health and well-being by performing various functions ranging from digestion, protection against pathogen colonization to host immunity and central nervous system regulation (Huttenhower *et al.* 2012). Effect of different confounding factors on the human microbiome is well studied: the association of specific diet and the microbiome is well known (Turnbaugh *et al*. 2009; Singh *et al* 2017).

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Ayurveda is one of the ancient well-written medical sciences, widely practiced in India (Chopra *et al.* 2010). It has an individualized approach towards management of health, and prevention and curing of illness/disease (Chopra *et al.* 2010). *Prakriti* is one of the important concepts of Ayurveda that defines personalized approach in health and diseases (Chopra *et al.* 2010). It is the basic constitution of an individual which is decided at the time of conception and remains unchanged throughout the life. According to Ayurveda, *prakriti* are classified into seven types: *vata*, *pitta*, *kapha*, *vata-kapha*, *vata-pitta*, *kapha-pitta* and *sama prakriti* (all three, i.e., *vata-pitta-kapha*). These *prakriti* exhibit specific functions, mainly structure, behaviour, response to environmental stimuli, susceptibility to diseases, etc. *Prakriti* types explain the physiological variations (Rotti *et al.* 2014). An individual may have a dominance of one or more *doshas* (bio physiological forces). Balance of the *doshas* results in homeostasis and good health, while vitiation or depletion of *doshas* leads to the disease (Govindaraj *et al.* 2015). Over time, the natural balance of the *doshas* in an individual can be disturbed by a number of factors, such as ageing, improper diet, lifestyle, stress levels and environmental pollution (Lakhotia 2014). Human microbiome is also known to differ in response to above-mentioned factors (Conlon and Bird 2015). The clinical manifestation of disease and its severity is determined by origin and mechanism of perturbation of *doshas* (Prasher *et al.* 2016). A recent study in the Indian rural population has showed that, although a substantial portion of gut microbiome is shared across the population, different *prakriti* types illustrate enrichment of specific bacterial taxa (Chauhan *et al.* 2018). With this preliminary information we decided to explore the association among the *prakriti* of an individual with the gut, skin and oral microbiome. In the present study, we provide a comprehensive analysis of the human microbiome from the gut, oral and skin ecosystems from 18 healthy individuals. 16S rRNA gene amplicon sequencing based microbiome analysis was done to understand the association between human microbiome and Ayurvedic *prakriti*.

2. Materials and methods

2.1 *Approval of the study*

The study was approved by the ethics committees of National Centre for Cell Science (NCCS) and King Edward's Memorial Hospital Research Centre (KEMHRC). Written informed consent from the study participants or parents of the study participants was obtained. All methods and experiments were performed by following the approved guidelines.

2.2 *Sample collection site*

The Vadu HDSS (health and demographic surveillance system) study site lies within two administrative blocks (Shirur and Haveli), which is about 40 km from Pune city. *Prakriti* assessment and sample collection was done from 53 individuals belonging to the HDSS area.

2.3 *Assessment of Prakriti and participant recruitment*

Prakriti assessment of study participants were performed by Ayurveda physician who were trained and experienced in assessing the *prakriti* as per the traditional practice in Ayurveda. These Ayurveda physicians used few clinical parameters for assessing the *prakriti*, which primarily includes observation, palpation, percussion, auscultation and asking questions regarding appetite, likes–dislikes, exercise, mental strength and diseases. For this, a *prakriti* assessment questionnaire was prepared using Ayurveda *Samhita* references which describe detailed *lakshanas* (characteristics) of *prakriti* (Rotti *et al.* 2014).

2.4 *Sample collection*

A questionnaire was filled during sample collection, seeking answers to questions regarding use of antibiotics, general health status, and sanitary practices. Freshly voided, early morning faecal samples were collected in sterile containers, early morning oral washings before brushing or gargling was collected in the form of washings using freshly prepared sterile 1X PBS (pH 7.4) from each study participant in sterile container, and skin samples were collected from 11 different body sites including forearm volar, palm, umbilicals, popliteal fossa, forehead, retro-auricular crease, manubrium, armpit, antecubital fossa, back, and anterior nares belonging to three different regions, i.e. moist region, oily region and sebaceous region. All samples were stored at −80°C temperature until further processing.

2.5 *Sample processing and next generation sequencing*

DNA extraction from faecal (representative of gut), oral and skin samples was done using QIAamp stool DNA mini kit, QIAamp DNA mini kit and QIAamp blood and tissue DNA extraction kit, respectively (Qiagen, USA). DNA extraction was done according to manufacturer's instruction. 16S rRNA gene amplicon sequencing based microbiome analysis was done to understand the correlation of microbiome with the *prakriti* types. Sequencing of V3-V4 region of 16S rRNA gene (average read length = 450 BP) was done using illumina Miseq paired end (2 * 300) sequencing technology.

2.6 *Pre-processing of read and bioinformatics analysis*

Assembly of forward and reverse reads for each sample was carried out using FLASH (Fast Length Adjustment of SHort

reads) (Magoc and Salzberg 2011). Microbial diversity analysis was done using standard QIIME (v1.8.0) pipeline (Navas-Molina *et al*. 2013) on the high-quality sequences. Closed reference based OTU picking approach was used to cluster reads into Operational Taxonomic Units (OTUs) at 97% sequence similarity using UCLUST algorithm (Edgar 2010) and greengene database (13.8) and representative sequences (repset) from each OTU were selected for taxonomic assignment. For the beta diversity analysis R scripts and R packages such as Phyloseq (McMurdie and Holmes 2013), online tool Calypso (Zakrzewski *et al.* 2017) were used. Statistical analysis was also performed using STAMP (Parks *et al.* 2014) and graphpad Prism (*www.graphpad.com*). Additionally, gut microbiome data of western Indian population was also surveyed using similar analysis pipeline for the presence and abundance of specific bacterial taxa across different *prakriti* types (Chauhan *et al.* 2018).

3. Results

Prakriti assessment of total 53 Individuals was done. Among these, 40 individuals having *pitta* pradhan *prakriti*, seven individuals has *vata* pradhan *prakriti* while only six study individuals has *kapha* pradhan *prakriti*. Randomly, six participants were selected from the *vata* and *pitta prakriti* to meet the number of participants in *kapha* pradhan *prakriti* for the microbiome analysis. Both male (n = 8) and female (n = 10) participants were included in the study (table 1).

3.1 *Association of human gut microbiome and prakriti type*

In total 28,31,418 good-quality sequences were obtained from the 35,49,865 raw sequences generated using 16S rRNA gene amplicon sequencing of the stool samples (n = 18). These sequences were clustered into 5,066 OTUs. Data normalization was done keeping 74,512 sequences per sample for the further microbiome analysis. Bacteria belonging to 21 different phyla were detected. Bacterial phyla Bacteroidetes (47%), Firmicutes (42%) and Proteobacteria (05%) were found to be highly dominant. Overall, higher abundance of bacterial genera *Prevotella* (43%), *Bacteroides* (14%) and *Dialister* (12%) in gut microbiome samples was observed. Preliminary investigations suggested high abundance of phyla Proteobacteria and Elusimicrobia in the *vata prakriti* samples, while Fusobacteria and Verrucomicrobia were highly abundant in the *pitta* and *kapha prakriti,* respectively (figure 1A). Presence of five statistically significant (ANOVA, $p \leq 0.05$) differentially abundant genera including *Bacteroides*, *Desulfovibrio, Parabacteroides, Slackia* and *Succinivibrio* (figure 1B) was observed across the three different *prakriti* types. *Bacteroides* and *Parabacteroides* were highly abundant in the *pitta prakriti* individuals while *Desulfovibrio, Slackia* and *Succinivibrio* were highly dominant in the *vata prakriti* individuals.

Analysis of gut microbiome data of earlier study by Chouhan *et al.* (2014) also showed the abundance of *Parabacteroides* and *Bacteroides* in the *pitta prakriti* individuals but those differences were not statistically significant (ANOVA, $p > 0.05$) (supplementary figure 1). Beta diversity analysis using bray-Curtis PCoA plot showed homogeneity in the microbiome composition of the *vata prakriti* samples by forming tight cluster separating the samples from *pitta* and *kapha prakriti* samples. *Pitta* and *kapha prakriti* samples were spread cross the plot (figure 1C). Shared and unique bacterial genera across the *prakriti* types revealed 53.6% sharing while 10%, 10.7% and 12.9% unique bacterial genera in the *vata*, *pitta* and *kapha prakriti* samples, respectively (figure 1D) (supplementary file 1). Genera *Enterobacter, Mogibacterium, Serratia, Pyramidobacter, Scardovia, Rhodococcus, Propionibacterium, Allobaculum, Methylobacterium, Eikenella, Zoogloea, Cronobacter* and *Dickeya* were only present in the *kapha prakriti* individuals. *Enterococcus, Lactococcus, Moryella, Pseudoramibacter, Cloacibacterium, Dermabacter, Flavisolibacter, Chlamydia, Planomicrobium, Trichococcus, Erysipelothrix, Hyphomicrobium, Novosphingobium, Acinetobacter, Anaeroplasma* and *Thermus* were only present in the *pitta prakriti* Individuals and genera *Anaerotruncus, Anaerofustis, Cetobacterium, Brachyspira, Robiginitalea, Alloiococcus, Carnobacterium, Sarcina, Pseudobutyrivibrio, Schwartzia, Gallicola, Desulfococcus, Psychrobacter and Meiothermus* were exclusively present in the *vata prakriti* individuals (supplementary file 1).

Table 1. Characteristics of the study participants

Sr. no	Participant ID	*Prakriti* type	Sex
1	D802	*Kapha*	Female
2	S102	*Kapha*	Female
3	S106	*Kapha*	Female
4	S107	*Kapha*	Male
5	S604	*Kapha*	Female
6	S618	*Kapha*	Male
7	D306	*Pitta*	Male
8	D308	*Pitta*	Female
9	D309	*Pitta*	Female
10	S104	*Pitta*	Female
11	S108	*Pitta*	Male
12	S607	*Pitta*	Female
13	D1001	*Vata*	Male
14	D101	*Vata*	Male
15	D106	*Vata*	Male
16	D302	*Vata*	Female
17	S105	*Vata*	Female
18	S601	*Vata*	Male

3.2 *Association of human oral microbiome and prakriti type*

Genera level microbiome analysis in the oral samples revealed abundance of *Neisseria* (22%), *Streptococcus*

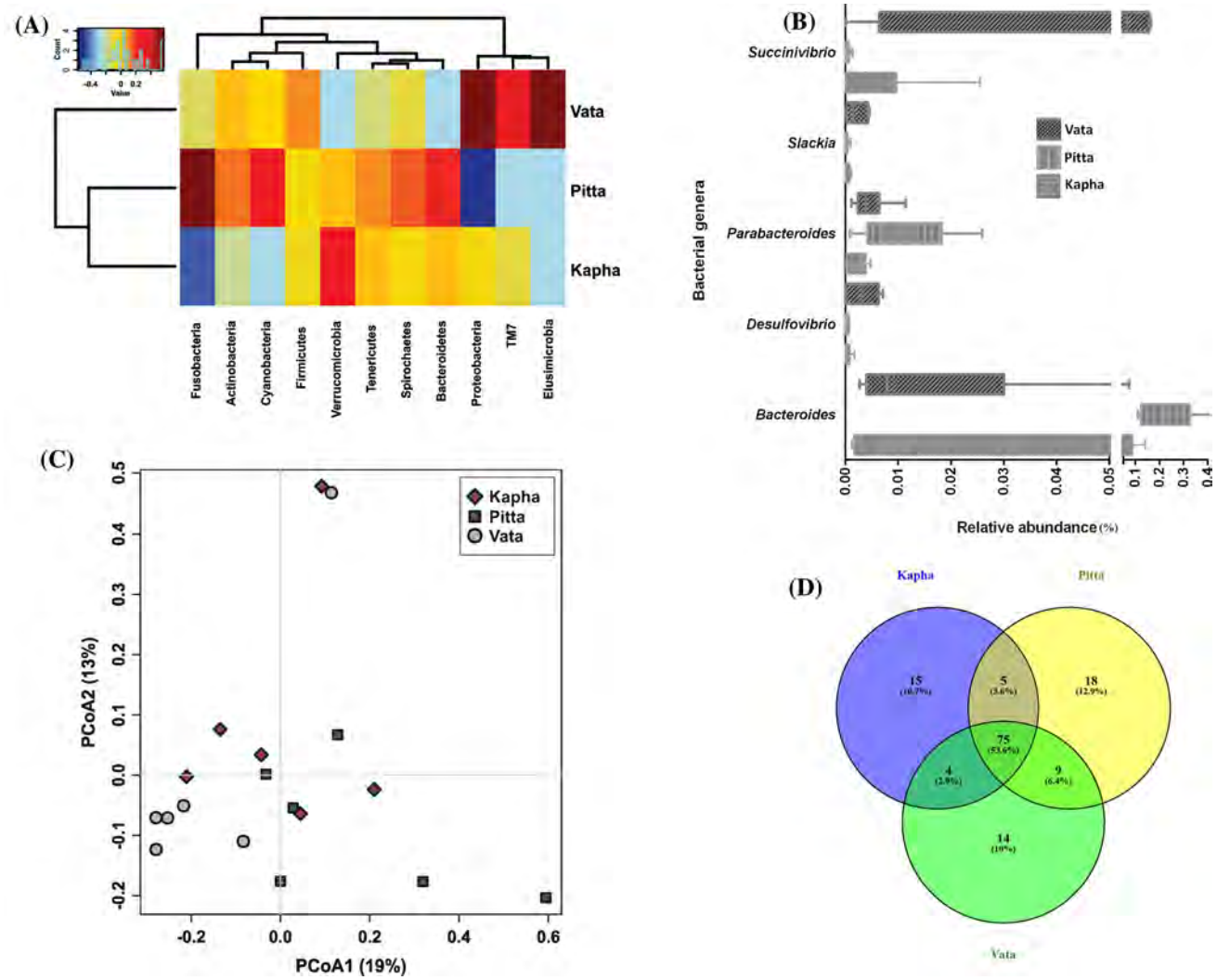

Figure 1. (**A**) Phylum-level distribution of bacterial populations in the *vata*, *pitta* and *kapha prakriti* types. (**B**) Differentially abundant bacterial genera in human gut microbiome across the *vata*, *pitta* and *kapha prakriti* individuals. (**C**) Multivariate analysis of beta-diversity: two-dimensional scatter plots of bacterial community (PCoA of 16S rDNA data) composition across the three different sample groups. Blue, red and grey colour represents samples from *vata*, *pitta* and *kapha prakriti* individuals, respectively. (**D**) Venn diagram of shared and *prakriti*-specific unique bacterial genera in the human gut microbiome. The numbers represent the *prakriti*-specific genera and total no of shared genera across all the study groups.

(15%), *Prevotella* (13%), *Haemophilus* (10%) and *Porphyromonas* (09%) across the samples. ANOVA analysis showed three statistically significant (ANOVA, $p < 0.05$) differently abundant genera based on the *prakriti* type. Wherein, genus *Leptotrichia* showed higher abundance in *kapha prakriti* samples, while *Gemella* and *Enhydrobacter* were dominant in *pitta prakriti* and *Campylobacter* and *Bifidobacterium* were dominant in *vata prakriti* samples (figure 2A). These three genera in addition to *Salenomonas* have showed differential abundance in the 2 group comparisons across the three *prakriti* types (figure 2B). The shared and unique bacterial genera analysis showed that 64 bacterial genera were common to all the three *prakriti* types and 21 genera were unique to *kapha*, 30 were unique to *pitta* and six genera, i.e. *Geobacillus, Lachnospira, Caulobacter, Hyphomicrobium, Mesorhizobium* and *Stenotrophomonas* were unique to *vata prakriti* samples (figure 2C) (supplementary file 2).

3.3 *Association of human skin microbiome and prakriti type*

Microbiome analysis of the skin samples revealed the differences in the mean relative abundance of bacterial genera *Corynebacterium*, *Streptococcus, Staphylococcus, Peptoniphilus, Alloiococcus, Anaerococcus, Porphyromonas, Paracoccus, Novosphingobium* and *Neisseria* in *vata, pitta* and *kapha prakriti* samples (figure 3A). Analysis of differentially abundant bacterial genera revealed presence of five

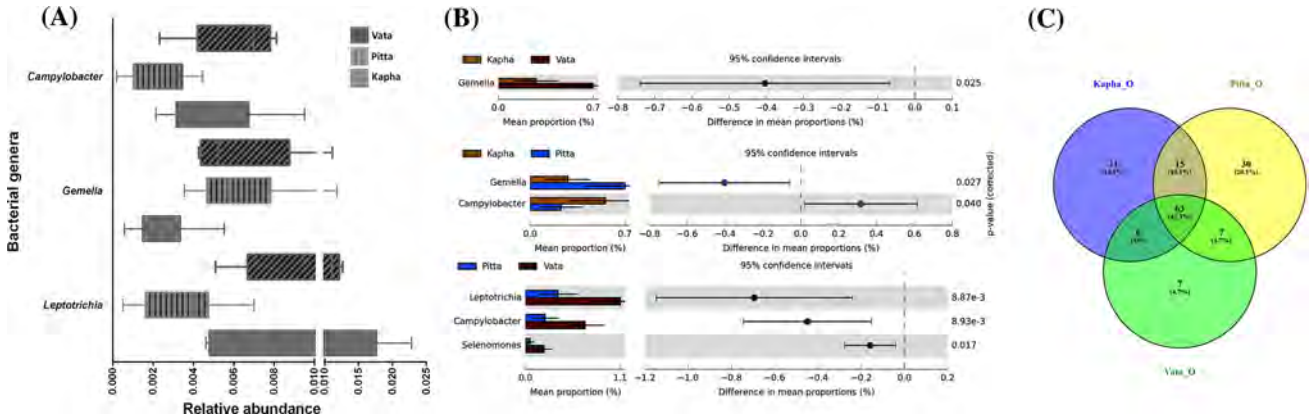

Figure 2. (**A**) Differentially abundant bacterial genera in human oral microbiome across the *vata*, *pitta* and *kapha prakriti* individuals. (**B**) Differentially abundant bacterial genera in human oral microbiome across the *vata*, *pitta* and *kapha prakriti* individuals in the 2 group comparisons using Welch t test analysis. (**C**) Venn diagram of shared and *prakriti*-specific bacterial genera in the human oral microbiome. The numbers represent the *prakriti*-specific genera and total no of shared genera across all the study groups.

bacterial genera (ANOVA, P<0.05). These genera include *Ruminococcus, Lysobacter, Mesorhizobium, Brevundimonas* and *Salegentibacter*, and all showed higher abundance in the skin microbiome of the *pitta prakriti* samples. Total 250 bacterial genera in the skin microbiome were shared in the three *prakriti* types, while 25, 72 and 22 genera were unique to the *pitta, kapha* and *vata prakriti,* respectively (figure 3B) (supplementary file 3). Beta dispersion analysis showed that *pitta prakriti* samples having less inter-sample variation, while *kapha prakriti* samples showed high inter-sample variation in the skin microbiome (figure 3C).

4. Discussion

Ayurveda is one of the oldest health sciences of the world. It is based on the concepts of *tridosha* and *prakriti* as the central philosophies. The primary aim of Ayurveda is maintenance of health and improvement of disorders in diseased people. Modernized practices derived from Ayurveda traditions are on similar lines with modern clinical practices (Sen and Chakraborty 2017). The present study is the first report explaining the detailed correlation of predominant Ayurvedic *prakrities* (*vata*, *pitta* and *kapha*) with the multiple human microbiomes (gut, oral and skin) of the individuals for unravelling the microbiome and *prakriti* associations. Ayurveda describes three fundamental entities that govern our inner and outer environments, viz. movement, transformation and structure, and are known in Sanskrit as *vata*, *pitta* and *kapha,* respectively (Pal 1991). These primary forces are responsible for the characteristics of our mind and body. And each of us has a unique proportion of these three forces that shapes our nature.

Here, analysis of human gut microbiome revealed five differentially abundant genera across the three *prakriti* types. Wherein, *Bacteroides* and *Parabacteroides* were found to be dominant in the *pitta prakriti* individuals (figure 1B). Earlier studies on the human gut microbiome reported that *Bacteroides* is one of the most abundant anaerobic organisms in the human gut (Wexler 2007). Members of genus *Parabacteroides* were found more in the *pitta prakriti* individuals. Gut microbiome studies exhibited that members of genus *Parabacteroides* play a key role in preventing gut inflammation by digesting the resistant starch (Hu *et al.* 2016), and are low abundant or absent in the IBD and ulcerative colitis patient (Noor *et al.* 2010). Ayurveda literature suggests that *pitta prakriti* individuals are more prone to develop gut inflammation related disorders like gastric ulcers (Dey and Pahwa 2014). Together, the altered human gut microbiome structure and Ayurveda literature substantiates high abundance of gut inflammation preventing organisms (*Parabacteroides*) in the *pitta prakriti* individuals. Microbiome data analysis of the study by Chauhan *et al.*, exploring gut microbiome and *prakriti* association, showed high abundance of *Parabacteroides* (statistically non-significant, ANOVA, $p > 0.05$) in the *pitta prakriti* individuals (supplementary figure 1) based on 4,000 reads per samples (Data normalization at 4000 reads/samples) using 29 samples each for *vata, pitta* and *kapha* (Chauhan *et al.* 2018). While, here in the present study, statistically significant differences were observed. We analysed less number of samples at high sequence depth ($\sim$ 74,000 sequences per sample), while in the earlier study, Chauhan *et al.* have analysed relatively more samples at lower sequence depth ($\sim$ 4,000 per sample). For this reason, future studies with additional samples at higher sequence depth are needed for precise understanding of microbiome and *prakriti* association. It is known that enteric nervous system is responsible for digestion and interaction with gut microbiome for modulation and activity of immune functions (Sharon *et al.* 2016). The *vata* brain-type exhibits a high range of digestive power, leading to an irregular appetite, bowel movements and frequent gas (Travis and Wallace 2015), and bacterial genus *Desulfovibrio* known for their ability for the production of H_2S (Motamedi and Karsten 1998) and methane were specifically

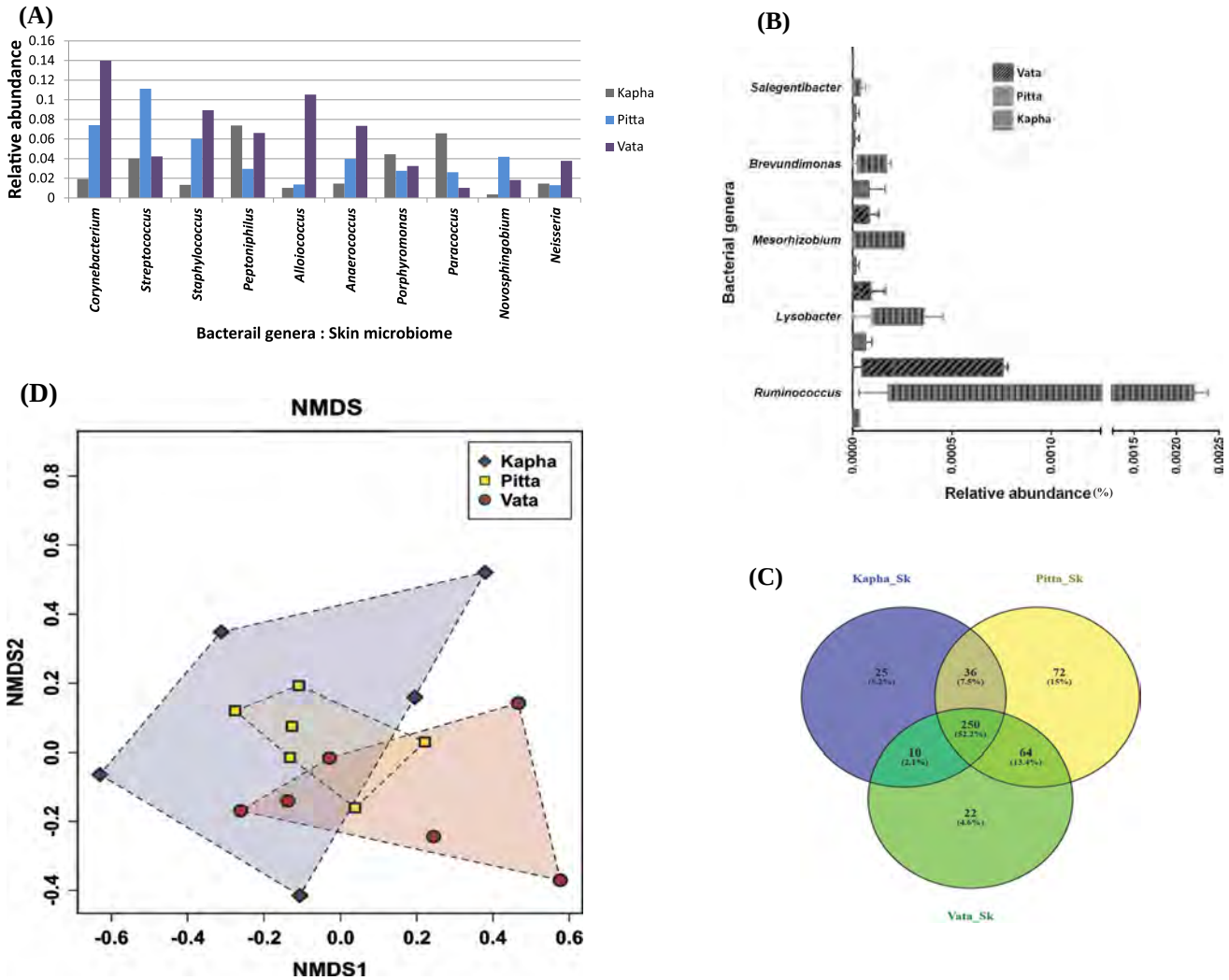

Figure 3. (**A**) Difference in the mean relative abundance in the bacterial genera in human skin microbiome across *the vata*, *pitta* and *kapha prakriti* individuals. (**B**) Differentially abundant bacterial genera in human skin microbiome across the *vata*, *pitta* and *kapha prakriti* individuals. (**C**) Venn diagram of shared and *prakriti*-specific bacterial genera in the human skin microbiome. The numbers represent the *prakriti*-specific genera and total no of shared genera across all the study groups. (**D**) Multivariate analysis of beta-diversity: two-dimensional scatter plots of bacterial community (NMDS of 16S rDNA data) composition across the three different sample groups. Blue, red and yellow colour represents samples from *vata*, *pitta* and *kapha prakriti* individuals respectively.

recorded in high abundance in the *vata prakriti* individuals, explaining the association of gut microbiome and Ayurvedic *prakriti*. Analysis suggested that overall most of the microbiome members are common across the samples of different *prakriti* and difference exists in the presence and abundance of key bacterial genera as largely the samples of the three *prakriti* types were dispersed across the PCoA plot and only 32% variation was explained (figure 1C). Bacteria interact exclusively within and between the species while they are responding to external stimuli. Human physiological responses changes with the *prakriti* type and it is the reason for *prakriti*-specific presence of few bacteria in the oral, gut and skin microbiome. However, studying one bacterium at a time or known consortium of bacteria and host physiological responses will help in understanding their precise associations. In addition to the gut microbiome, oral and skin microbiomes of these individuals were also studied. Oral microbiome analysis revealed the abundance of genera *Neisseria, Streptococcus, Prevotella, Haemophilus* and *Porphyromonas.* These are the most abundant organism's plays most important role in the formation of the healthy oral microbiome (Chen and Jiang 2014). Larger proportion the oral microbiome (63%) is shared across the three *prakriti* types, whereas *pitta prakriti* individuals showed most number of the unique bacterial genera (30 genera) and high inter-individual variation in the microbiome of *pitta prakriti* individuals is one possible explanation.

Analysis based on the abundance of the organisms revealed three differentially abundant genera (figure 1A). Among the three, *Leptotrichia* were found dominant in the

kapha prakriti individuals. These organisms are common inhabitant of the oral cavity. These organisms are opportunistic pathogens and ferment carbohydrates and produce lactic acid which may eventually be involved with tooth decay (Emenike and Olsen 2017). Genera *Gemella* and *Campylobacter* were also relatively high in the *pitta prakriti* individuals. *Gemella* were also the opportunistic pathogens (Jayananda *et al.* 2017). *Pitta prakriti* individuals are more prone to the disorders related to gums and teeth; here the abundance of opportunistic pathogens represents the putative *prakriti*-specific characteristics (Pravin *et al.* 2015) and the human oral cavity is a reservoir for the different *Campylobacter* species.

Complexion of the skin changes with the *prakriti* (Umarkar *et al.* 2013). *Vata prakriti* individuals show lustreless skin having hairs, skin and nails rough in texture and develop cracks due to dryness (Umarkar *et al.* 2013). Similarly, *pitta prakriti* person has fair body colour; they have a tendency for wrinkles and the hairs to turn gray at an early age, while *kapha prakriti* individuals have oily skin. Human skin microbiome showed the association with the characteristics of the skin (Prasuna and Srinivasulu 2013). Skin microbiome analysis of the abundant genera showed the differences in their relative abundance across the three *prakriti* type. Among the 479 bacterial genera, 5 genera showed statistically significant differential abundance in the skin microbiome. All these 5 genera have high abundance in the *pitta prakriti* samples (figure 3B). '*Pittam sasneha tikshnoshnam laghu visram, saram dravam*'(Ashtanga Hrdayam: Sutrasthana I:11) explains the main characteristics of the *pitta prakriti,* i.e. *pitta* is oily, sharp, hot, light, fleshy-smelling, spreading, and liquid. Here, the oily quality allows skin softness, the liquid quality exhibits excess sweating and fleshy-smelling indicates strong body odor. Bacteria including *Lysobacter, Rhizobium, Ruminococcus* were relatively high in the skin microbiome of *pitta prakriti* individuals (figure 3B). The bacteria like *Lysobacter* and *Rhizobium* (Yan *et al.* 2016) detected in agricultural soils and *Ruminococcus* is associated with the domestic animals like cattle (Guo *et al.* 2010). The present study population is rural agricultural population and the dominant bacteria present in their environment get adhered to the skin due to oily skin of the *pitta prakriti* individuals. However, samples from only three *pradhan* (dominant) *prakriti* types were included in the present study. Thus, microbiome analysis of study participants from all the seven *prakriti* types with additional sample size will be helpful for the precise understanding of these associations. In summary, human gut, oral and skin microbiome showed *prakriti*-specific presence and relative abundance (high or low abundance) of signature bacterial taxa. Microbiome structure of healthy individuals belonging to three different *prakriti* is explored so the findings of the study will further help in understanding and treating the specific diseases in future using Ayurveda treatment regimes by keeping microbiome knowledge as a base.

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Letters in Applied Microbiology

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ORIGINAL ARTICLE

Functional characterization and *in vitro* screening of *Fructobacillus fructosus* MCC 3996 isolated from *Butea monosperma* flower for probiotic potential

M. Patil[1], A. Jadhav[2] and U. Patil[2]

1 Department of Microbiology, R. C. Patel Arts, Commerce and Science College, Shirpur, India
2 Department of Microbiology, Government Institute of Science, Aurangabad, India

Significance and Impact of the Study: This study provided *in vitro* evidence that *Fructobacillus fructosus* MCC 3996 have endurance in acidic gastric juice, better co-aggregation, auto-aggregation properties, splendid antagonistic activities against several bacteria involved in food spoilage/human infections, pertinent antibiotic susceptibility profile and no haemolytic activity. Also, *F. fructosus* have the capability to survive in the appreciable amount of fructose, and this advocates that the strain could be used as starter culture and/or the active ingredient of fructose-rich foods. The current *in vitro* study provided a strong basis for further in vivo research to identify the health beneficial characteristics of *F. fructosus* and its potential could be effectively utilized as health-boosting ingredient in food and pharmaceutical industries.

Keywords
Butea monosperma, fructose, *Fructobacillus fructosus*, fructophilic lactic acid bacteria, probiotic.

Correspondence
Ulhas K. Patil, Department of Microbiology, Government Institute of Science, Aurangabad 431004 (M.S.), India.
E-mail: ulhaskpatil@gmail.com

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Abstract

The fructophilic bacterium *Fructobacillus fructosus* MCC 3996 described in the present investigation was isolated from the nectar of *Butea monosperma* flower and evaluated *in vitro* for the manifestation of probiotic features. The strain utilizes fructose faster than glucose and is capable to grow in the range of 1–35% fructose concentration (optimum 5% w/v) and thus denotes its fructophilic nature. *In vitro* assessments of the strain have examined for the endurance in acidic environment/gastric juice, the better auto-aggregation ability even in the presence of hydrolytic enzymes, co-aggregation with pathogenic bacteria, hydrophobicity properties and no haemolytic activity to elucidate its feasible probiotic use. The significant antagonistic activity against several detrimental bacteria, despite lacking the bacteriocin secretion, is an astonishing feature. Owing to the indigenous origin of the isolate, it could be used as a probiotic, starter culture, and/or the active ingredient of food formulation may contribute to improve the desirable fermentation, long-term storage and nutritional benefits of foods especially rich in fructose.

Introduction

The *Fructobacillus* bacteria are found in fructose-rich niches such as flowers, fruits and fermented foods (Endo and Okada 2008; Verón *et al.* 2017; Sakandar *et al.* 2019). All *Fructobacillus* bacteria ferment glucose; however, fructose is fermented faster than glucose and they also survive in relatively higher fructose concentration (~40%, w/v; Endo *et al.* 2011). The preferential utilization of fructose by *Fructobacillus* would be due to loss of alcohol/acetaldehyde dehydrogenase (*adhE*) gene in the period of adaptation to survive a fructose-rich habitat, and this gene is not needed to metabolize fructose (Maeno *et al.* 2018).

Although the taxonomic characteristics of genus *Fructobacillus* were well documented, the health-promoting probiotic potential and commercial applicability are the least explored area. Recently, Sakandar *et al.* (2019) advocated usefulness of two strains of *Fructobacillus fructosus* for their use in food for human consumption.

This study consists of a systematic characterization and evaluation of *in vitro* assessment for probiotic capabilities

of *F. fructosus* isolated from the nectar of *Butea monosperma* flower. On the basis of *in vitro* tests recommended for affirming the probiotic nature of the strain, the *F. fructosus* MCC 3996 has been screened and proposed to be a potential candidate as probiotic. The current *in vitro* study outcome provides strong basis for further cell culture/animal model research to identify the health beneficial characteristics and the strain could be conceivably utilized as effective probiotics for future food applications for improving the natural fermentation and refining the nutritional properties of foods especially rich in fructose (e.g. high-fructose syrup, honey, fruit drinks, jellies and ice creams).

The functional properties of fructose have extended its option as a key and healthy food ingredient in many food industries. The technical and functional characteristics of fructose over other sweetener are as follows: low molecular weight, flavour enhancer, smooth consistency, good humectant, high osmotic pressure, high solubility, no crystal formation, stable in acidic foods, etc. (Singh *et al.* 2018). Also, fructose plays beneficial physiological roles in the human body such as (i) bypassing metabolic pathway of glucose, (ii) have a low glycaemic index, (iii) increases the bioavailability of iron by forming an iron-chelate complex, (iv) accelerates ethanol metabolism, etc. (Singh and Chauhan 2018). The excess consumption of fructose-rich food was linked with obesity in human (Bray *et al.* 2004). Also, Park *et al.* (2013) suggested the utility of *Lactobacillus curvatus* HY7601 and *Lactobacillus plantarum* KY1032 for prevention of the development of high-fructose diet-induced metabolic syndrome including obesity, while no sufficient statistics are available to establish a direct relation between high-fructose intake and health risk (Rizkalla 2010). The influence of microbiota on the host metabolism, the regulation of energy homeostasis and its antagonistic role are systematically documented recently, while this review also identified the need of additional studies to establish the utility of probiotics for the treatment of obesity (Fontané *et al.* 2018).

The fructophilic feature is the most significant aspect related to the *F. fructosus* MCC 3996 and it encouraged the expectation to launch the strain as a next-generation probiotic. In recent years, the use of fructose as food ingredient has been significantly increased due to its cost-effectiveness and relatively higher sweetening index compared to glucose and sucrose. The fructose-containing sweeteners were preferred in the global market due to its availability, lucrative and greater sweetening competence; these are known as high-fructose corn syrup in the United States, iso-glucose in European countries, and dextrose/fructose and fructose/dextrose syrup in other countries (Bode *et al.* 2014). The performance of *in vitro* and *in vivo* studies are required to scrutinize and establish the utility of any strain as probiotics (de Almada *et al.* 2015).

A fructophilic probiotic could be useful as health-boosting ingredient to expand the benefits of high-fructose formulations currently available in the market. Hence, fructophilic *F. fructosus* MCC 3996 could be a better alternative in fruit-canning and high-fructose syrup manufacturing at this juncture if probiotic potential of the strain will be recognized in vivo studies.

Results and discussion

Isolation and identification of strain

The strain MPP-76 was newly isolated from the nectar of *B. monosperma* flower. The *B. monosperma* Lam. (Family: Fabaceae) is a medium-sized tree of the Indian subcontinent. The flowers of the plant are scentless, have dark velvety green cup-shaped calices and five petals. The keel petals contain copious amounts of nectar. The *Fructobacillus* might have evolutionarily adapted to the fructose-rich niche and might possess fructophilic and several niche-specific characteristics. Previously, the fructophilic lactic acid bacteria were isolated from a flower of *Tropaeolum majus* (Endo and Okada, 2008; Endo *et al.* 2011). The strain was identified as *F. fructosus* on the basis of the morphological, cultural, biochemical and the 16S rRNA partial gene sequencing (1490 bp; accession number: MH509400) (Fig. 1). The strain was deposited at the National Centre for Microbial Resources (NCMR), Pune, India and now designated as *F. fructosus* MCC 3996.

Biochemical and physiological profile of strain

The strain *F. fructosus* MCC 3996 requires 5% fructose for optimum growth and was not capable to grow in absence of the fructose. The maximum concentration of fructose which supported growth was 35% (Table S1). Although the strain ferments glucose, the fructose was fermented faster than glucose. The strain is facultative aerobic. The major acid produced during fermentation was lactic acid and also strain not produces catalase and oxidase enzymes. These all features signify that *F. fructosus* MCC 3996 is obligatory fructophilic lactic acid bacteria. The fructophilic behaviour and adaptation to high-fructose concentration by *F. fructosus* MCC 3996 could be better explored to promote the strain as an effective probiotic ingredient in conjunction with fructose/fruits containing food preparation as vehicle.

Acid and gastric juice tolerance

The reported *F. fructosus* MCC 3996 strain survived 67–68% at pH 2 and 3, while it did not survive at pH 1 after 3 h exposure (Table S2). Even in synthetic gastric juice,

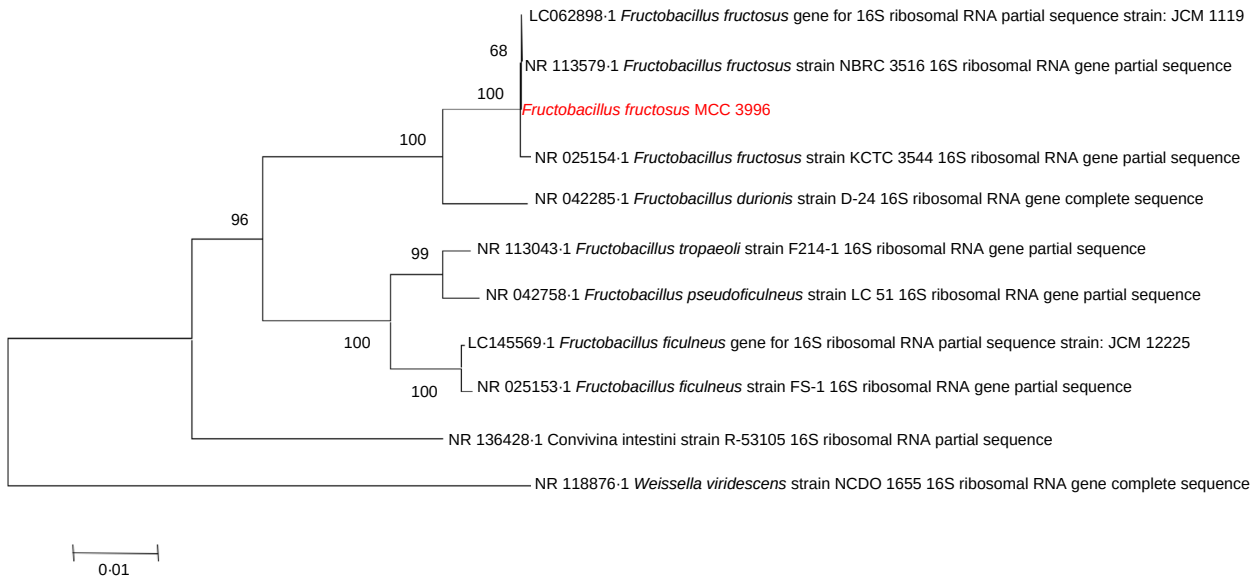

Figure 1 Phylogenetic relationship of strain *Fructobacillus fructosus* MCC 3996 to related species of *Fructobacillus* strains based on 16S rRNA gene sequences. The tree was reconstructed using the neighbour-joining method. *Weissella viridescens* NCDO 1655 was used as outgroup. A bootstrap percentage (68%) is given at branching points. Bar, 0·01 substitutions per nucleotide position. [Colour figure can be viewed at wileyon linelibrary.com]

the strain showed 81% survival after 3 h. The enhanced survival in synthetic gastric juice (pH 2) compare to acidic pH might be due to the presence of compatible solutes such as dextrose and several metal ions. The endurance for a prolonged period at low pH is desirable and the crucial property for any probiotic strain for survival during the stomach passage. The pH of the human stomach ranges from 1·5 (fasting stage) to 4·5 (after a meal) while the approximate time for food ingestion is about 3 h (Jacobsen *et al.* 1999). The health-boosting formulation of *F. fructosus* MCC 3996 consumed with a dietary supplement with appropriate buffering capacity could give desirable results.

Bile salt tolerance

Fructobacillus fructosus MCC 3996 showed appreciable tolerance for bile salt. In the presence of bile salt −0·05, 0·1, 0·15, 0·3, 1·0 and 2·0 (%, w/v), survival percentages of bacterium were 98, 98, 97, 96, 68 and 52%, respectively, after 24 h. Also, the growth curve patterns were determined using the various concentration of bile salt (0·05, 0·1, 0·15 and 0·3% w/v) for *F. fructosus* MCC 3996. The growth of *F. fructosus* MCC 3996 in fructose-yeast extract-peptone (FYP) media containing 0·05, 0·1, 0·15 and 0·3% (w/v) bile salt was delayed by 6, 54, 90 and 118 min, respectively, as compared to control (FYP broth without bile salt) (Fig. 2). This suggests that the growth kinetics of strain was not affected significantly in the range of 0·05–0·3% bile salts.

The range of bile salt concentration found in the human intestine is varied from 0·05 to 0·3% (Graciela *et al.* 2001). The bile salt tolerance is an important property of probiotic bacteria used as food adjuncts. The bile salt tolerance empowers them to survive, grow and to perform their favourable action in the human gastrointestinal tract.

Auto-aggregation and co-aggregation activity

Aggregation of bacterial cells of the same strains is called as auto-aggregation. The bacterial cells have also a property to aggregate with genetically divergent strains and this property is called as co-aggregation. Aggregation and co-aggregation properties of strain suggest adherence capabilities in the human gut environment. The aggregation profile of *F. fructosus* MCC 3996 revealed that greatest auto-aggregation percentage (44·64%) was detected after 24 h. The consequences of adherence are also determined by several digestive enzymes such as pepsin, trypsin and bacterial protease (alcalase®). These enzymes have lowered the percentage (~10%) of auto-aggregation (Table 1).

Also, *F. fructosus* MCC 3996 showed co-aggregation with various pathogenic strains: *Escherichia coli*, *Salmonella typhimurium* and *S. aureus*. A relatively high percentage of *F. fructosus* MCC 3996 and *S. aureus* were co-aggregated, compare to *S. typhimurium* and *E. coli* (Table 1). The co-aggregated cells of *F. fructosus* MCC 3996 with respective pathogenic strains were visualized under a scanning

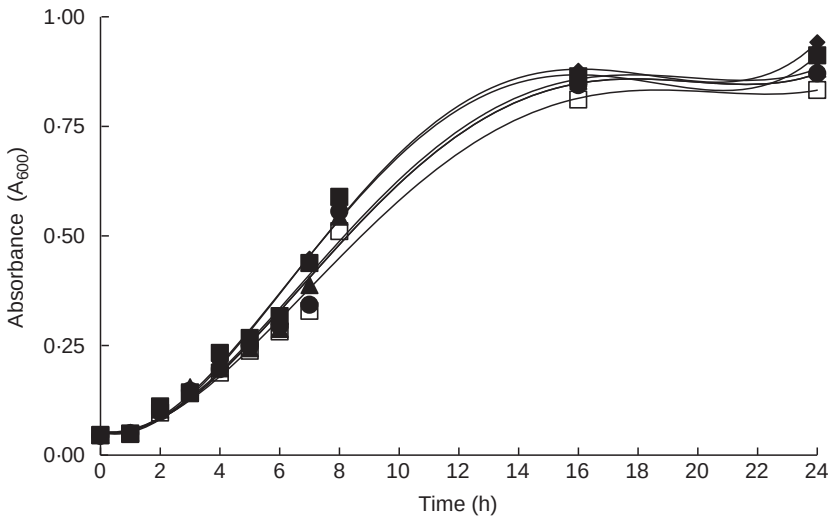

Figure 2 Growth curve pattern of strain *Fructobacillus fructosus* MCC 3996 in the presence of bile salt (0·05, 0·1, 0·15 and 0·3%) at 37°C for 48 h. All the values are representing mean ± SD (♦ bile salt (0%), ■ bile salt (0·05%), ▲ bile salt (0·1%), ● bile salt (0·15%) and □ bile salt (0·3%)).

Table 1 Aggregation and co-aggregation profile of *Fructobacillus fructosus* MCC 3996

	Aggregation (%)			
	0 h	8 h	16 h	24 h
1. Auto-aggregation	0·00	37·55	44·06	44·64
2. Auto-aggregation in presence of digestive enzymes				
Protease	0·00	31·51	31·76	30·74
Pepsin	0·00	40·82	42·09	35·84
Trypsin	0·00	36·61	33·67	30·74
3. Co-aggregation				
E. coli (NCIM 2109)	4·11	18·80	29·16	58·41
S. aureus (NCIM 2079)	7·08	13·08	20·51	70·71
S. typhimurium (NCIM 2501)	16·91	34·00	35·38	64·84

electron microscope (S4800 Type II; Hitachi, Hitachinakashi, Japan) (Fig. 3). The outcomes also revealed that the co-aggregation property (i) depends on the specific type of pathogen strain and (ii) progressively increased by incubation time.

Cell surface hydrophobicity

The ability of auto-aggregation, co-aggregation and binding capability to mucus membrane is depending on hydrophobic/hydrophilic interactions contributed by proteins and polysaccharides on the bacterial cell surface. The cell surface hydrophobicity/hydrophilicity characteristics of the bacterial surface were assessed using chloroform, ethyl acetate and xylene (Kos *et al.* 2003). The strain *F. fructosus* MCC 3996 showed greater affinity towards the organic solvents: chloroform (66·41%), ethyl acetate (85·31%) and xylene (97·48%).

The ability of *F. fructosus* MCC 3996 to co-aggregate with these pathogens may assist them to develop a barrier that prevents colonization by pathogens as suggested by Schellenberg *et al.* (2006). The adhesion to xylene (apolar solvent) validates the hydrophobic surface of bacteria. The hydrophobic lining of the human gut is contributed by the surface-active phospholipids known to be present in both the gastric mucosa and juice. Hence, *F. fructosus* MCC 3996 could colonize with mucosal surface of the stomach which has a hydrophobic lining of the human gut.

Antagonistic activity

The studied strain effectively inhibited various bacterial pathogens such as *Bacillus pumilus*, *E. coli*, *S. typhimurium*, *Staphylococcus aureus*, *Proteus vulgaris* and *Pseudomonas aeruginosa*. The *F. fructosus* MCC 3996 lacks the ability to secret bacteriocin as detected by available methods; still, the superior antagonistic activity against these detrimental bacteria is astonishing property (Fig. S1). The effect of *F. fructosus* MCC 3996 for inhibiting the pathogens was probably due to the production of various antimicrobial substances viz. organic acids (lactic acid and acetic acid), OH-phenyl lactic acid, bacteriocin, sugar catabolite, hydrogen peroxide, fat and amino acid metabolites, phenyl-lactic acid, reuterin and reutericyclin (Servin 2004). The active inhibitory mechanisms of the *F. fructosus* MCC 3996 strain are under investigation.

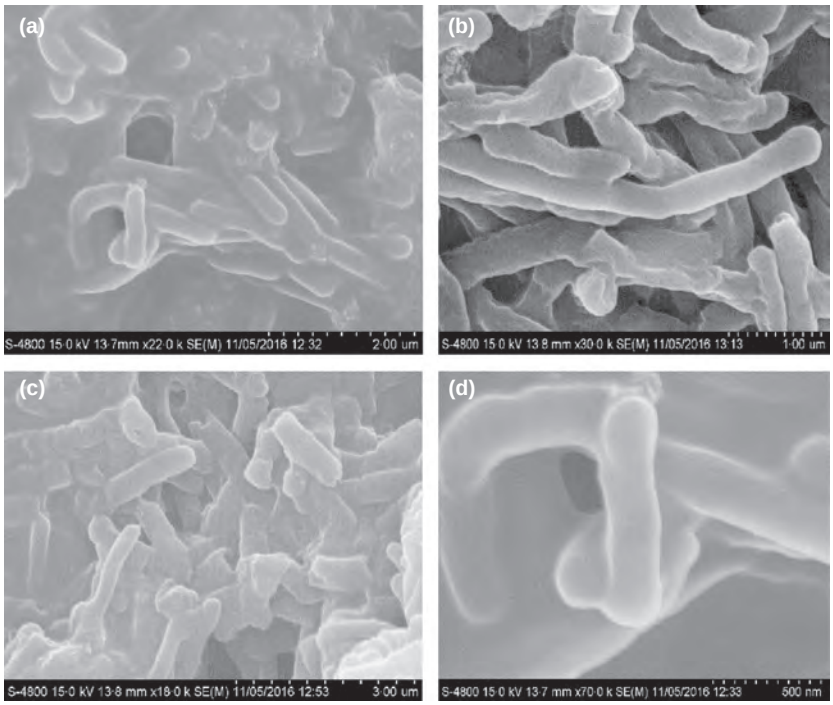

Figure 3 Scanning electron micrograph of (a) auto-aggregation of *Fructobacillus fructosus* MCC 3996, and co-aggregation of *F. fructosus* MCC 3996 with (b) *Salmonella typhimurium* (NCIM 2501), (c) *Escherichia coli* (NCIM 2109) and (d) *Staphylococcus aureus* (NCIM 2079).

Antibiotic susceptibility

The *F. fructosus* MCC 3996 could be suitably prescribed during antibiotic therapy using amoxyclav, carbenicillin, cefotaxime, ciprofloxacin, colistin, co-trimoxazole, co-trimazine, gatifloxacin, nitrofurantoin, norfloxacin, oxacillin and streptomycin as the strain showed resistance against these antibiotics based on the sensitivity and resistance pattern (Table S3). The antibiotic resistance-conferring genes in probiotics should be non-transferable to other bacteria. The frequency of gene transfer might negligible as the strain *F. fructosus* is physiologically, genetically and taxonomically not related to common human pathogens/opportunistic pathogens. Also, the evaluation of antibiotic markers is important safety criteria to confer the 'qualified presumption of safety' as per the European Food Safety Authority (2008).

Haemolytic activity

In establishing and assuring the safety, even among a group of bacteria that is 'Generally Recognized as Safe (GRAS)', it is recommended that probiotic strains should be characterized for the absence of haemolytic activity (Guidelines for the evaluation of probiotics in food, 2006). The isolate *F. fructosus* MCC 3996 did not show any type of haemolysis even after 72 h when cultured aerobically and micro-aerobically on blood agar. This emphasizes that the strain is safe for probiotic utility.

Materials and methods

Sample collection

Totally, five fresh flowers of single shrub of *B. monosperma* were collected from Shirpur, India (21°24'38·4″N 74°58'04·0″E). The nectar (~0·5 ml) was inoculated aseptically in 20 ml sterile FYP broth having the following composition (g l^{-1}): fructose, 10; yeast extract, 10; peptone, 5·0; beef extract, 0·5; sodium acetate, 2·0; Tween-80, 0·5; $MgSO_4 \cdot 7H_2O$, 0·2; $MnSO_4 \cdot 4H_2O$, 0·01; $FeSO_4 \cdot 7H_2O$, 0·01 (pH 6·8) and incubated aerobically, anaerobically and microaerophilically for 48 h at 30°C. An enriched sample was streaked on FYP agar plates and was incubated at 30°C for 48 h. The well-isolated colonies were picked up and further subcultured on FYP plates to ensure the purity of strain. The isolated strain designated as MPP-76 and was maintained at 4°C on FYP agar medium.

Identification of isolate

The isolated strain was identified on the basis of various morphological, cultural and biochemical characteristics as

per key is given by Endo *et al.* (2011). Also, the phylogenetic analysis was conducted on the basis of 16S rRNA partial gene sequence.

Optimization of growth parameters

The optimum temperature of strain was evaluated by culturing the strain at different temperatures 15, 30, 37, 40 and 50°C. Also, optimum pH evaluated by culturing strain in FYP broth having pH 4·0, 5·0, 6·0, 7·0, 7·5 and 8·0. The strain was cultured at respective temperature and pH in aerobic and microaerophilic conditions.

The sugar utilization profile was determined using Hi-Carbo kit (Hi-media, Mumbai, India). The fructose utilization profile of *F. fructosus* MCC 3996 strain was determined by inoculating 2·5 ml 24 h pre-grown culture (1×10^7 CFU per ml) into 50 ml separate flasks of FYP broth containing varied concentration of D-fructose: 1, 5, 10, 15, 20, 25, 30, 35 and 40% (w/v).

Evaluation of potential probiotic properties

The set of several *in vitro* tests is recommended to screen potential probiotic strain (FAO/WHO, 2006). Based on these recommendations, these *in vitro* tests were performed to propose the probiotic potential of an isolated strain.

The inoculum used for these tests consists of 24 h pre-grown culture (2×10^7 CFU per ml) prepared in phosphate buffer (pH 6·8). In these respective tests, the FYP agar plates were incubated for 48 h at 30°C*aerobically*. After incubation, the total viable count of strain was enumerated as colony forming units per millilitre (CFU per ml). The results of each parameter were graphically correlated with $\log_{10}$ of CFU per ml.

Acid and gastric juice tolerance

Acid tolerance of strain *F. fructosus* MCC 3996 was determined as per Ren *et al.* (2014). For this, glycine-HCl buffers with pH 1·0, 2·0 and 3·0 were used. A suitable inoculum (2×10^7 CFU per ml) was added to the respective buffer solution. These buffered cell suspension solutions were kept at 30°C for 3 h. Diluted aliquots ($1 : 10^7$) of respective cell suspension were spread on FYP plates at the interval of 1, 2 and 3 h. The inoculated FYP plates were incubated at 30°C for 48 h and the CFU per ml were enumerated. The $\log_{10}$ of CFU per ml in respective buffered cell suspension was determined.

Gastric juice tolerance of strain *F. fructosus* MCC 3996 was determined using a synthetic gastric juice having the following composition: protease peptone, 0·83%; dextrose, 0·35%; NaCl, 0·2%; KH_2PO_4, 0·06%; $CaCl_2$, 0·011%; KCl, 0·037%; ox-bile, 0·005%; lysozyme, 0·01% and pepsin, 1·33%; pH 2·0. A suitable inoculum was added to adjust cell density ~2×10^7 CFU per ml of synthetic gastric juice solution. This gastric juice containing cell suspension was kept at 30°C and for 3 h. A diluted aliquot ($1 : 10^7$) of the cell suspension was spread on FYP plates at the interval of 1, 2 and 3 h. The inoculated FYP plates were incubated at 30°C for 48 h and the CFU per ml were enumerated.

Bile salt tolerance

Bile salt tolerance of strain *F. fructosus* MCC 3996 was determined against various concentrations of bile salt: 0·05–2·0 (%, w/v) as per Ren *et al.* (2014). A dense inoculum was added to adjust cell density ~2×10^7 CFU per ml of bile salt-containing FYP broth. This inoculated FYP broth was kept at 30°C for 24 h. Diluted aliquots ($1 : 10^7$) of the cell suspension were spread on FYP agar plates. The inoculated FYP agar plates were incubated at 30°C for 48 h and CFU per ml were enumerated.

Also, the growth delay kinetics was determined in the presence of bile salt. The absorbance (A_{600}) determined against un-inoculated broth. The growth curve graph was plotted as absorbance versus incubation time. The growth delay time (min) at various concentrations of bile salts was calculated by comparing with growth in the absence of bile salt (Graciela *et al.* 2001).

Auto-aggregation and co-aggregation assays

Auto-aggregation and co-aggregation assays were carried as per Collado *et al.* (2007). The pre-grown culture of *F. fructosus* MCC 3996 strain was centrifuged at 10 000 ***g*** rev min^{-1} for 15 min to get cell pellet. The cells pellet was then washed thrice with PBS (0·08 g l^{-1} NaCl, 0·0121 g l^{-1} K_2HPO_4 and 0·0034 g l^{-1} KH_2PO_4, pH 6·8), followed by centrifugation. The cell pellet then re-suspended in the same buffer to reach the absorbance of 0·5 ± 0·05 at 600 nm. From this, 4 ml of bacterial suspension was gently vortexed for 10 s. The bacterial suspension was stood stable at 30°C for different time intervals (8, 16 and 24 h). The upper part of bacterial suspension was withdrawn gently with a micropipette (2 ml) and its absorbance was recorded. The auto-aggregation percentage was calculated as $1-(A_t/A_0) \times 100$, where A_t represents the absorbance at time t = 2, 8, 16 and 24 h while A_0 is the absorbance at t = 0 h.

Similarly, auto-aggregation was also studied in the presence of hydrolytic enzymes. The pre-grown culture of *F. fructosus* MCC 3996 strain was centrifuged and washed thrice with PBS (pH 6·8). The cell pellet then re-suspended in the same buffer containing hydrolytic enzymes

(250 U ml^{-1}) viz., pepsin, trypsin and bacterial protease (food grade alcalase; Novozyme, Bagsværd, Denmark). The absorbance of suspension was adjusted to 0·5 ± 0·05 at 600 nm. Then 4 ml of the bacterial cell suspensions containing respective hydrolytic enzymes was incubated at 30°*C* for 10 min. After incubation, the upper suspension was removed carefully and its absorbance was recorded. The auto-aggregation percentage was calculated as described previously.

For the co-aggregation assay, the equal volumes harvested cells of *F. fructosus* MCC 3996 and different pathogens: *E. coli* (NCIM 2109), *S. typhimurium* (NCIM 2501) and *S. aureus* (NCIM 2079) were mixed together in separate tubes by vortexing for 10 s. Then, these tubes were incubated at 30°C for different time intervals 8, 16 and 24 h. After incubation, the supernatant was removed carefully and its absorbance (A_{600} nm) was measured. The co-aggregation percentage was determined using the following formula.

$$\text{Co} - \text{aggregation\%} = \left[\left(A_{\text{pat}} + A_{\text{isolate}}\right) - 2(A_{\text{mix}})\right]/\left[\left(A_{\text{pat}} + A_{\text{isolate}}\right)\right] \times 100$$

where A_{pat} and A_{isolate} represent absorbance of pathogen and probiotic strain at 600 nm and A_{mix} represents the absorbance of a mixture of pathogen and probiotic strain at 8, 16 and 24 h.

Also, to visualize the co-aggregation phenomenon, the pre-grown and 10^{-4} diluted cultures (200 µl) of *E. coli, S. typhimurium* and *S. aureus* were mixed separately with *F. fructosus* MCC 3996 by electron microscopy. The mixed culture was fixed with 1 ml, 3% glutaraldehyde for 24 h. Then the treated cells were washed with PBS (0·1 mol l^{-1}, pH 6·8). These washed cells were dehydrated using various concentration of ethanol (10–100%, v/v) for 15 min each. Finally, the cells were dehydrated in 100% ethanol for 30 min for two times. The co-aggregated specimens were allowed to air dry, and then coated with gold-mounted stubs using double-sided carbon tape. The co-aggregated cells of *F. fructosus* MCC 3996 with pathogens were observed separately using a Scanning Electron Microscope (FE-SEM—S4800 Type II; Hitachi).

Cell surface hydrophobicity

Bacterial cell surface hydrophobicity was determined by measuring microbial adhesion to hydrocarbons as described by Kotzamanidis *et al.* (2010). A grown culture of *F. fructosus* MCC 3996 was harvested by centrifugation at 10 000 ***g*** rev min^{-1} for 15 min. The cell pellet was washed thrice and suspended in sterile PBS (pH 6·8). The absorbance of suspension was adjusted 0·5 ± 0·02 (~10^8 cells per ml) at 600 nm using a spectrophotometer (UV-Vis 2700, Shimadzu, Japan) and designated as A_0. The standard bacterial suspension (1 ml) was mixed with 3 ml of organic solvent (ethyl acetate, xylene and chloroform) separately. This mixture was pre-incubated for 10 min at room temperature. A two-phase system developed was then mixed by vortexing for 2 min, and then the mixtures stabilized for 20 min to get two phases (water and ethyl acetate/xylene/chloroform phases). An aqueous phase was carefully removed and its absorbance was measured at 600 nm (designated as *A*1). The cell surface hydrophobicity percentage (H%) was calculated using the following formula:

$$\text{Hydrophobicity\%} = (1 - A_1/A_0) \times 100$$

Detection of antagonistic activity

Antagonistic activity of *F. fructosus* MCC 3996 strain was challenged with several detrimental bacterial strains: *B. pumilus* (NCIM 2327), *E. coli* (NCIM 2109), *S. typhimurium* (NCIM 2501), *S. aureus* (NCIM 2079), *Proteus vulgaris* (NCIM 2172) and *P. aeruginosa* (NCIM 2036) as described by Schillinger and Lucke (1989). The strain *F. fructosus* MCC 3996 to be tested for antagonistic activity was spotted onto the surface of FYP agar plates. These plates were then incubated aerobically for 48 h at 30°C. After growth on FYP plates, the 0·1 ml (10^8 cells per ml) of the detrimental bacterial strains listed as above, to be tested for sensitivity were inoculated into 7 ml of liquefied nutrient agar medium containing tubes (42°C). This mixture then poured over the plate and allow to solidify. The inoculated plates were further incubated aerobically for 24 h at a respective growth temperature of food pathogenic strains.

Antibiotic susceptibility

The inoculum (0·1 ml) was uniformly spread on FYP agar plates (90 mm). Then with sterile forceps, the commercially available octa-discs of standard antibiotics (Himedia) were placed on the surface of FYP agar plates. After incubation, sensitivity/resistance against the respective antibiotics was determined by observing zones of inhibition.

Haemolytic activity

For determining haemolytic activity, a strain *F. fructosus* MCC 3996 was cultured on FYP agar plates supplemented with 5% sheep blood. The sheep blood was collected from domesticated sheep available locally; sterile defibrinated blood was used for blood agar preparation. These plates were incubated aerobically and micro-aerobically for 48 h

at 30°C and examined for sign of haemolysis on the plate (Maragkoudakis *et al.* 2006).

Conflict of Interest

The authors declare that they have no conflict of interest.

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Figure S1. Antagonistic activity of *F. fructosus* MCC 3996 against a: *Bacillus pumilus,* (NCIM 2327), b:, *Escherichia coli* (NCIM 2109), c: *Salmonella typhimurium* (NCIM 2501), d: *Staphylococcus aureus* (NCIM 2079), e: *Proteus vulgaris* (NCIM 2172), f: *Pseudomonas aeruginosa* (NCIM 2036).

Table S1. Morphological, cultural, and biochemical characteristics of *Fructobacillus fructosus* MCC 3996.

Table S2. Survival profile of *Fructobacillus fructosus MCC* 3996 at acidic pH and in synthetic gastric juice.

Table S3. Antibiotic susceptibility of *Fructobacillus fructosus* MCC 3996.

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A GEOGRAPHICAL STUDY OF DISTRIBUTION OF POPULATION IN NANDED DISTRICT

Dr. P. A. Khadke,
Assistant Professor,
School Of Earth Sciences,
Swami Ramanand Teerth Marathwada University,
Nanded, Maharashtra, 431606

Waghmare P. B.
Research Scholar,
School Of Earth Sciences,
Swami Ramanand Teerth Marathwada University,
Nanded, Maharashtra, 431606.

.ABSTRACT

The present study has aimed to explain the distributional patterns of population in Nanded district during 1981 - 2001. Distribution of population refers to the way of people are spaced over the surface of the earth. The areal population distribution of Nanded district is not unevenly throughout the district. In general, the concentration of population is denser in the urban region and sparse towards the rural areas, which itself is a very common phenomenon observed in cases of all the urban communities of the country. In Nanded tehsil a dense concentration is found in all decades, and Bhokar, Deglur are sparse distribution. The years 2001 observed that 20.82 per cent Population in Nanded tehsil and lowest population was 2.99 in Umri tehsil. This variation is mainly associated with the topographical characteristics of the different parts of the district; demographic factors such as birth, death rate and migration, process of economic development, scarcity of water are some of the problems in the study area.

KEY WORDS: Distribution of population, Analysis, Urban region, phenomenon, communities.

INTRODUCTION

The present study has aimed to explain the distributional patterns and spatio -temporal changes of population in Nanded district. Population is unevenly distributed throughout the district. This variation is mainly associated with the topographical characteristics of different parts of the district. The distribution denotes the spatial pattern due to dispersal of population, formation of agglomeration, linear spread etc. The several methods of describing the distribution of population the simplest way is percentage distribution of population over the geographical areas. Economic characteristics play an important role in the overall development of an area. These characteristics reflect on the economic status of any region at given point of time. Hence, it is essential to study the distribution of population in the study area. In most tehsil of the district geographical distribution of population is not even with varying degrees of concentration of population giving rise to varying densities in the different parts of the district. The population distribution in district has been determined by availability of land for cultivation, quality of soil, availability of water resources, topography and availability of transportation and urban facilities.

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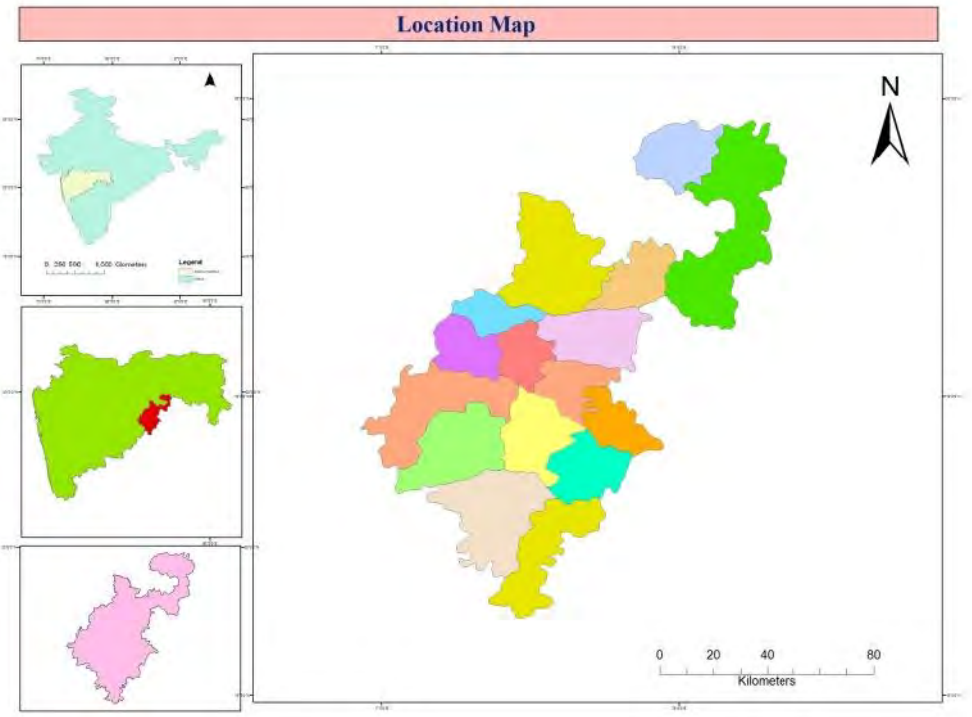
OBJECTIVES

1) To analyze Tahsilwise distribution and concentration of Population in Nanded district.
2) To find out distribution pattern of Population in Nanded district.

STUDY AREA

Nanded district is part of Marathwada Region in Maharashtra. For the present study in and around area of Nanded district is selected. Nanded district is situated on the bank of Godavari River. Nanded district has a geographical area of 10,5,28 Sq. Km. which forms 3.41% of the total geographical area of Maharashtra State. The district is situated in the Deccan Plateau. The district of Nanded has between 18°.15' and 19°.55' North latitude and 77°.7' to 78°.15' East longitudes. *The total population of the districts was 33, 56,566 persons according to 2011 census and male i.e. 1732567 and female are 1623999.*



DATA BASE AND METHODOLOGY

The present study is based on secondary data collected from census Reports of Government of India. Covering distribution of population in Nanded district census handbook (1981, 1991, and 2001), Socio-economic review, district statistical abstract. The Geographical study of over census of 1981 to 2001 has been analysed. For detailed study of changes patterns of population distribution in Nanded District. The collected data has been processed and analysed by using different quantitative, statistical technique. The tabulated data has been presented by Maps using Arc GIS. To make the comparative analysis of population distribution in Nanded district.

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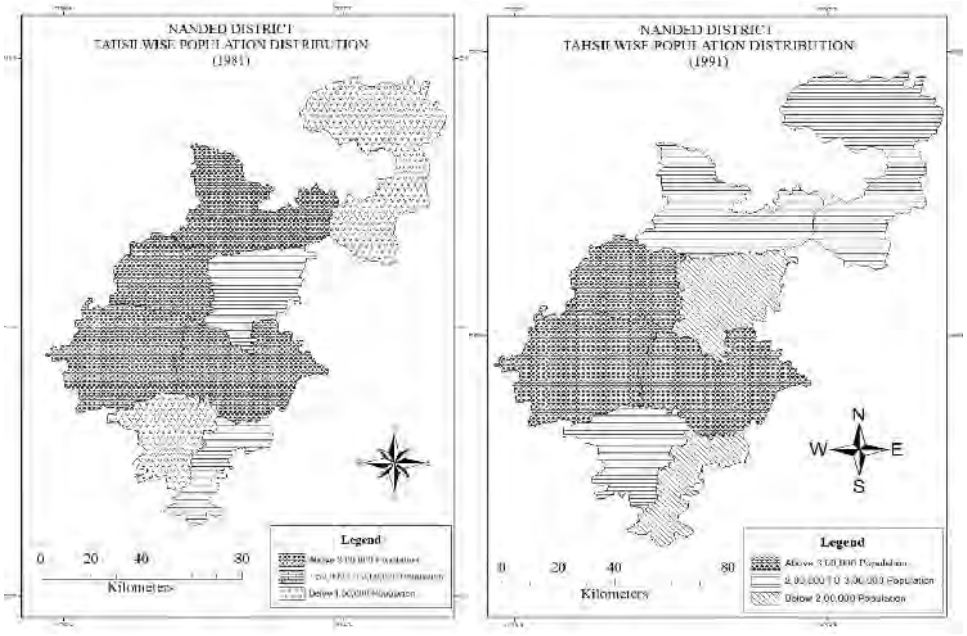
TAHSILSWIES DISTRIBUTION OF POPULATION

NANDED DISTRICT
TAHSILSWIES DISTRIBUTION OF POPULATION YEAR (1981)

Sr. No	Tahsils	Persons	Total Per cent	Males	Per cent of Male	Females	Per cent of Females
1	**Kinwat**	198999	11.37	100841	50.67	98158	49.32
2	Mahoor						
3	**Hadgaon**	208498	11.91	105625	50.65	102873	49.34
4	Himayatnagar						
5	**Nanded**	388002	22.17	201102	51.83	186900	48.16
6	Ardhapur						
7	Mudkhed						
8	**Bhokar**	134138	7.66	68030	50.71	66108	49.28
9	Umri						
10	**Biloli**	266019	15.25	134782	50.66	131237	49.33
11	Dharmabad						
12	Naigaon						
13	**Kandhar**	266534	15.23	136147	51.08	130387	48.91
14	Loha						
15	**Mukhed**	157134	8.98	80063	50.95	77071	49.04
16	**Deglur**	130010	7.43	65827	50.63	64183	49.36
	District	**1749334**	**100**	**892417**	**51.01**	**856917**	**48.98**



According to 1981 census, it is observed that the more concentration of population is found in the tahsils Nanded which is 22.17 per cent. The sparse population is observed in the tahsils Bhokar and Deglur i.e. 7.66 and 7.43 per cent. The tahsils Biloli and Kandhar has 15.25 and 15.23 per cent. Population and tahsils Kinwat and Hadgaon was 11.37 per cent and

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11.91 per cent. Higher concentration of population is observed in the tahsils Nanded because it is a district head quarter of the district.

The sex wise distribution of population is also uneven. According to 1981 census, the Nanded district has 51.01 per cent male and 48.98 per cent females. A comparative analysis of Tahsilwise distribution of population indicates that, the percentage of male population is highest i.e. 51.83 per cent in Nanded tahsil and lowest i.e. 50.63 per cent in Deglur in tahsils Nanded, Biloli and Kandhar have highest percentage of male population it's average i.e. (51.01 per cent) of the district. The percentage of female population is highest (i.e. 49.36 per cent) in the tahsil Deglur and lowest (i.e. 48.16 per cent) in the Nanded tahsil. Tahsil Kandhar has higher percentage of female's population than the average (i.e. 48.96 per cent) of the female population in the study area.

NANDED DISTRICT
TAHSILSWIES DISTRIBUTION OF POPULATION YEAR (1991)

Sr. No	Tahsils	Total	Total Per cent	Males	Percentage of Males	Females	Percentage of Females
1	**Kinwat**	243158	10.43	123917	50.96	119241	49.03
2	Mahoor						
3	**Hadgaon**	263330	11.29	134293	50.99	129037	49.00
4	Himayatnagar						
5	**Nanded**	579436	24.86	300789	51.91	278647	48.08
6	Ardhapur						
7	Mudkhed						
8	**Bhokar**	175804	7.54	89834	51.09	85970	48.90
9	Umri						
10	**Biloli**	341405	14.65	174772	51.19	166633	48.80
11	Dharmabad						
12	Naigaon						
13	**Kandhar**	352514	15.15	181778	51.56	170736	48.43
14	Loha						
15	**Mukhed**	204607	8.78	105230	51.43	99377	48.56
16	**Deglur**	170120	7.3	87263	51.29	82857	48.70
	District	**2330374**	**100**	**1197876**	**51.40**	**1132498**	**48.59**

According to 1991 census, it is observed that the more concentration of population is found in the tahsils Nanded which is 24.86 per cent. The sparse population is observed in the tahsils Deglur and Bhokar i.e. 7.31 per cent and (7.59 per cent). Tahsil Kinwat and Hadgaon was 10.43 per cent and 11.29 per cent of the total population and tahsil Biloli and Kandhar was 14.65 per cent and 15.15 per cent. Higher concentration of population is observed in the tahsil Nanded i.e. 24.86 per cent. And lowest population was Deglur tahsil i.e. 7.3 per cent.

The sex–wise distribution of population is also uneven. According to 1991 census, the Nanded district has 51.4 per cent male and 48.59 per cent female. A comparative analysis of Tahsilwise distribution of population indicates that, the percentage of male population is highest i.e. 51.91 per cent in tahsils Nanded and lowest i.e. 50.96 per cent in tahsil Kinwat, Hadgaon and Kandhar have highest percentage of male population in the average (i.e. 51.40

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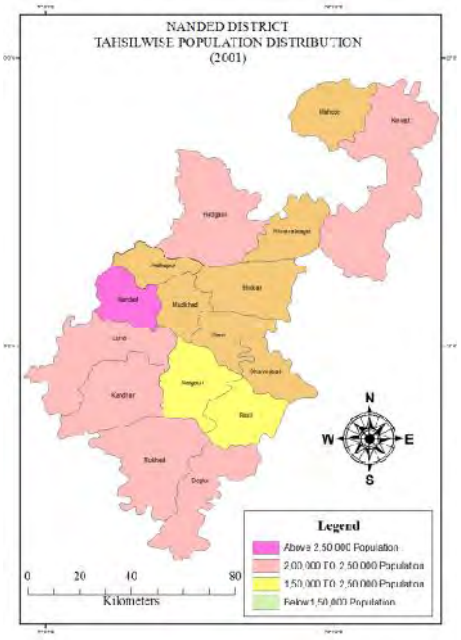
per cent) in the tahsil Biloli, Hadgaon and Deglur have highest percentage of the female population it's average (i. e. 48.59 per cent) of the female population in the study area.

NANDED DISTRICT
TAHSILSWIES DISTRIBUTION OF POPULATION
YEAR (2001)

Sr. No	Tahsils	Total Persons	Percentage of Persons	Males	Percentage of Males	Females	Percentage of Females
1	Kinwat	210630	7.32	107337	50.95	103293	49.04
2	Mahoor	86782	3.01	44774	51.59	42008	48.40
3	Hadgaon	224354	7.8	115568	51.51	108786	48.48
4	Himayatnagar	88924	3.09	45621	51.30	43303	48.69
5	Nanded	598969	20.82	311875	52.06	287094	47.93
6	Ardhapur	98755	3.43	50958	51.50	47797	48.39
7	Mudkhed	97286	3.38	50049	51.44	47237	48.55
8	Bhokar	119229	4.14	61078	51.22	58151	48.77
9	Umri	86206	2.99	43920	50.94	42286	49.05
10	Biloli	155318	5.4	79731	51.33	75587	48.66
11	Dharmabad	86362	3.07	43596	50.48	42766	49.51
12	Naigaon	161134	5.6	83103	51.57	78031	48.42
13	Kandhar	211347	7.34	109747	51.92	101600	48.07
14	Loha	207306	7.2	106663	51.45	100643	48.54
15	Mukhed	243030	8.44	124613	51.27	118417	48.72
16	Deglur	200627	6.97	102725	51.20	97902	48.79
	District	**2876259**	**100**	**1481358**	**51.51**	**1394901**	**48.49**



According to 2001 census, it is observed that, more than 20.82 per cent of the total population of Nanded district. The tahsil Mukhed and Kandhar was 8.44 per cent and 7.34 per cent population of the district, and other reaming are below the 8 per cent population of the district. The tahsil Nanded was observed highest concentration of population i.e. 20.82

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per cent of total population and lowest population observed in the tahsil Umri i.e. 2.99 per cent. Biloli and Naigaon Tahsils 5.4 per cent, and 5.6 per cent population growth respectively.

The district as wholes has 51.51 per cent males and 48.51 per cent females in 2001. The highest percentage of males has observed in Nanded tahsil (i.e. 52.06 per cent) and lowest (i.e. 50.48 per cent) in tahsil Dharmabad. The figure of percentage of female is highest (i.e. 49.51 per cent) in tahsil Dharmabad and lowest (i.e. 47.93 per cent) in tahsil Nanded in most of the tahsils are higher percentage of male population than the average. (i.e. 51.51 per cent) male population of the study area. In whole district seven tahsils are highest percentage of female population (i.e.48.49 per cent).

CONCLUSIONS

The whole population distribution in 1981 its Male population is 51.40 per cent and female 48.59 per cent. The population concentrations are observed in Nanded, Biloli, Kandahar, Kinwat and Hadgaon tehsil. The district as wholes has 51.51 per cent males and 48.51 per cent females in 2001. The highest percentage of males has observed in Nanded tahsil (i.e. 52.06 per cent) and lowest (i.e. 50.48 per cent) in tahsil Dharmabad. The study of Tahsilwise distribution of population in year 1981, 1991 and 2001 is reveals that tahsils Nanded has 24.86 per cent population of total in 1981, which is decrease in 2001 up to 20.82 per cent. Because of 2001 census Nanded tahsils divided in the other three tahsils i.e. Nanded, Ardhapur and Mudkhed are newly created in the 2001 census. The 1981 and 1991 tahsils are 8 and 2001 was tahsils are 16.

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अहिराणी लोकगीतातून खानदेशी लोकसंस्कृतीचे ऐतिहासिक दर्शन

प्रा.डॉ. रमाकांत अंबादास चौधरी
इतिहास विभाग,
आर.सी.पटेल कला, वाणिज्य व विज्ञान महाविद्यालय शिरपूर

प्रास्ताविक :-

लोकगीतांना इंग्रजीत Folksong असे म्हटले जाते, लोकगीतांच्या संदर्भात British Dictionary ने व्याख्या केलेली आहे ती अशी "A song which the music and text have been landed down by oral tradition among the common people." तर Standard Dictionary of Folklore Mythology and Legends च्या अनुषंगाने लोकगीत म्हणजे ज्या समूहाचे वाङ्मय अलिखित आणि मौखिक परंपरेने चालत येते त्याचे संगीतमय गीत होय. कुंजबिहारी दास यांनी लोकगीताची केलेली व्याख्या ही प्रसिध्द इंग्रजी कवी विल्यम वर्डस वर्थ यांच्या कवितेच्या व्याख्येशी मिळती जुळती आहे. ते म्हणतात, A Folk song is spontaneous out flow of life of the people that live in more of less primitive condition cut side the sphere of sophisticated influences. उत्स्फूर्तपणे लोकगीतांची निर्मिती होत असून लोकगीतांचा प्रवाह अखंडपणे वाहत असतो. यात आदिम जीवनाचे अवशेष दिसतात. लोकगीतांची निर्मिती लोकसमूहात स्वाभाविकपणेच होत असते. लोकगीतांच्या विषयासंबंधी ग्रीम म्हणतो, लोकगीत अकृत्रिम असतात. ती सहजपणे स्वयंनिर्माण होतात. तर पॅरीच्या मते लोकगीत म्हणजे आदिमानवांचे आल्हाददायी संगीत होय.

उद्देश :-

खानदेशातील लोकवाङ्मयावर प्रकाश टाकणे.
खानदेशातील लोकगीतांचे स्वरूप समजून घेणे.
खानदेशातील लोकसंस्कृतीचे महत्व समजून घेणे.

खानदेशातील लोकांची विशिष्ट मानसिक जडणघडण, विशिष्ट जीवनप्रणाली, परंपरा लोकगीतात प्रतिबिंबीत झालेल्या दिसतात. खानदेशात लोकगीतांचे दालन समृध्द आणि संपन्न असून ते विविध वैशिष्ट्यांनी नटलेले आहे. या लोकगीतांची परंपरा फार जुनी आहे. लोकगीताबाबत सुलक्षणा कुलकर्णी म्हणतात की, या लोकगीतांची परंपरा फार जुनी आहे. मानवाच्या आदिम अवस्थेत त्याच्या मनातील भावना जेव्हा माणूस शब्दातून व्यक्त करू लागला तेव्हा भावनांच्या प्रकटीकरणासाठी त्याने जी गाणी गायली तीच ही लोकगीते असू शकतील. खानदेशची बोलीभाषा अहिराणी असल्याने लोकगीतेही त्याच भाषेत मोठ्या प्रमाणात आहेत. त्यामुळे अहिराणी लोकगीते ही खानदेशातील अहिराणी लोकसंस्कृतीची अमूल्य अशी संपत्ती आहे. या लोकगीतांमधून खानदेशी लोकजीवनाचे व्यवहार प्रतिबिंबात होतात. खऱ्या अर्थाने सांगावायाचे झाल्यास अहिराणी लोकगीते म्हणजे खानदेशच्या एकूणच परिसरातील समूहजीवनाचे दर्शन म्हटले पाहिजे. खानदेशातील सण-उत्सव, विधी, परंपरा, संकेत या सर्व लोकतत्त्वाचे दर्शन या गीतांमधून घडते. म्हणून लोकगीते ही या लोकतत्त्वाचा अभ्यास आहे. या लोकगीतांना फार प्राचीन अशी परंपरा आहे. लोकगीतांचा इतिहास अभ्यासतांना जाणवते की, जेव्हा लोक एकत्र येवून समुहाने राहू लागलेत तेव्हापसून लोकगीतांची परंपरा प्रचलीत आहे. आदिमानवाच्या कंठातून पद्यमय लयबध्द ध्वनी बाहेर पडला आणि त्या ध्वनींनी भावना आणि विचार व्यक्त करायला सुरुवात केली आणि आपोआप पुढेजावून त्या ध्वनी अक्षर शब्दांनी लोकगीते झालीत. पुढे ही गाणी लोकमुहातील प्रत्येक मानवी घटकांच्या मुखातून येऊ लागली आणि रानावनातून डोंगरमाथ्यांमधून, वृक्ष-वल्लीतून ती निनादू लागलीत. शेवटी हा विरळ वस्ती करुन राहणारा मानवी समुदाय मोठ्या संख्येने एकत्र येवून राहू लागला, कालांतराने शेती करू लागला पुढे अग्नीचा शोध लागला म्हणून अन्न शिजवून खावू लागला. दळणवणाचो साधने चाकाचा शोध लागल्यावर निर्माण झालीत आणि या प्रत्येक प्रसंगी त्याच्या मुखातून सूर बाहेर पडू लागलीत. शेतीची गीते, बैलगाड्यावरचो गीते, पेरणीची गीते, हंगामाची गीते, गाऊ लागलेत. कालांतराने हा मानवी समुह संस्कारक्षम झाला. प्रत्येक मानवीसमुहाच्या परंपरा, रिती, संस्कृती बनल्या त्यातून तंत्र मंत्र ही पुढे आलीत चराचर सृष्टीतील अनेक घटकांना पुजू लागला. सूर्य, चंद्र, धरा, पाणी, वायु, अग्नी अशा अनेक देव देवता त्यांनी कल्पिल्या आणि त्याच्याशी निगडीत आरत्या, गाणी, प्रार्थना पुढे रचल्या गेल्यात, म्हटल्या गेल्यात.

खानदेशातील लोकगीतांचे वैभव अनन्य साधारण असे आहे. संत तुकाराम आणि संत ज्ञानेश्वरांच्या रचनांमध्ये आहिराणी शब्दांचा उल्लेख आढळतो. खानदेशची प्रसिध्द कवयित्री बहिणाबाई चौधरी यांनी खानदेशी लोकगीतांना त्यांच्या लेखनातून चालना दिली

व ती परंपरा बालकवी ठोंबरे पासून ना.दो. महानोरांपर्यंत चालत आली. मानवीसमुहातील गरजा बदल जावून आज या प्रदेशातील लोक भौतिक जीवनाच्या सुखाकडे वळून आधुनिक तंत्रज्ञानातून करमणूक करायला लागली आहेत. घरा घरात टिव्ही, टेपरेकॉर्डर, संगणक सी.डी., डी. व्ही. डी., पोहोचले असून पाश्चिमात्य तालावरील गाणी ऐकण्यात दंग झालेली आढळतात. भाद्रपदात अहीराणी गायल्या जाणाऱ्या गुलाबाईची गाणी कालवश होत असून लग्नाची गाणी देखील आज सी.डी द्वारे गायली जातात. असे असले तरी लोकगीतांचे वैभव चिरंतर असे आहे. खानदेशचे स्वत:चे असे सांस्कृतिक वैभव असून नागरी, ग्रामीण आणि वन्यक्षेत्रात राहणाऱ्या लोकसमुहाची आपली स्वत:ची लोकगीते आहेत. खानदेशातील लोकगीतांचे वर्गीकरण अनेक दृष्टीकोनातून करता येते यात

विधीगीते - यात, जन्म, सटी, लग्न, मुंज आणि संस्कार संबंधित गीते येतात.

श्रमगीते :- विविध क्षेत्रात काम करणाऱ्या क टकरी मानवीसमुहाचे कामानुरुप गीते येतात जसे जातीवरील गाणे, कांडणीची गीते, पेरणीची गीते, गुरांची गीते.

उत्सवाची गीते :- वर्षभरात विविध सण साजरे केल्या जातात यात नागपंचमी, हरतालीक, गौरी, गौराई, होळी, पोळा, कानबाई, रानबाई, देवीची गीते.

स्त्रीगीते :- खानदेशात स्त्रियांशी निगडीत अनेक लोकगीते असून त्याचा भंडार मोठा आहे.

बालगीते :- यात लहान मुलांसाठी गाणी आहेत तर काही अंगाई गीते. पाळणा गीते आहेत.

वरील वर्गीकरण केलेल्या गीतातून खानदेशातील भौगोलीक, सांस्कृतिक, सामाजिक, आर्थिक वैशिष्ट्ये स्पष्ट होतात. यावरुन येथील व्यक्तीजीवनाचा आढावा घेता येतो.

स्त्रीजीवनाचे अत्यंत सूक्ष्म वर्णन बहिणाबाईने केले आहे. स्त्रीला माहेरची ओढ असते ती घाईघाईने माहेरी यायला निघते तेंव्हा धडपडते तेंव्हा रस्त्यावरचा दगड म्हणतो.

"नीट जाय मायबाई, नको करु धडपड
तुझ्याच मी माहेरच्या वाटेवरला दगड"

तर पतीच्या निधनांतर त्या संसाराबद्दल सांगतात

"सांग धरणीमाय, अशी कशी जादू झाली.
झाड गेला निघीसनी, मागे सावली उरली"

स्त्रीगीतातून खानदेशातील समाज व्यवस्थेतील व कुटुंब व्यवस्थेतील स्त्रीचे असणारे स्थान याचा परिचय होतो. पूर्वी एकत्र कुटुंब पध्दत होती आजही अनेक ग्रामीण क्षेत्रात मोठे कुटुंब एकत्र राहत असते. अशा या मोठ्या कुटुंबात स्त्रीचा वाटा मोठा असतो. तीला कुटुंबातील सगळ्यांशी जुळवून घ्यावयाचे असते. त्यातून जीवनाचे सौदर्य बाहेर पडते.

"सोयिल दयन फेकी दिन्ह आडसन
कुजात नारीन बायी दिन्ह दरसन"

सांसारीक जीवन जगतांना स्वत:चा स्वार्थ बाजूला ठेवून जीवनाचे सत्य पाळायचे हे गुण तिला माहेरुन शिकवल्या जातात. वाईट टाकून द्यावयाचे हा कर्मयोग तिला खालील ओळीतुन समजतो.

"नको करु नारी गर्व गमानना धडा,
सवसार शे वं थंडा पानीना बुडबुडा"

घरातील, गल्लीतील, तरुण मुलींकडून अक्षम्य चुक झाली असे प्रत्यक्ष मुलीला बोलावून सांगणे म्हणजे मुलीवर अविश्वास दाखवणे ठरते. शिवाय तिच्या चारित्र्यावि यी मातेनेच कसे साशंक असावे यावेळी मात्र त्या मुलीला सल्ला पुढील ओवीतून दिसतो.

"पाची पकवानन जेवन उल्ट झाय हूई माखीन
तानीया बाय मन्हा, संदी सोडी दे दासीन"

म्हणजे पंचपक्वान्न खाल्ले त्यात माशी खाण्यात गेली म्हणून तुला ओकाऱ्या होत आहेत पण छकुले तू दासीची संगत सोड हा उपदेश आईला आपल्या मुलीला करायचा आहे.

कुटूंबसंस्था म्हणजे खानदेशी संस्कृतीचा प्रमुख पाया होय. कुटूंबसंस्थेतून तयार झालेल्या रक्ताच्या जिव्हाळ्याचा नात्यातून नातेवाईकांचा जो गोतावळा तयार होतो त्याला खानदेशी संस्कृतीत अधिक महत्व प्राप्त झाले. बालकांवर सुसंस्कार करण्यात आईची भूमिका सर्वात महत्वाची ठरली आहे. त्यामूळेच सासुरवासीनीला आईची हरघडी आठवण येत असते. म्हणूनच आईवि यीच्या जात्यावरील अहिराणी ओव्या सर्वात जास्त आढळतात.

माय माय करु, माय साखरनं पोत।
मायनं नाव लेता, मना हिरदे बये ज्योत।।
माय माय करु, माय सोनानी परात।
मायना बिगर, माल्हे गमेना घरात।।
माय माय करु, माय सोनानी पालखी।
मायना बिगर, कोन करेना आलोखी।।
माय माय करु, माय नदीमानी शाहू।
मायना पोटे ऊंनू, एक बहिण दोन भाऊ।।
माय माय करु, माय चवदा रतन।
हिरदना आंगोठीमा, कशी करुन मी जतन।।

आईविषयीच्या अशा अनेक ओव्यांमध्ये 'माय माय करु' अशी आईविषयीची हृदयापासूनची तळमळीची हाक, उत्कट प्रेम,

आई विषयी पुन्हा पुन्हा येणाऱ्या आठवणी लक्षात येतात. आईला अनेक उपमा देवून आईचा गोडवा, प्रेम, वात्सल्य, त्याग किती मोठा आहे याचे वर्णन केले आहे. आईविषयी श्रेष्ठ कवींनी गाईलेल्या महतीपेक्षा खानदेशातील अहिराणी निरक्षर स्त्रियांनी आईवि यी गाईलेली महती कमी वाटत नाही. म्हणूनच आईवि यीच्या ओव्या ऐकतांना, वाचतांना आपल्यालाही गहिवरल्याशिवाय रहावत नाही. आईचे उपकार कधीही फिटणार नाही याची जाणीव या गीतांतून प्रकट होते.

खानदेशी अहिराणी संस्कृतीत आईप्रमाणेच पुढील ओव्यांवरुन वडीलही पूजनीय आहेत असे लक्षात येते.

बाप कसा म्हणे, ठेव लेकी मनी बनी।
जाणार नाही म्हनी पगडीनं पानी।।
बाप कसा म्हणे, लेक भंडारीनं सोनं।
सोनं झाय जूनं, लेक परायानं धन।।
बाप कसा म्हणे, लेकी नांदीसन काढ नांव।
शिवना शेजार, सगा सोयरानं गांव।।
आईबा कसा म्हणे, बेटी चांगली ऱ्हायजो।
पोटपाट झाकीसन, पानी तापीनं व्हायजो।।
आईबा आईबा करु, आईबानी दगडनी छाती।
कलेजा ना धड, धड सोपा जवाईना हाती।।
डोकावरनां पदर, खांदावर ना लेवू।
आयबा तुन्हा, तुन्हा मरजीले भ्यावू।।

मुलीच्या सासरी वागण्यावरुन बापाची मान खाली जाणार नाही याची शिकवण या गीतातून वडिल मुलीला देतात. मुलीने आईवडिलांना दुःख सांगायचे नाही. त्यांना मानसिक त्रास द्यायचा नाही. सांगितले तर "आंडेरनी जात नांदती बरी का मरती बरी" अशी भावना होती. डोक्यावरचा पदर खांद्यावर येऊ देऊ नकोस, कुणाच्या डोळ्याळा डोळा देवू नकोस, रित सोडून वागू नकोस, आयु यभर पवित्र रहा, सासर व माहेर दोन्ही कुळांची किर्ती वाढव असा बापाचा मुलीसाठी या गीतांमधील उपदेश म्हणजे संपूर्ण आयु यभर प्रेरणादायी ठरणारा आहे. आजच्या आधुनिक स्त्रियांना हा उपदेश नक्कीच मार्गदर्शक ठरणारा आहे.

संसार मझार, कितला येतस नातागोता।
बहिण नी भाऊ माणिक मोतीसना पोता।।
भाऊ रे पाव्हना, घोडा बांध बा जाईले।
पयले सोयराले रामराम, मग भेटजो बाईले।।
बहिणले भाऊ, एक देव बा वशिंद्राले ।
चोईना एक खन, एक रातना ईसावाले।।
आंबानी कयरी आंबाले झायी जड।
बहिणना साठे हाऊ सोयरा लागे गोड।।
सासरे जास बहिण, तिन्हा डोयामा पानी।
लाडका भाऊ सांगे, जलम बाईना बंगयवानी।।

आईवडिलानंतर बहिणीचे माहेरपण करणारा, बहिणीची हौसमौज पुरवणारा, माहेरचा बहिणीला जवळचा वाटणारा म्हणजे भाऊ होय. भावाबद्दल सार्थ अभिमान या गीतांतून ओसंडतांना दिसतो.

सासु सतनी रखमा, सासरा इठोबा मन्हा।
याद मायनी ना ये आसा सुखे संसार मन्हा।।
सासु नी सासरा, मन्हा जीवले आसरा।
माता ना पिता मना जन्म देणार दुसरा।।
सासू नी सासरा सुरतीना सोनार।
त्यासनी घडावन कोनले नही येणार।।

आई सारखीच प्रेमळ माझी सासु आहे. नेहमीच माझ्यावर माया करते. सासु सत्यवान रुखमाई तर सासरे विठोबा आहेत. त्यांच्यामुळे मला आईवडिलांची आठवण येत नाही. पारंपारिक आराध्य दैवतांची उपमा ती सासुसासऱ्यांना देवून त्यांचे कौतुक या गीतातून केलेले आहे.

नजीकथीन देखू, मन्हा रामनी नवती।
नव लाख मोती, मन्हा कुकुना भवती।।
आईबानं राज, राज लोकले सांगाले।
भरतारनं राज उभा जलम भोगाले।।
शेरभर सोनं घाली नार दिशे किरियालिंग।
कुकुनं लावू बोट, मी चांद सुऱ्यानी बहिण।।
मानता मानीसन, बेलव्हास संकरले।
कपयना कुकु, आयु यभर मांगस भरतारले।।
सर्गेना देवले, देवले सांगी वनू।
रामले आयु य, माले मरन मांगी वनू।।

अहिराणी ओवी गीतात पतीचे भावविश्व "पती" भोवती गुंफले आहे. पतीशिवाय पत्नीला अस्तित्व नाही. असेल तर त्याला अर्थच नाही. अशी अहिराणी स्त्रीची मानसिकता आहे. पतीचा उल्लेख 'देव', 'राम' असाच आदरपूर्वक होतांना दिसतो. पती म्हणजे स्त्रिचे सौभाग्य लेणे समजले जाते. पती जिवंत असेपर्यंत पत्नीने कपाळाला कुंकु लावण्याची रित आहे. पतीचे आयु य वाढविण्यासाठी देवालाही ती प्रार्थना करते. आजच्या संगणक युगातील पती-पत्नीच्या नात्यातील प्रेमाचा दुरावा कमी करण्यासाठी हे गीते महत्वाचे ठरणारे आहेत.

निष्कर्ष :

भारतीय संस्कृती जगात श्रेष्ठ व पवित्र संस्कृती समजली

जाते. प्राचीन ऋषीमुनींच्या ज्ञानसाधनेतून तिचा उदय झाला. चार वेद, रामायण, महाभारत, आरण्यके, उपनिषदे, गीता इत्यादी सर्व ग्रंथसंपदा म्हणजे भारतीय संस्कृतीचे मुर्त स्वरुप आहे. या भारतीय संस्कृतीच्या कुशीतच विकसित झालेली स्वतंत्र अशी एक खानदेशी संस्कृती उदयास आली. खानदेशी संस्कृतीच्या विकासात अहिराणी भाषेने आपली महत्वाची भूमिका बजावली आहे.

स्वातंत्र्योत्तर काळात मराठी, हिंदी, इंग्रजी भाषांना शासनमान्यतेच्या वाढत्या प्रभावामुळे औपचारीक शिक्षणात या भाषांना दिलेल्या महत्वामुळे अहिराणी भाषेतून विकसिकत झालेल्या खानदेशी संस्कृतीकडे दुर्लक्ष झाले. औपचारीक शिक्षण घेऊन पुढारलेल्या सुशिक्षित वर्गाने खानदेशातील ग्रामीण भागातून विकसित झालेल्या संस्कृतीवर घाव घालून गावंढळ, अशिक्षित अशी टिकाटिपण्णीही केली. जून्या रुढी-परंपरांना दोष देवून या संस्कृतीला हिनवले. आधुनिक सुधारणांच्या नावावर घट्ट विणलेल्या खानदेशी संस्कृतीचे धागे अतिशय ढिले व कमजोरझालेले दिसतात. अशा कठिण परिस्थितीतही खानदेशी संस्कृतीचे थोडेफार अवशेष खानदेशातील ग्रामीण भागात अद्यापही पहायला मिळतात. त्यातूनच खऱ्या खानदेशी संस्कृतीचे दर्शन घडते.

संदर्भ -

British Dictonary (१९९८) Folk song

पगारे, म.सु. (२००५) अहिराणी लोकगीते आणि लोकभाषा, वाङ्मय सेवा प्रकाशन, नासिक

व्यवहारे, शरद (१९९०) मराठी लोकगीत - स्वरूप-विशेष, विश्वभारती प्रकाशन, नागपूर

कुलकर्णी, सुलक्षणा (२००५) स्त्री गीतांतील लोकमानस, द.ता.भोसले (संपा) लोकजीवन आणि लोकसंस्कृती, महाराष्ट्र राज्य साहित्य आणि संस्कृती मंडळ, मुंबई

सावंत, उषा (२००५) खानदेशी अहिराणी स्त्री गीते, प्रतिमा प्रकाशन, पुणे,

सूर्यवंशी, रमेश (२०१०) लोकसाहित्य आणि अभ्यास विषय (खानदेशी), प्रकाशक सौ.मीना सूर्यवंशी, कन्नड जि.औरंगाबाद

पगारे, म.सु (२००३) अहिराणी लोकगीतातील लोकतत्व, इहवाद आणि लोकभाषा, प्रशांत पब्लिकेशन्स, जळगांव,

पगारे, म.सु. (२००५) अहिराणी लोकगीते आणि लोकभाषा, वाङ्मय सेवा प्रकाशन, नासिक

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अभंगकर चन्नांच्या शिवदैवताची विविध रूपे

प्रा. डॉ. प्रवीण कारंजकर
श्री साईबाबा लोकप्रबोधन कला.
महा. वडनेर जि. वर्धा

चन्नाणा शिवबसाप्पा वारद हे मराठवाडयातील वीरशैव अभंगकार त्यांचा जन्मकाल व मरत्युकाल उपलब्ध नाही. सुप्रसिध्द वीरशैव साहित्य संशोधक डॉ. सुधाकर मोगलवारांनी त्यांच्या पीएच. डी. प्रबंधात १९ व्या शतकातील अर्वाचीन ग्रंथकार या प्रकरणात त्यांच्या साहित्याचा समावेश केला आहे. डॉ. मोगलवारांच्या मते, ''त्यांनी लिहीलेल्या अभंगाची संख्या सुमारे ३५०० एवढी आहे पण त्यातले सुमारे १५०० अभंगच प्रकाशित झाले आहेत.''(०१)माजलगाव येथील मठा कडून श्री चनाकृत अभंगाचा गाथा मानावाने फेब्रु १९८४ मध्ये प्रकाशित करण्यात आला यावी पश्ष्ठ संख्या ३५८ पेक्षा जास्त आहे यातील अभंगाचे विषय आणि त्यांची संख्या पुढील प्रमाणे आहेत गुरूपर – ६५, गणपतीपर – २, सरस्वतीपर – १, देवीपर – २, नामपर – ४४, उपसपेपर –५२,भक्तीपर – १४९, करूणापर – १९५, उपदेशपर – ३४७, अनुभवपर – १८०, वैराग्यपर – १३, संतपर – ९६, अष्टावरणपर – १२, वैद्यलायपर – २०, कपिलधारपर – ९, भल्लीणीपर – ८, विनवणीपर – ६, निंदकपर – ३, टोणपेपर – ९९, लळीतपर – ७०, पद – १०३, दोहरे – ३२, आर्या – ५, साकी – ७, श्लोक – ५, पाळणा – १, आरती – १४, असे विषय व त्यांची अभंग संख्या आहे.

या अभंगगाथेत चन्नास्वामी यांनी मराठी, हिंदी व काही प्रमाणात कन्नड भांषांतही अभंग लेखन केलेले दिसून येते. यावरून तीनही भाषा अवगत

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A Geographical Study of Bajra Productivity in Solapur District

Dr.P.Y. Magare
Head Department of Geography, R. C. Patel Arts Commerce &Science College Shirpur Tal Shirpur Dist. Dhule

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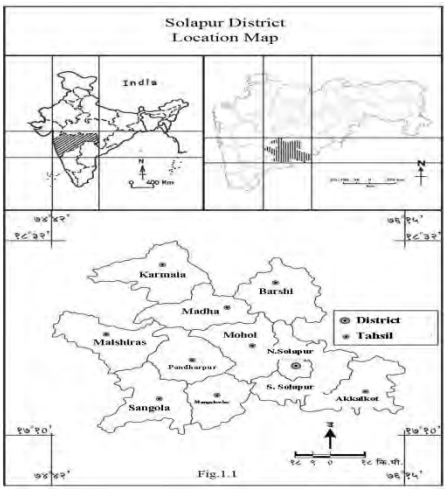
1.1 Introduction :

The overall growth of the Indian economy has depended much on the performance of agriculture. It is the single largest source of employment in India, even though is contribution. Agriculture is backbone of many developing countries. Most of the population is engaged in primary activity in India. The state of development of a country can be assessed on the basic of development in agriculture. Agriculture production is influenceby physical, socio-economic, technological and organization factors. Endeavour is made to study Bajra productivity in Solapur district of Maharashtra state for the year 2005-2010 to 2010-15. Bajra crops is dominant food crop in the study region and near about 60 percent people used it. Farmers are growing numerous crops in the field rather than single crops. The distributional pattern of crops in any region is an outcomes of predominance of certain crops. Bajra is an important crop in the cropping pattern of the study region. Bajracrops is raised in only kharip season in the study region. It is well adopted to the environment in this region.

1.2 Study Region

The district Solapur is one of the most important districts of the Maharashtra state both in terms of area and population. It is a part of Bhima basin. Solapur district is selected as a study region for the present investigation. It is lives between $17^0$10' North to $18^0$32' North latitude and $74^0$42' East to $76^0$15' East longitude and comprising by eleven tahsils. The total geographical area of the Solapur district is about 14895 square kilometers with a population 4317756 according to 2011 census. The region under study constitutes 4.88 percent area and 3.97 percent population of the Maharashtra state. Physiographically, the region is divide into three major divisions such as hilly region, the plateau region and low land plain region. The region derived by the river Bhima and its tributaries. The climate of Solapur district is monsoon climate. The district entirely lives in drought prown area. The annual temperature ranges between 10^0cg to 44^0 cg. The annual average rainfall is 667.10 mm. Three types of soil of the district are confirmed to the hilly region shalow soil, to plateau region medium black soil and the river valley, deep black soil. The district possesses 2.14 percent forest land of the total geographical area. (Fig. 1.1)

Map 2.1



Source : Survey of India, Solapur District

1.3 Objectives :

In the present research paper following main objectives is taken in to consideration.

1) To study the spatial pattern of bajra productivity index in the study region.

2) To analyze the spatio temporal changes of bajra cultivation during the investigation period in Solapur district.

1.4 Data base and methodology

The present research study is mainly based on the secondary sources of data. The data regarding agriculture has been derived from socio-economic review, district census hand book, crop seasons reports. All tahsilwise statistical information calculated with the help of suitable method and find out productivity index.

Productivity index calculated by Prof. Yenedy's formula

Formula :

$$\text{Productivity Index(PI)} = \frac{Y}{Yn} \div \frac{T}{Tn} \times 100$$

Where,

PI=Productivity Index

Y=Production of the selected crop in component arial unit.

Yn=Total production of the selected crop in the entire region

T=Area of the selected crop in component arial unit.

Tn=Total area of the selected crop in the entire region.

1.5 Area under Bajra Crop

In the year of 2005 to 2010 total area under bajra is 43846 hectors. The highest area under bajra crop has 33.65 percent in Sangola tahsil and the lowest area under bajra crops is 0.58 percent in North Solapur tahsil out of the total bajra area of the study region. Remaining nine tahsils namely Malshiras (23.25), Mangalvedha (20.17), Karmala (9.25), Akkalkot (4.20), Pandharpur (3.61), Mohol (1.79), Madha 1.56), South Solapur (1.17) and Barshi (0.72) tahsils are found in 0.72 to 23.25 percent area under the bajra crops.

In the study region during the study period in 2010 to 2015 the total area under bajra is 37163 hector. The highest area under bajra has 27.86 percent in Malshiras tahsil and lowest area under bajra is 1.95 percent in North Solapur tahsil. Remaining nine tahsils namely Sangola (21.52), Karmala (12.20), Mangalvedha (7.80), Pandharpur (6.18), Akkalkot (5.55), Madha (5.19), Mohol (4.28), South Solapur (3.81) and Barshi (3.60) tahsils are found in 3.60 to 21.52 percent area under bajra crop.

1.6 Production of Bajra Crop :

In the study region bajra production is 166077 quintal during the year 2005 to 2010. In this period highest production of bajra out of the study area is 30.54 percent in Sangola tahsil and lowest production of bajra is 0.66 percent in North Solapur tahsil. Remaining nine tahsils i.e. Malshiras (24.29), Mangavedha (21.17), Karmala (9.44), Akkalkot (4.44), Pandharpur (3.83), Mohol (2.01), Madha (1.56), South Solapur (1.21) and Barshi (0.80) tahsils are found in the moderate production of bajra crop.

In the year 2010 to 2015 total bajra production is 132232 quintal. In this period highest bajra production out of the district is 24.70 percent in Malshiras tahsil and lowest bajra production is 2.33 percent in North Solapur tahsil. Remaining nine tahsils Sangola (19.59), Karmala (12.60) Mangalvedha (8.75), Pandharpur (6.75), Akkalkot (6.19), Madha (5.81), Mohol (4.52), South Solapur (4.45) and Barshi (4.26) tahsilsare found in moderate production of bajra crop.

1.7 Productivity Index

The study region i.e. Solapur district has productivity index calculated for the year 2005to 2010 and 2010 to 2015. In the year 2005-10 out of all tahsils the highest productivity index is found in North Solapur (113.7) tahsil and the lowest productivity index is recorded in Sangola(90.7) tahsil.The above analysis of the tahsil wise productivity index is high $\bar{x} + 2S.D.$ is observed in three tahsils in this period i.e. North Solapur (113.7), Barshi (111.1) and Mohol (112.2) tahsils.The moderate

productivity index $\bar{x}+1S.D.$ is observed in three tahsils i.e. Pandharpur (106.0), Akkalkot (105.7) and South Solapur (103.4) tahsils.The moderate productivity index in these tahsils is due to fertile and plain soil and agriculturally prosperous and also connected by transportation network as well as developed in agro based industries.The low productivity index $\bar{x}-1S.D.$ is observed in four tahsils these are Mangalvedha (104.9), Malshiras (104.4), Karmala (102.0) and Madha (100.00) tahsils and very low productivity index $\bar{x}-2S.D.$ is observed in only one Sangola (90.7) tahsil.

In the year 2010 to 2015 out of all tahsils the highest productivity index is found in North Solapur tahsil 119.4 and the lowest productivity index is recorded in Malshiras tahsil 88.6 The above tahsil wise analysis of the productivity index is high $\bar{x}+2S.D.$ is observed in two tahsils these are North Solapur (119.4) and Barshi (118.3)tashils in this period.

The moderate productivity index $\bar{x}+1S.D.$ is observed in five tahsils i.e. South Solapur (116.7), Mangalvedha (112.1), Madha (111.9), Akkalkot (111.5) and Pandharpur (109.2) tahsils and low productivity index $\bar{x}-1S.D.$ is observed in two tahsils i.e. Mohol (105.6) and Karmala (103.2) tahsils. Very low productivity index $\bar{x}-2S.D.$ is observed in two tahsils these are Sangola (91.0) and Malshiras (88.6) tahsils.

Table No.1
Productivity Index

Table No.1

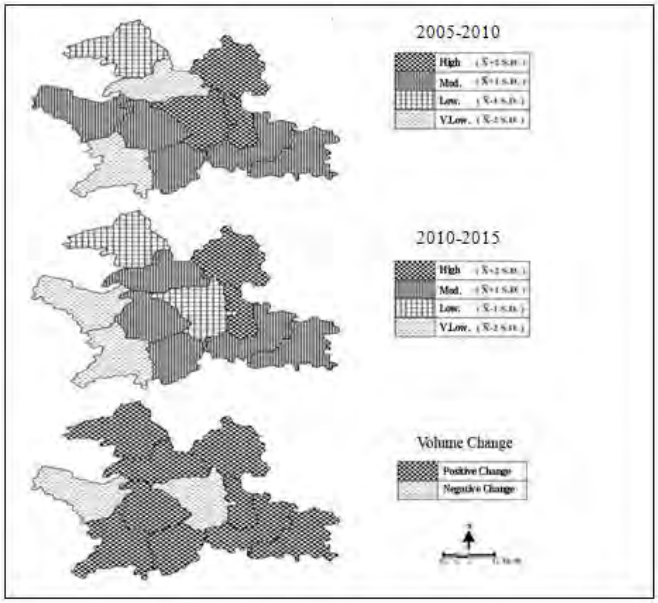
Productivity Index

Tahsil	2005-2010				2010-2015				Productivity Index		Change
	Area	Percent	Production	Percent	Area	Percent	Production	Percent	2005-2010	2010-2015	
N.Solapur	258	0.58	1110	0.66	728	1.95	3085	2.33	113.7	119.4	+5.7
Barshi	319	0.72	1345	0.80	1339	3.60	5634	4.26	111.1	118.3	+7.2
Akkalkot	1842	4.20	7381	4.44	2065	5.55	8194	6.19	105.7	111.5	+5.8
S. Solapur	515	1.17	2017	1.21	1416	3.81	5891	4.45	103.4	116.7	+13.3
Mohol	789	1.79	3339	2.01	1593	4.28	5984	4.52	112.2	105.6	-6.6
Mangalvedha	8845	20.17	35173	21.17	2100	7.80	11573	8.75	104.9	112.1	+7.2
Pandharpur	1584	3.61	6361	3.83	2300	6.18	8934	6.75	106.0	109.2	+3.2
Sangola	14755	33.65	50727	30.54	7999	21.52	25917	19.59	90.7	91.0	+0.3
Malshiras	10198	23.25	40347	24.29	10355	27.86	32662	24.70	104.4	88.6	-15.8
Karmala	4057	9.25	15678	9.44	4537	12.20	16666	12.60	102.0	103.2	+1.2
Madha	688	1.56	2599	1.56	9931	5.19	1378	5.81	100	111.9	+11.9
District	**43846**	**100**	**166077**	**100**	**37163**	**100**	**132232**	**100**			

Source : Socio-economic review of Solapur District 2005 to 2017

Map 1.2

Solapur District : Bajra Productivity Index



Source : Compiled by Author

1.8 Volume Change of Productivity Index

The average volume of change of productivity index is positive changes in nine tahsil and negative changes in two tahsils.

The positive change of productivity index are observed in nine tahsils. The highest positive change in North Solapur (13.3) tahsil and lowest positive change in Sangola (0.3) tahsil. Remaining seven tahsils are positive change of productivity
ndex i.e Madha (11.9), Bharshi (7.2), Mangalvedha (7.2), Akkalkot(5.8), North Solapur (5.7), Pandharpur (3.2) and Karmala (1.2) tahsils.

The negative change of productivity index are observed in only two tahsils. The highest negative change in Malshiras (15.8) tahsil and the lowest negative change in Mohol (6.6) tahsil. (Fig. 1.2)

1.9 Conclusion

In the study region during the study period in 2005 to 2010 the total area under rice is 43846 hector. The highest area under bajra has 33.65 percent in Sangola tahsil and lowest area under bajra is 0.58 percent in North Solapur tahsil. In the year of 2010 to 2015 total area under bajra is 37163 hectors. The highest area under bajra crop has 27.86 percent in Malshiras tahsil and the lowest area under bajracrops is 1.95 percent in North Solapur tahsil out of the total bajra area of the study region.
In the study region bajara production is 166077 quintal during the year 2005 to 2010. In this period highest production of bajra out of the study area is 30.54 percent in Sangola tahsil and lowest production of bajra is 0.66 percent in North Solapur tahsil. In the year 2010 to 2015 total bajra production is 132232 quintal. In this period highest bajra production out of the district is 24.70 percent in Malshiras tahsil and lowest bajra production is 2.33 percent in North Solapur tahsil.

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Study of Tribal and Non-Tribal Population Distribution and Sex Ratio in Nandurbar District (Maharashtra)

Mr. Ramesh P. Chavan
Assistant Professor Department of Geography
S.S.V.P.S Arts, Comm. And Science College
Shindkheda Dist. Dhule, M.S., INDIA.

Dr. P. Y. Magare**
**Associate Professor & Head department of Geography R.C. Patel Arts, Science And Commerce College , Shirpur Dist Dhule , M.S. INDIA.

Introduction-

There are a number of tribal groups in India,they known by different names such as the Adiwasis-the original inhabitants, Vanya jati (live in the forest), AdimJati-primitive people, etc. Tribal community is very primitive and backward in India. The largest concentration of scheduled tribe is confined to central India, particularly in Madhya Pradesh and in its adjoining states like Maharashtra, Gujrat, Rajasthan, Andhra Pradesh, Jharkhand, Orissa and Bihar. In Maharashtra, according to 1991 census, the concentration of tribal population is mostly confined to north-eastern and north western parts.In the northwestern part of the state, particularly Thane, Nashik, Dhule and Nandurbar districts where more 43 percent (43.09) and in the eastern part (Wardha, Nagpur, Bhandara, Chandrapur and Gadchiroli districts), 21.69%, concentration of tribal population to the total tribal population of the state. In Maharashtra the schedule tribe population was 73.18 lakhs (1991), which constituted 9.27 percent of the total population of the state. It has now increased to 85.77 lakhs in 2001 but the proportion has reduced to 8.85 % and 9.35 percent in 2011 (105.10 lakhs). (S. K. Pawar, K. C. Ramotra 2017).

No less impressive is the pattern of their spatial distribution, it has been commonly observed that the tribes reveal strong tendencies of clustering and concentration in the hilly, forested and the geographically inaccessible tracts of the country (Ahmad, 1999). This is the main cause for their backwardness. The growth of the tribal population would be necessary for Understanding the cause of illiteracy, poverty and discrimination.

The tribal people distinct by their own cultures, traditions and occupation and scattered all over the world. The scheduled tribes from the most socially and economically backward sections of Indian society, illiterate, underdeveloped, primitive and predominantly concentrated

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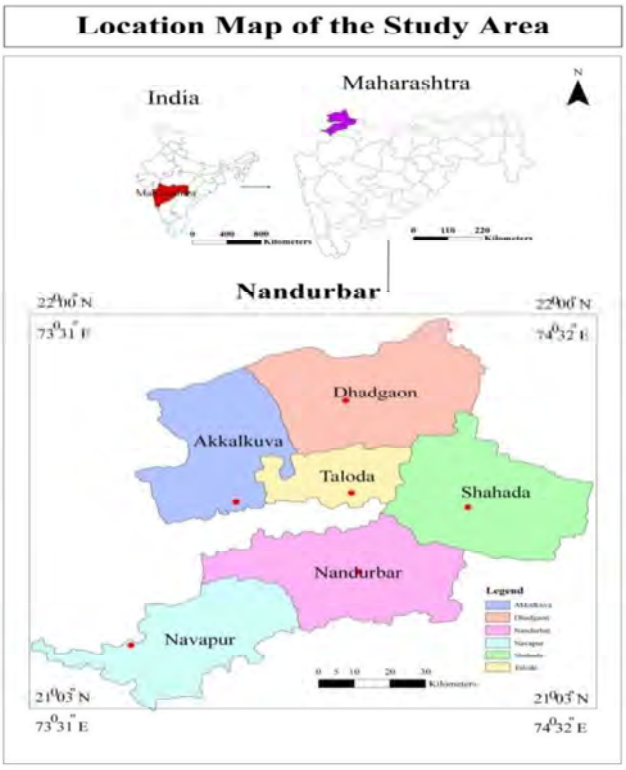
in thick forested and hilly areas, which hampered interaction with the outside world.The tribes are the economically backward ethnic group in India. They are food gatherers, hunters, forestland cultivators and minor forest product collectors. They live in isolation with near to nature, hence, called the son of the soil. Tribes constituted separate socio-cultural groups having distinct customs, tradition, marriage, kinship, property inheritance system and living largely in agricultural and pre-agricultural level of technology.

Tribal society is defined as a collection of families bearing a common name, speaking a common dialect, occupying a common territory. The world tribe means a group of families, living in a contiguous region, speaking a common language and having a historical past.

Study Area-

Nandurbar district is located in northern part of Maharashtra. The geographical location is 21º00′ North latitude to 22º03′ North latitude and 73º31′ East longitude to 74º32′ East longitude. The study area occupies an area 5034.30 sq. km.



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The population according to census 2011 is 16, 48,295. Out of total population 83.29 % are rural and 17.71 % urban population. Nandurbar district separated from formerly Dhule district on 1 July 1998. Nandurbar district is bounded at north and west by Gujrat state, South and South East border demarcated by Dhule district, Madhya Pradesh on North and North East. Nandurbar district consist by 6 tehsil which is Dhadgaon (Akrani), Taloda, Shahda, Nandurbar, Akkalkkuwa and Navapur.

Physiographically, the study region is peculiar in nature. The district forms part of Tapi and Narmada basins. The Narmada River flows in the north and forms boundary between the study region and Gujrat state. The northern part of the district is covered with Satpuda mountain ranges. The altitude of this region is between 300 and 1200 meters from MSL. It is characterized by deep vally with steep slopes. Tapi River flows from the east to west in the southern part of the Satpuda. The region to the south of river Tapi is plain with soils.

The climate of the district is characterized by hot summer and general dryness throughout the year except during the south west monsoon season i.e. June to September. In Nandurbar district the average of rainfall is 801 mm, the rainfall in the eastern part of the district is minimum and shahada comes under this category. The rainfall increase in the westwards of the district. Akkalkuwa and Navapur comes under the major rainfall area in the district.

Objectives-

1) To study the tehsil wise distribution of tribalpopulation in Nandurbar District.

2) To study of sex ratio of tribal and non-tribal population in Nandurbar district.

Database & Methodology-

The present study is mainly based on Secondary data, which is collected from the District Census Handbook, Census of Maharashtra and Statistical Abstract of Nandurbar district. 1981 to 2011 period is selected for the present study. An attempt has been made to tabulate process, analyze and interpret the data by applying suitable statistical and cartographic techniques.

Explanation :

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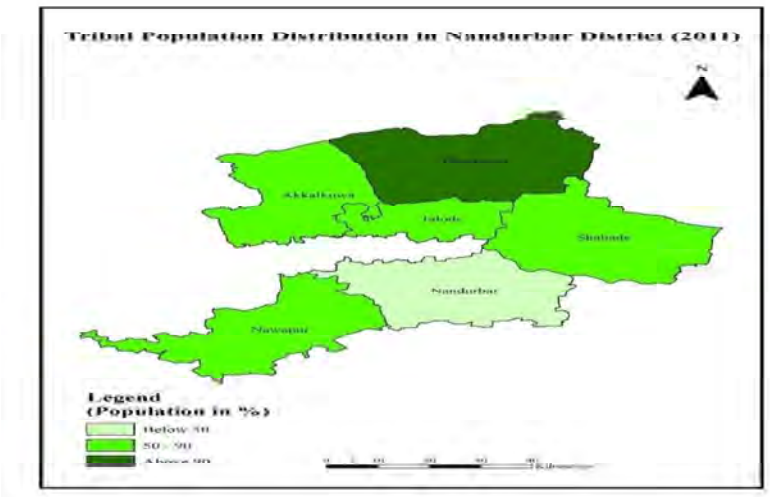
According to 2011 census, the population of Nandurbar district is 1648295 and the population density is 277 persons per sq. km. The sex ratio favoring in males i.e. 978. The proportion of schedule tribe's population to the total tribal population of the districts is 69.28 percentages (1141933). Majority of the population belongs to tribal communities. The northern and southern tahsils namely Akkalkuwa, Dhadgaon (Akrani), and Nawapur have higher proportion of population. The lower proportion of schedule tribe population found in Shahade and Nandurbar tahsil. The literacy rate of the district is 64.38 percent and scheduled tribes literacy which is lower than the district its 55.03. Agriculture is the main occupation of the people.

The study of tribal population distribution is carried out for 1981 to 2011.

Tribal Population Distribution In Nandurbar District (1981-2011)

Sr.No.	Tehsils	1981	1991	2001	2011
1	Navapur	85.43	85.04	84.88	85.52
2	Nandurbar	38.04	39.28	40.82	45.57
3	Talode	65.98	67.85	72.29	77.44
4	Akkalkuwa	87.21	81.22	84.76	85.25
5	Dhadgaon	95.23	86.13	94.96	95.94
6	Shahade	47.19	47.78	48.62	54.20

Source: Census of India, Nandurbar and Dhule district census handbook 1981, 1991, 2001, and 2011.



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In the study of distribution of tribal population in Nandurbar district from 1981 to 2011, the population distribution in all the tehsils does not appear to change much over time. A similar percentage is seen in the tribal population distribution in Navapur tehsil from 1981 to 2011.

The southern part of Navapur tehsil is covered by the Sahyadri Range and the northern part is covered by the Tapi valley. In this tehsil, according to the census of 2011 have 85.52 percent population is the tribal population. Much of Nandurbar and Shahada tehsil is covered by the Tapi valley. In these tehsils, urbanization appears to have taken place in large numbers. The tribal population in these tehsils is less than the other tehsil. Nandurbar tehsil has the lowest number of tribal population its only 45.57 %. The percentage of Shahada tehsil is 54.20%.

The northern part of Taloda tehsil is covered by the Satpuda Mountains and the tribal population is 77.44 %. The whole area of Dhadgaon (Akrani) tehsil is covered with mountain ranges. This is known as the wooded area. The tribal population is 93.95% of the population of this tehsil.The northern part of Akkalkuwa tehsil is covered by mountains. The tribal population here is 85.25% .The study of tribal and non-tribal population sex ratio is carried out for 1991 to 2011.

Sex ratio of Non-tribal and tribal population in Nandurbar district.

Sr. no.	Tehsils	Tribal population sex ratio 1991	Non-Tribal population sex ratio 1991	Tribal population sex ratio2001	Non-Tribal population sex ratio2001	Tribal population sex ratio2011	Non-Tribal population sex ratio2011
1	Navapur	1006	930	1006	929	1023	940
2	Nandurbar	1015	939	1010	938	1022	928
3	Talode	1014	954	1008	934	1014	946
4	Akkalkuwa	1010	873	1021	674	997	601
5	Dhadgaon	1003	929	1013	917	1001	958
6	Shahade	984	933	998	938	1008	949
	Nandurbar District	1005	926	1009	988	1010	910

Source: Census of India, Nandurbar and Dhule district census handbook 1991, 2001, and 2011.

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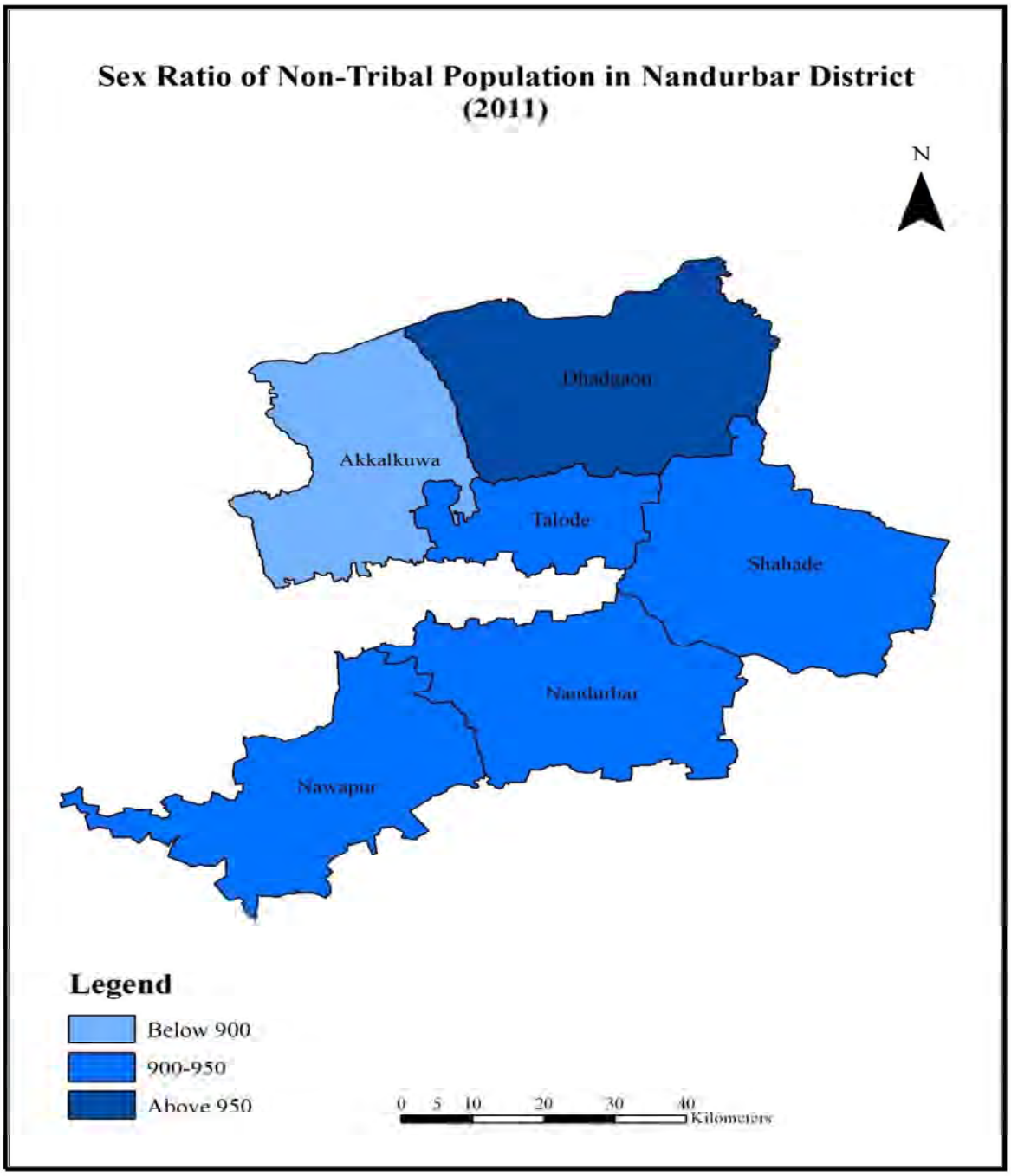

In this above map according to the 2011 census the highest non-tribal population sex ratio occur in Dhadgaon tehsil while lowest non-tribal population occur in Akkalkuwa tehsil.

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कल्पवृक्ष ठरला आहे.

निष्कर्ष :-

मोहाच्या झाडाचे फुल हे आदिवासी लोकांचे आर्थिक स्त्रोत आहे.

मोहाच्या फळामध्ये असणाऱ्या बीजाला टोळी असे म्हणतात. टोळीपासून तेल काढले जाते. या तेलाचा खाद्य तेल म्हणुन वापर करतात. तेल काढल्यावर बियांची पेढ बनविली जाते. तिचा खतासाठी उपयोग केला जातो.

टोळीच्या आतल्या बियांपासून साबण तयार केला जातो. मार्च ते एप्रिल महिन्याच्या कालावधीत या झाडापासून फुले व फळे मिळतात.

गरोदर स्त्रिला मोहाचे फुल खायला देतात कारण मोहाच्या फुल अधिक पोष्टिक असते.

या वृक्षाचे आयु यमान जवळपास ६० ते ७० वर्षापर्यत आहे.

मोह वृक्ष हा डेरेडार असून तो जवळपास ४० ते ६० फुट उंच वाढतो.

आदिवासीसाठी हा वृक्ष वरदान ठरला आहे त्यामुळे हा आदिवासींसाठी कल्पवृक्ष ठरला

संदर्भ :-

जोशी महादेवशास्त्री (१९७०) भारतीय संस्कृतीकोश खंड ६, प्रकाशक पंडित महादेवशास्त्री, कार्यवाह भारतीय संस्कृतीकोश मंडळ, पुणे,

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चितमपल्ली मारूती (१९८५) जंगलाचं देणं, साहित्य प्रसार केंद्र, नागपूर

मेहता प्रकाशचंद्र (१९९३) भारत के आदिवासी, शिवा पब्लिशर्स डिस्ट्रीब्यूटर्स, उदयपूर

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भूराजनितीच्या संदर्भात बलुचिस्थानचे महत्व - एक अभ्यास

प्रा.डॉ. आर. एस. पवार
संरक्षणशास्त्र विभाग प्रमुख,
आर.सी.पटेल महाविद्यालय शिरपूर, जि.धुळे

भूराजनितीच्या संदर्भात भारत पाकिस्तान संबंध अभ्यासतांना बलुचिस्थानचे भूराजनैतिक महत्व वाढलेले दिसते. जम्मु कश्मीर प्रश्न, ईशान्य भारत दहशतवाद व अन्यत्र अस्थैर्य पसरविण्याचे पाकिस्तानचे प्रयत्न सुरू आहेत. भूराजनैतिक दृष्ट्या बलुचिस्थानचा पाकिस्तानी कुरापतींना पर्याय भारत आपल्या परराष्ट्रीय धोरणात बदल करून अल्पकालीन राष्ट्रीय हितासाठी उपयोग करू पाहत आहे. १५ ऑगस्ट २०१६ रोजी स्वातंत्र्य दिनाच्या भा ाणात पंतप्रधान नरेंद्र मोदींनी बलुचिस्थानचा उल्लेख करून इतिहासाची पुर्नरावृत्ती होवू शकते. बलुचिस्थानाच्या स्थानिक संघर्षाला पाठिंबा देत पाकिस्तानच्या राजकीय व लष्करी गोटात धडकी भरली आहे. बांगलादेशासारखी पुर्नरावृत्ती होवू शकते. भारताचे राष्ट्रीय सुरक्षा सल्लागार अजित डोवेल यांनी पाकिस्तानी भारताविरूध्दच्या कटकारस्थानांना पर्याय म्हणून 'बलुचिस्थान कार्ड' चा उल्लेख केला आहे. पाकिस्तान ने कार्यवाह्या थांबविल्या नाहीत तर बलुचिस्थान गमवावा लागेल.

उद्देश :-

भारत पाकिस्तान संघर्षावर प्रकाश टाकणे.

बलुचिस्थानची भूराजनिती समजून घेणे.

बलुचिस्थानचा भौगोलिक व ऐतिहासिक घटकांवर प्रकाश टाकणे.

भारत पाकिस्तान संबंधाचा आढावा

भारत व पाकिस्तानचे विभाजनातूनच संघर्षाची सुरूवात झाली. १९४७ पासूनच पाकिस्तानने आक्रमक भुमिका घेतली. संबंधाचा इतिहास हा सुरूवातीपासूनच अविश्वासाने भरलेला आहे. या अविश्वासामुळे उभय देशांमध्ये सतत तणावपूर्ण वातावरण राहिलेले आहे. भारताने ज्या ज्या वेळेस विश्वास दाखविला त्या प्रत्येक

वेळेस पाकिस्तानने विश्वासघात केला आहे. सिमला करार, लाहोर करार, पाणी वाटपाचा करार या साऱ्यांवर पाकिस्तानने पालन केले नाही. कश्मीर धोरण १९४७ पासून तर आजपर्यंत विश्वासघातावर आधारलेले आहे. त्याकरीता भारताविरुध्द चार युध्दात पाकिस्तानला पराभवाचा सामना करावा लागला आहे. भारताचा विकास आणि लढायातील पराभवाचा बदला घेण्यासाठी पाकिस्तान सतत भारताविरुध्द कटकारस्थान करीत आला आहे. विभाजनानंतर कश्मीरचा प्रश्न निर्माण झाला. उभय देशातील तणाव युध्दाचे कारण बनून आजही कश्मीर प्रश्न आहे तसाच आहे. भारतात कश्मीरचे विलीनीकरण कश्मीरचे राजे हरिसिंग, शेख अब्दुल्ला व कश्मीरी जनता यांच्या इच्छेनुसार झाले आहे. पाकिस्तानी टोळीवाल्यांनी १९४७ च्या ऑक्टोबर महिन्यात मुजफराबाद व डोमेल टेकडी हस्तगत केली. मोठ्या संख्येने घुसखोरांपुढे कश्मीरी सैन्याचा टिकाव लागणार नाही म्हणून राजा हरिसिंग यांनी भारतात विलिनीकरणाची तयारी दर्शविली. २६ ऑक्टोंबर १९४७ रोजी राजा हरिसिंग व पंडीत नेहरू यांनी विलिनीकरणाच्या मसुद्यावर स्वाक्षरी केली आणि कश्मीरच्या रक्षणासाठी भारतीय सैन्य रवाना झाले. तो पर्यंत ३० टक्के कश्मीर पाकिस्तानने गिळकृंत केला होता. तोच भाग आज आझाद कश्मीर म्हणून ओळखला जातो. पाकिस्तानने भारताविरूध्द १९४७, १९६५, १९७१ व १९९९ अशी समोरासमोरील युध्द भारतावर लादली. चारही युध्दात पराभवाचा सामना करावा लागणाऱ्या पाकिस्तानला भारताविरुध्द कटकारस्थान करण्यापलिकडे मार्ग नाही. दहशतवादाचा आधार घेऊन भारता विरुध्द नेहमीच आतंकी कारवाया केल्या आहेत. भारत पाकिस्तानच्या ह्या कारवायांना यशस्वी तोंड देत आहे. दक्षिण आशियात अस्थैर्य निर्माण करण्याचे काम पाकिस्तान करीत असला तरी भारताने जगाच्या मंचावर दहशतवादी राष्ट्र म्हणून सिध्द करून दिले आहे.

बलुचिस्थान व भूराजकीय महत्व

बलचिस्थान हा दक्षिण पश्चिम आशियातील डोंगराळ प्रदेश आहे. या प्रदेशात बलुची नावाच्या जमाती राहतात. सिंध, खैबर-पख्तून व पंजाब या पाकिस्तानी प्रांताच्या जोडीला चौथा भौगोलिक दृष्ट्या सर्वात मोठा प्रांत म्हणजे बलुचिस्तान. पाकिस्तानच्या एकुण भूभागाच्या ४४ टक्के भाग या प्रातांने व्यापला आहे. मात्र पाकिस्तानच्या एकुण लोकसंख्येपैकी फक्त पाच टक्केच वस्ती या प्रातांत आहे. नैसर्गिक वायु, सोने, तांबे इत्यादी खनिज संपत्तीने हा प्रांत समृध्द आहे. बलुचिस्तानच्या उत्तरेस व वायव्येस अफगाणीस्तान आहे. या प्रातांची नैऋत्य सीमा इराणला भिडलेली पंजाब सिंध, खैबर पख्तून व फाटा हे विभाग बलुचिस्थानच्या ईशान्येला आहेत. ऐतिहासिक दृष्ट्या बलुचिस्थान हा पर्शियन साम्राज्याचा व नंतर भारतावर आक्रमण करून येथे झालेल्या सत्ताधारींचा साम्राज्याचा भाग बनत गेला. ब्रिटिशांनी १८३९ साली हा प्रांत आपल्या ताब्यात घेतला त्यानंतर पुढील जवळ जवळ तीन दशके या प्रांतातील आपला अंमल बसविला. फाळणीच्या वेळी भारतातील संस्थानांना आपला अंमल बसविला. फाळणीच्या वेळी भारतातील संस्थानिकांना त्यांचा सार्वभौमत्वाचा अधिकार परत मिळाला. बलुचिस्थानातील ब्रिटिशांच्या प्रत्यक्ष अंमलाखाली नसलेला पण स्थानिकांच्या हाती देऊन त्यांना आपल्या देखरेखीखाली ठेवलेला प्रदेश पाकिस्तानात सामील व्हायला हवा होता. पण जसे कश्मीरच्या राजाला स्वतंत्र रहायच होते तसेच बलुचिस्थानातील नेतृत्वाला आपला प्रदेश स्वतंत्र हवा होता. परंतु कश्मीरप्रमाणे १९४८ साली पाक सैन्याने या प्रांतातील स्वतंत्र राहू इच्छिणाऱ्यांचा प्रदेश ताब्यात घेतला आणि नंतर तो १९५५ साली पाकिस्तानात विलीन करून टाकला. त्या काळापासून स्वतंत्र राहण्याची उर्मी होती. त्यानंतर १९४८ पासून आजपर्यंत अस्थिर राहिला आहे.

बलुचिस्थानचे ऐतिहासिक महत्व

जग जिंकण्याच्या उद्देशाने युरोपातल्या मॅसिडोनियाचा राजा अलेक्झांडर हा पुर्वेकडे निघाला. पॅलेस्टाईन, अनातोलिया, बॅबिलोनिया, असीरीया इत्यादी प्रदेश जिंकत तो प्रचंड अशा पर्शियन साम्राज्यावर धडकला. भीषण युध्द झाले आणि पर्शियन सम्राट दुसरा दारियस याच्या सैन्याचा पराभव झाला. विशाला पर्शियन साम्राज्य अलेक्झांडरच्या एकाच धडकेत कोसळले. गर्वाने, बलाने उन्मत झालेला अलेक्झांडर भारताच्या वेशीवर येऊन धडकला. इथे त्याची गाठ अनेक छोट्या गणराज्यांशी झाली. एक नगर म्हणजे एक राज्य इतकी छोटी असणारी ही गणराज्ये तलवारीला भलतीच तिखट होती. त्यांनी अलेक्झांडरला दमवले, रडवले. सिंधु नदीच्या काठावर राजा पौरसाची गाठ पडण्या आधी अलेक्झांडर अर्धा खचला. यातच एक किरात जमातीचे राज्य पाकिस्तानच्या बलुचिस्थान प्रांतातले कलात नावाचे एक शहर प्राचीन किरातांप्रमाणे आधुनिक बलुची देखील उत्तम लढवय्ये आहेत. इंग्रजांनी भारतातल्या काही जमातींना लढवय्या जाती 'मार्शल रेसेस' असे नाव दिले होते. अशा जमातीमधून बलुच रेजिमेंट देखील होती.

बलुचिस्थानची अंतर्गत समस्या :-

आजवर बलुचिस्थानात १९४८, १९५७-५८, १९६३-६९, १९७३-७७ आणि २००४ ते आजपर्यंत असे अनेक उठाव होत आले आहेत. आधीच्या उठावापेक्षा सध्याचा उठाव किती गुणात्मक आहे याचं विश्लेषण 'इकॉनामिष्ट' या साप्ताहिकाने एप्रिल २०१२

च्या अंकात केले आहे. सर्वत्र पसरलेली बलुच मध्यम वर्ग या संघर्षाला आर्थिक व इतर प्रकारचे बळ कसा प्राप्त करतो शिवाय तारिक फतेह सध्या भारतीय वाहिन्यांवर झळकत आहे. आता या साऱ्या संघर्षात भारताच्या भूमिकेमुळे आगीत तेल ओतले जाणार आहे. बलुचची मागणी आहे ती 'आझादी' ची अर्थात स्वतंत्र बलुचिस्थानची आहे.

ग्वादर बंदर आर्थिक महामार्ग

पाकिस्तान व चीन आर्थिक महामार्ग ग्वादर बंदरातून जाणार आहे. बलुच संघर्षाचा फटका पाकला जोडणारा आर्थिक महामार्ग बांधण्याच्या चीनच्या अतिमहत्वाकांक्षी योजनेला बसतो. या बंदराचा विकास करण्यात चीनला सर्वात मोठा अडथळा येत आहे. म्हणुन चीनचा आर्थिक महामार्ग हा चीनच्या दृष्टीने अती महत्वाचा आहे.

पाकिस्तानच्या दृष्टीकोनातून बलुचिस्थानचे महत्व

अमेरिकेच्या मदतीने अफगाण जिहादला हातभार लावणाऱ्या पाक सेनेने तीन दशकापूर्वी बलुच भूमी वापरली होती. जगभराच्या कोणत्याही मुस्लीम तरुणांना तिथे आणुण जिहादसाठी प्रशिक्षण दिले जात होते. त्यांच्या सोबत जवळपासच्या जगणाऱ्या बलुच टोळीमध्ये जिहादची मानसिकता रूजली त्याचे रूपांतर बंडखोरीत झाले. आजही अनेक तहरिके तालिबान अशी संघटना अस्तित्वात आली. तहरिके तालिबान ही पाकव्याप्त भूमीत बलुच स्वातंत्र्य मागणारी संघटना आहे. परंतु पाक सेना त्यांचे निर्दालन करण्यासाठी सतत हिंसेचे थैमान घालत असते. तेथील आपल्या अपयशाचे खापर भारतावर फोडत असते. तिथल्या हिंसाचाराला भारत जबाबदार असल्याचे आरोप पाक करीत असतो. कश्मीर मधील हिंसाचार हा बलुचिस्थानमधील हिंसाचाराशी कधीच बरोबरी होवु शकत नाही. मात्र पाक राज्य व्यवस्थेला हे कधीच कळले नाही. तसा पुरावाही देता येत नाही.

इतिहासाची पुर्नरावृत्ती होऊ शकते म्हणजेच दुसरा बांगलादेशही निर्माण होऊ शकतो अशी भिती पाकच्या राजकीय व लष्करी गोटात भरली आहे. म्हणुन बलुचिस्थान सांभाळून ठेवण्याचा आटापिटा पाकिस्तान करीत आहे. हिंदुस्थानचे तुकडे व्हावेत असे स्वप्न बाळगणाऱ्या पाकिस्तानमधुन पाकव्याप्त कश्मीर व बलुचिस्थान फुटून वेगळे होण्यासाठी सज्ज असल्यामुळे पाक समोर देश विभाजनाचे संकट उभे राहिले आहे. पाकव्याप्त कश्मीरला तर आपल्या कश्मीरमध्ये विलिन व्हायचे आहे. अशावेळी पाकिस्तानच्या अखंडतेसाठी शरिफ हे हार्ट ऑफ एशियन कॉन्फरन्सची भाषा करीत आहे. आज पाकिस्तान प्रचंड तणावात आहे. पाकिस्तानला सावरण्याकरीता अमेरिकेच्या दोन भेटी देखील घेतल्या आहेत. परंतु ओबामा यांनी अणुकरार पाकिस्तान सोबत केला नाही.

आज पाकिस्तानला पाकव्याप्त कश्मीर वाचविणे मुश्किल आहे. निर्माण केलेले दहशतवादी थकले आहेत. शिवाय बलुचिस्थानचा प्रश्न अतिशय उग्र झालेला आहे. बलुचला आता पाकिस्तानमध्ये राहायचे नाही. त्यांना पाकमधून फुटून वेगळे राहायचे आहे. आणि यामागे भारताचा पाठिंबा आहे. म्हणूनच अमेरिकेच्या मदतीने अण्वस्त्रांचा उपयोग भारताविरूध्द करण्याशिवाय शरिफांना मार्ग उरला नाही. परंतू तेथूनही त्यांना अपयश मिळाले. शरिफ इस्लामच्या नावाने बलुचिस्थान वाचविण्याचा प्रयत्न करतील परंतु प्रत्यक्षात बलुच जनतेला आता मात्र पुर्ण स्वातंत्र्य हवे आहे. त्यामुळे कितीही प्रयत्न केले तरी पाकिस्तानचे पुन्हा एकदा विभाजन होणे अटळ आहे. बलुचिस्थान हे पाकिस्तानचे आकारमानानुसार सर्वात मोठे राज्य तेच फुटून वेगळे पडल्यास पाकिस्तान एकदम संकुचित होवून जाईल. आंतरराष्ट्रीय राजकारणातून बाहेर पडेल. जगात पाकिस्तानला कोणतीही किंमत राहणार नाही.

सारांश

पाकव्याप्त कश्मीर आणि बलुचिस्थान स्वातंत्र्याची मागणी पाकिस्तान दडपून टाकत आहे. तेथे मानवी हक्कांची पायमल्ली होत आहे.

बलुचिस्थान हे कश्मीर आहे असा भ्रम निर्माण केला जात आहे. बहुसंख्येच्या एकसाची सांस्कृतिक राष्ट्रवादाच्या चौकटीत सर्वांना कोंबायच म्हणजे इतर सांस्कृतिक गटांनी बहुसंख्येच्या परंपरा प्रथा स्विकारण्याचा हट्ट भारत सरकारचा आहे.

प्रत्यक्षात बलुचिस्थान कश्मीरला पर्याय असू शकत नाही. अशाने भारताला पाकिस्तानच्या रांगेत उभे राहण्यासारखे आहे. जगात भारताची किंमत कमी होऊ शकते.

भूराजनैतिक दृष्ट्या बलुच भूमीचा वापर आणि त्यांच्या स्वातंत्र्य महायज्ञात सहभागी असल्याचे भाकीत हे पाकिस्तानच्या छुप्या कारवाहिंना प्रतीउत्तर असु शकते. भितीचा सिध्दांत आणि लवचिक राष्ट्रहितापोटी धमकविणे या पलिकडे याचा उपयोग होवु शकत नाही.

चीनच्या ग्वादर बंदराचा 'आर्थिक महामार्ग' याला मोठा अडसर भारत होवू शकतो आणि चीन सामरिकी शक्तीच्या तुलनेने भारत अतिशय कमजोर आहे. चीनच्या परराष्ट्र धोरणाचा भारतला मोठे नुकसान होवू शकते.

बलुचिस्थान वाचविण्यासाठी शरीफ यांनी हार्ट ऑफ एशियन कॉन्फरन्स भरविण्याची तयारी सुरू केली आहे. अफगणिस्थानला

पुढे करून बलुचचे ग्वादर बंदर या कॉन्फरन्सचा केंद्रबिंदु आहे. या बंदरावर ज्या ज्या देशाचा व्यापार अवलंबून आहे त्या सर्व देशांना म्हणजे तुर्कमेनिस्तान, उजबेकीस्तान, ताजिकीस्तान, कजाकिस्तान, खिरगीस्तान या सारख्या देशाचा समावेश आहे. म्हणून रशियासह चीन अफगणिस्तान या देशांना ग्वादर बंदराचे महत्व आहे.

भारत-पाक संघर्षातील बलुचिस्थानचा मुद्दा भारताच्या दृष्टीने चीनला इशारा देत पाकिस्तानला कश्मीरातील हिंसाचाराचे जशाच तसे उत्तर देणे असे काही उद्देश असु शकतात. परंतु यात भारताची संरक्षण क्षमता तपासून पाहणे गरजेचे आहे.

संदर्भ :-

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बलुचिस्थान विकिपिडीया

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मराठा घराण्यातील स्त्रियाचे लोकोपयोगी व सार्वजनिक हिताची कामे - एक दृष्टिक्षेप

प्रा. डॉ. रमेश धनराज जाधव
इतिहास विभाग प्रमुख,
आर.सी.पटेल कला, वाणिज्य व विज्ञान महाविद्यालय शिरपूर, जि.धुळे

प्रस्तावना

मराठा घराण्यातील स्त्रियांनी अनेक लोकोपयोगी व सार्वजनिक हिताची कामे केलेली दिसून येतात. त्यांनी देखील मंदीर बांधणे, जून्या मंदीराची डाकडूगी करणे यासाठी खर्च केलेला दिसून येतो. मराठा सरदारांनी देखील अशा स्वरूपाची मंदीरे बांधलेली आढळून येतात. देवालये, घाट इत्यादी बांधण्यावर पेशवे, त्यांचे सरदार यांनी बराच खर्च केलेला आढळतात. मराठा सरदारांच्या स्त्रियामध्ये शिंदे, होळकर व भोसले घराण्यातील स्त्रियांनी मंदीरे व घाट बांधण्यात त्यांनी मोठा सहभाग घेतल्याचे दिसून येते.१

उद्देश -

मराठा घराण्यातील स्त्रियांच्या धार्मिक जीवनावर प्रकाश टाकणे.

मराठा घराण्यातील स्त्रियांच्या लोकोपयोगगी कार्याचा आढावा घेणे.

मराठी कालीन सार्वजनिक हिताच्या कार्यात मराठा स्त्रियांच्या योगदानावर प्रकाश टाकणे.

विषय विवेचन -

छत्रपती शाहू महाराजांनीही राज्यकारभार करतांना लोकोपयोगी कार्याला त्यांनी प्राधान्य दिलेले दिसून येते. छत्रपती शाहूमहाराजांनी आपल्या राज्यात देवालय, वापीकूप, तयार केलेले दिसून येतात. तसेच ठिकठिकाणी झाडी लावून फुले झाडे लावण्याची शाहू महाराजांनी खास करून आवड होती. त्यांनी विविध ठिकाणी फूल झाड्यांची रोपे लावण्यासाठी मागविलेली दिसून येतात. त्यावरून त्यांची फुलझाडे लावण्याची त्यांची आवड लक्षात येते.२ शाहूमहाराजांनी त्यांच्या कारकिर्दीत ब्रम्हेंद्रस्वामींचे म्हणणे त्यांना मनापासून पसंत होते. त्यांनी जागोजागी देवालये बांधली आणि

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पाकिस्तानी परमाणु शक्ति के विकास में चीन की विशेष भूमिका

प्रा.डॉ. आर. एस. पवार
संरक्षणशास्त्र विभागप्रमुख,
आर.सी.पटेल महाविद्यालय शिरपूर, जि.धुळे

जैसे-जैसे भारत-पाक तथा भारत-चीन सम्बन्धों में कटुता आती गयी वैसे-वैसे पाक-चीन सम्बन्ध और मधुर होते गए। ७० के दशक में पाक-चीन के मध्य राजनीतिक, सैनिक, आर्थिक, वैज्ञानिक, सांस्कृतिक और तकनीकी सम्बन्ध अधिक प्रगड हुए। अफगनिस्तान और कश्मीर के मुद्दे पर चीन पाकिस्तानी नीतियों का समर्थक रहा। सम्बन्धों को मजबूती प्रदान करने हेतु उच्चस्तरीय दौरों के अलावा निम्न स्तर पर प्रतिनिधि मण्डलों का आदान-प्रदान होता रहा। पाक-चीन गठजोड अन्तर्राष्ट्रीय के बवण्डर में दोनों देशों को स्थिरता प्रदान किये हुए है। यह गठजोडस दोनों देशों के आन्तरिक शासन-तन्त्रो में फेर बदल और परिवर्तन के बावजूद फला-फूला है। विपरीत परिस्थितियों के बाद भी पाक-चीन गठबन्धन टूटा नहीं है। अपने अस्तित्व के प्रारम्भ के दिनों से पाकिस्तान चीन के साथ अच्छे सम्बन्ध कायम रखने के प्रति सजग रहा है, इसलिए सन् १९५० में उसने चीन लोक गणराज्य को मान्यता प्रदान कर राजनीतिक सम्बन्धों की शुरूवात की, सन् १९५४ में पाकिस्तान के 'सीटो' का सदस्य बनने पर चीन नाखुश अवश्य हुआ, लेकिन सम्बन्धों में कटुता नहीं आयी, क्योंकि चीन जानता था कि पाकिस्तान के इस कदम के मूल में भारत विरोधी भावना काम कर रही है, इसलिए चीन ने पाकिस्तान का खुलकर विरोध नही किया। सन् १९८५ में प्रधानमंत्री बनते ही मुहम्मद खान जुनेजो ने चीन की यात्रा की और नये आर्थिक समझौते पर हस्ताक्षर किये, साथ ही चीन द्वारा पाकिस्तान को दी जाने वाली एक मुश्त सहायता की घोषणा की, अक्टूबर सन् १९८६ में पाकिस्तान विदेश मंत्री याकूब खाँ की चीनी सहायता की आशा बढ गयी। चीनी प्रधानमंत्री चाओ-चियाग ने भी पाकिस्तान की उच्चस्तरीय यात्रा कर दोनों देशों के सम्बन्ध में सुदृढ बनाने में मुख्य कडी का काम किया। आर्थिक, वैज्ञानिक और तकनीकी सहयोग सम्बन्धी संयुक्त आयोग के ढाँचे के जरिये दोनों देशों के आर्थिक सहयोग और व्यापार के क्षेत्रों का पता लगाने का पर्याप्त प्रयास किया।

इतना ही नहीं पाकिस्तान का आणविक कार्यक्रम भी चीनी सहायता से चल रहा है, जिसकी शुरूवात सन् १९७६ में तब हुई थी जबकि तत्कालीन प्रधानमंत्री जुल्फिकार अली भुट्टो ने इसके लिए चीन से समझौता किया था सन् १९७८ में जेन बियांग की इस्लामाबाद यात्रा के दौरान इस बात की पुष्टि हो गयी थी। सन् १९८३ में संयुक्त राज्य अमेरिका की संसद की विदेश मामलों की गुप्त बैठक में गुप्तचरों ने पाक चीन आणविक सहयोग की विस्तार से जानकारी दी गयी और ९ फरवरी सन् १९८४ को पाकिस्तानी आणविक कार्यक्रम के जनक डॉ. अब्दुल कादिर खान ने यह दावा किया था कि पाकिस्तान हथियारों के लिए उपयोगी परिष्कृत युरेनियम के उत्पादन में सफल हो गया है, उसे केवल आणविक ट्रिगर की जरूरत है यह कमी भी चीन ने पूरी कर दी है। इसके लिए चीन ने पाकिस्तान को ५००० रिंग मेंगनेट प्रदान किये है। चीन पाकिस्तान के खुशाब में ४० मेंगवाट क्षमता की परमाणु भट्टी बना रहा है जिसमें प्लूटोनियम तैयार किया जा सकेगा रक्षा के क्षेत्र में चीन पाकिस्तान का प्रमुख सहयोगी बन कर उभरा है। पाकिस्तान को लडाकू विमानों बख्तरबन्द गाडीयों से लेकर एफ-९ और एम-११ प्रेक्षपास्त्र प्रदान करने वाला चीन ही है। इतना ही नही पाकिस्तान के 'गोलरा' में चीनी सहायता से यूरेनियम परिष्कृत करने का संयत्र स्थापित किया गया है तथा चश्मा में ३०० मेगावाट का एक और परमाणु बिजली घर बनाया जा रहा है। रक्षा विशेषज्ञो का यह मानना है कि चीन ने अपने ४ परमाणु बम की प्रतिकृति पाकिस्तान को उपलब्ध कराई है और उसे दो परमाणु बम बनाने लायक परिष्कृत यूरेनियम भी उपलब्ध कराया है। संयुक्त राज्य अमेरिका सीनेटर एलन केस्टन ने सन् १९८४ में संयुक्त राज्य अमेरिकी सीनेट को अवगत करा दिया था कि पाकिस्तान चीन की मदद से एक दर्जन परमाणु बम बनाने की क्षमता हासिल कर चुका था। पाकिस्तानी सैनिकों ने भी पाकिस्तान के पास परमाणु बम होने की खुले आम घोषणा कर दी थी।

उल्लेखनीय है कि इस समय चीन पाकिस्तान के लिए वही कर रहा है जो एक समय रूस ने भारत के लिए किया था। पाकिस्तानी प्रेक्षपास्त्र कार्यक्रम को भी चीनी तकनीकी प्राप्त हुई। चीन की सहायता से उसने हत्फ-१, हत्फ-२ एवं हत्फ-३ जैसे प्रक्षेपास्त्र बनाये ये बैलेस्टिक मिसाइल है जिनके विकास में चीन ने तकनीकी सहायता प्रदान की है।

चीन और पाकिस्तान दोनो ने मिलकर मध्य दर्जे की मिसाइल एफ-१, एफ-२ तैयार कर रहे है और दोनो के सहयोग से विश्व का सबसे शक्तिशाली युध्द टैंक अलखखलिद तैयार किया जा रहा है। इसी तरह के टैंको ने खाडी युध्द के समय विनाश का दृश्य उपस्थित कर दिया था।

ज्ञातव्य है कि, मई सन् १९८८ में अमेरिका सीनेटर क्वाले ने तृतीय विश्व में बैलेस्टिक मिसाइलों के प्रसार के सम्बन्ध में अपनी एक प्रकाशित रिपोर्ट में बताया गया था कि पाकिस्तान द्वारा निर्मित हत्फ मिसाइले चीन के प्रेल मिसाइल की तकनीक पर निर्मित की गयी है तथा चीनी वैज्ञानिकों पाकिस्तानी मिसाइला निर्माण कार्यक्रम में प्रमुख रूप से सहायता दी है। यद्यपि चीन पाकिस्तान को मिसाइल बेचने की खबरों पर खण्डन करता रहा है किन्तु अमेरिकी उपग्रहों द्वारा लिये गये मिसाइलों के चित्रों से इसकी पुष्टि हो गयी जिसे अन्ततः पाकिस्तान को स्वीकार करना पडा। जून सन् १९९१ में अमेरिकी विदेश मंत्री रेजीनाल्ड बार्थोलोग्यू ने अपनी बीजिंग यात्रा के दौरान चीन सरकार को यह समझाने की कोशिश की थी कि वह पाकिस्तान व सीरिया को ऐसी मिसाइल न बेचे वास्तव मे अमेरिका सीरिया को प्राप्त हो रही चीनी मिसाइलों से चिन्तित था क्योंकि सीरिया को चीनी मिसाइलों की प्राप्ति से इजराइल पर सामरिक दबाव बढ जायेगा जिसे अमेरिका कभी सहन नहीं कर सकता। अमेरिकी विरोध के बावजूद चीन द्वारा पाकिस्तान को दी जा रही एम-११ मिसाइलों से भारत के प्रमुख शहरों पर आक्रमण कर सकता है।

उल्लेखनीय है कि चीन ने पाकिस्तान को कई बैलेस्टिक मिसाइलों की आपूर्ति की है तथा पाकिस्तान में मिसाइल में मिसाइल बनाने के लिए कारखाना भी स्थापित किया है। यह समाचार रह रहकर अमेरिका समाचार जगत में प्रकाशित होता रहा है। इतना ही नहीं स्वयं खुफिया एर्जेसियों के माध्यम से ये खबरे अमेरिकी समाचार जगत में प्रकाशित होती रही है। और सी.आई.ए. के सूत्रों के माध्यम से अमेरिकी सांसदो ने इस आशय की जानकारी भी दी है कि पाकिस्तान ने किस प्रकार चीन से मिसाइल प्राप्त की थी इतना होने के बावजूद भी अमेरिका कहता है कि उसके पास सबूतों का अभाव है। यदि अमेरिका वास्तव में बैलेस्टिक मिसाइलों के प्रसार को लेकर चिंतित है तो उसे पाकिस्तान को परमाणु और मिसाइल क्षमता हासिल करने से रोकना चाहिए। वास्तव में अमेरिका के इसी रवैये के कारण दक्षिण एशिया में मिसाइलो की प्रतिस्पर्धी बढती जा रही है।

विगत कुछ दिनों पूर्व ६५० कि.मी मारक दूरी की जिस मिसाइल के परीक्षण की खबर पाकिस्तान द्वारा मुखरित हुई थी। वास्तव में एम-९ किस्म की चीनी मिसाइल है। असल में पाकिस्तान का पूरा मिसाइल व परमाणु प्रोग्राम चीन से हासिल हुआ है।

चीन और पाकिस्तान का गुप्त सैन गठजोड एक बार फिर सार्वजनिक हो गया है। अमेरिका खुफिया एजेंन्सी सी.आई.ए. ने खुलासा किया है कि चीन पाकिस्तान ने जनसंहारक हथियार कार्यक्रमों को लगातार समर्थन दे रहा है। एजेंसी ने कहा कि वह चीन-पाक के बीच इस तरह के सहयोग पर लगातार निगरानी रखेगी। चीन ने इस मामले पर कोई टिप्पणी करने से इंकार कर दिया, लेकिन साथ ही काह है कि हथियारों की बिक्री के प्रति उसका रवैया सावधानीपूर्ण और जिम्मेदारी वाला है। जनवरी से जून १९८८ के बीच सयम में हुई इस सौदेबाजी के बारे में सी.आई.ए. ने अमेरिका कांग्रेस को सौपी अपनी रिपोर्ट में यह आरोप लगाया है। इसमें कहा गया है चीन ने पूर्व में पाकिस्तान को इस तरह की सहायता उपलब्ध करायी थी तथा अभी भी वह उसे कुछ हद तक जनसंहाकार के हथियार के विकास और निर्माण में मदद दे रहा है। रिपोर्ट में कहा गया है कि पाकिस्तान की इस तरह भारत अपने परमाणु तथा मिसाइल कार्यक्रम के लिए विदेशों पर निर्भर है। रिपोर्ट में कहा गया है कि पिछले वर्ष के प्रथम छह महीनों में पाकिस्तान पूरी दुनिया में विभिन्न स्त्रोतो के माध्यम से दोहरे इस्तेमाल के काम में आने वाली तकनीक तथा उपकरण जुटाने में लगा रहा। सी.आई.ए. के मुताबिक पाकिस्तान का परमाणु कार्यक्रम पूरी तरह विकसित श्रेणी का है और पिछले वर्ष २८ व ३० मई १९९८ को ६ परमाणु परीक्षण से इस बात की पुष्टि भी हो चुकी है।

ज्ञातव्य है कि चीन परमाणु कर्मचारियों के प्रशिक्षण के मदद के लिए पाकिस्तान को एक अत्याधुनिक प्रायोगिक परमाणु बिजली घर नियंत्रण कक्ष पी.३०० निर्यात करने की योजना बना रहा है यह जानकारी पेइचिंग में २९ सितम्बर १९९७ में दी गई थी। सरकारी समाचार एजेंसी शिन्हुआ के अनुसार पी.३०० चीन का सबसे बडा और अत्याधुनिक प्रायोगिक नियंत्रण कक्ष है। अमरीका इस बात पर चिन्ता जाहिर करता है कि चीन ने पाकिस्तान को सम्भवतः परमाणु हथियार बनाने में मददगार प्रौद्योगिकी दी है।

ज्ञातव्य है कि पाकिस्तानी सेना के लिए मुख्य युध्दक टैंक एम.बी.टी. २००० का शुरूवाती उत्पादन आरम्भ किया जा चुका है। जेम्स डिफेंस विकली ने खबर दी है कि उत्पादन अगस्त के पहले सप्ताह में चीन के उत्तरी औद्योगिक निगम (नौरिन्को) और पाकिस्तान के हैवी इंडस्ट्रीज टेक्सिला (एच.आई.टी.) के बीच औपचारिक समझौते पर हुये दस्तख्त के बाद शुरू किया गया। एच.आई.टी. की

शुरूआती चरणों में ५० फीसदी एम.बी.टी. के उत्पादन की योजना है।

उल्लेखनीय है कि अमेरिका में हाल ही में जारी एक खुफिया रिपोर्ट में यह स्पष्ट रूप से स्वीकार किया गया है कि पाकिस्तान ने कम दूरी के एम-११ प्रक्षेपास्त्र चीन से प्राप्त किए है। चीन प्रक्षेपास्त्रों की पाकिस्तान को बिक्री की बात अमेरिकी खुफिया रिपोर्ट में हल्के-फुल्के तरीके से पहले भी कही जाती रही है जिन्हें अमेरिका प्रशासन ने कभी गम्भीरता से नहीं लिया। चीन भी सदा ही ऐसी रिपोर्ट का जोरदार खण्डन करता रहा है तथा हमेशा यह कहा है कि पाकिस्तान के साथ उसका प्रक्षेपास्त्रों के लेन-देन से सम्बन्धित कोई रिश्ता नही है किन्तु इस बार चीन ने ऐसी रिपोर्ट का खण्डन नहीं किया है और अब पाकिस्तान चीन की मदद से युध्दक टैंक एम.बी.टी. का भी उत्पादन शुरू करने जा रहा है। रिपोर्ट पर प्रतिक्रिया व्यक्त करते हुए चीनी विदेश मंत्रालय की एक प्रवक्ता ने कहा है कि चीन ने अमेरिका की इस रिपोर्ट को गम्भीरता से लिया है।

साप्ताहिक ने इस्लामाबाद में एक पाकिस्तानी अधिकारी के हवाले से कहा है एम.बी.टी. अलखालिद का उत्पादन शुरू होना सैनिक उपकरणों के निर्माण के महत्वपूर्ण क्षेत्र में पाकिस्तान को आत्मनिर्भर बनने की दिशा में एक बडी सफलता है।. दूसरी महत्वपूर्ण बात है कि आलोचना के माहौल में पाकिस्तान स्वदेशी करण के आधा ार को व्यापक बना रहा है। अक्टूबर सन् १९८८ को पाकिस्तान ने इसकी घोषणा की थी और विकास अनुबंध पर चीन के उत्तरी औद्योगिक निगम नागरिकों के साथ सन् १९९० में दस्तखस्त किये जा चुके है। अलखालिद की विकास प्रक्रिया १९८९ में शुरू हुई थी और पाकिस्तान के रेतीले क्षेत्र में १९९८ की गर्मियों के दौरान उसके व्यापक परीक्षण भी किये गए।

साप्ताहिक अधिकारियों के हवाले से लिखा है कि ४० किलो मीटर प्रति घन्टे की रफ्तार से चलते समय अलखालिद दो किलोमिटर के दायरे में आने वाले ८० फीसदी लक्ष्यों को नष्ट कर सकता है।

अमेरिका में परमाणु शस्त्र नियंत्रण पर विस्कानसिन परियोजना के निदेशक विस्कानासिन ला स्कूल के प्रोसेसर मेरी मिलहोलिन यदि कहे कि चीन ने पाकिस्तान को सम्पूर्ण परामणु और मिसाइल तकनीकी की आपूर्ति की है और अमेरिकी प्रशासन गम्भीरता से नहीं ले तो उसमें अमेरिकी प्रशासन की अल्पकालिक और उसे अमेरिकी प्रशासन गम्भीरता से नहीं ले तो उससे अमेरिकी प्रशासन की अल्पकालिक और पूर्णत: स्वार्थी नीति का ही आभास होता है। १७ जून सन् १९९८ को मेरी मिलहोलिन ने अमेरिकी प्रतिनिधि सभा हाउस ऑफ रिप्रेजेंटिव्स की अन्तर्राष्ट्रीय मामलों और राष्ट्रीय सुरक्षा समिति की एक सुनवाई के दौरान यह साफ साफ कहा था कि चीन ने सन् १९९२ के उत्तरार्द्धमें पाकिस्तान को सम्पूर्ण मिसाइलों का ही निर्यात किया है। लेकिन इसके बाद से चीन ने निर्यात के इस तरीके में बदलाव किया और अब वह मिसाइलों का निर्यात टुकडों में अर्थात अलग-अलग हिस्सों को अलग-अलग खेप में भेज कर करता है। मिलहोलिन ने कहा इसका एक उदाहरण है। मिसाइल की निर्देशन प्रणाली चीन के निर्यात ही इस दुनियां में शस्त्र प्रसार के सबसे बडे खतरे है। १९९६ के मध्य तक अमरिका खुफियां एजेंसियों ने इस बात के पक्के सबूत इकट्ठे किए कि चीन ने पाकिस्तान को मिसाइल बनाने का कारखाना सौंपा है।

इस प्रकार चीन व पाक के मध्य पनपते सामरिक सम्बन्ध दोनों के व्यक्तिगत स्वार्थो को जहाँ उजागर कर रहे हैं। वहाँ दोनों देशों के सम्बन्धों में आती जा रही निरन्तर प्रगाढता भारत के सुरक्षा परिवेश के लिए नि:सन्देह घातक सिद्ध होगी पाकिस्तान चीन के गुप्त सहयोग से अपने परमाणु ठिकानों को निरन्तर परिष्कृत कर रहा है। पाकिस्तान पिन्सटेक में परमाणु पुन: संशोधन संयत्र काहुटा में यूरेनियम शोधक कराची में सवंर्धन, चस्मा में फ्यूल राड, लाहौर में यूरेनियम शोधक, कराची में परमाणु रिएक्टर, मुल्तान में खानें तथा खुशाब में नवनिर्मित परमाणु रिएक्टर के विकास में निरन्तर हर हथकणडे अपनाने को प्रयत्नशील है।

अत: चीन भारत की कमजोरियों का पूरा लाभ उठा रहा है और वह पाकिस्तान अथवा म्यानमार दोनों के साथ अपने सैन्य सम्बन्धों को सुदृढ कर रहा है तथा उन्हें सहायता भी दे रहा है। ऐसा करने में चीन इस बात की तनिक भी चिन्ता नहीं करता कि उसके इस तरह के रूख से भारत नाराज भी हो सकता है। पाकिस्तान में मिसाइल फैक्टरी कायम करने के मामले में चीन स्पष्टत: इसी तरह का दृष्टिकोण है। चीन पाकिस्तान को उसके पंजाब स्थि खुशाब नाभिकीय संयत्र और काहुटा स्थित खान अनुसन्धान प्रयोगशाला के निर्माण मं तकनीकी सहायता दे रहा है। जहाँ शस्त्रस्त्रों के लिए उन्नत यूरेनियम तैयार होगा नाभिकीय विशेषज्ञों का मत है कि इन संयत्रों से प्लूटोनियम और यूरेनियम को पिघलकार नाभिकीय बम बनाये जा सकते है और सामरिक मिसाइल भी तैयार हो सकते है। पाकिस्तान को परमाणु हथियार और प्रक्षेपास्त्र उपलब्ध कराकर और गौरी प्रक्षेपास्त्र के सफल परीक्षण में उसका हाथ बंटाकर चीन ने प्रमाणित कर दिया है कि वह भारत को कमजोर बनाए रखने का उतना ही इच्छुक है जितना कि पाकिस्तान।

वर्तमान समय में चीन और फ्रांस का पाकिस्तान के साथ दृढ मैत्री सम्बन्ध चल रहा है। और इसके अन्तर्गत चीन व फ्रांस पाकिस्तान को नाभिकीय अस्त्रों के निर्यात और विकास में भी भरपूर सहायता प्रदान कर रहा है। जो अन्तर्राष्ट्रीय नियमों के अनुसार उन्हें नहीं करना चाहिए।

संदर्भ ग्रंथ सूची

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९) दैनिक जागरण

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११) हिंदुस्तान टाईम्स, नई दिल्ली

१२) अमर उजाला समाचार पत्र

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ज्ञानेन्द्र पतिकी कविताओं में पर्यावरण विमर्श

प्रा.डॉ. सुनील एम. पाटिल
हिंदी विभागाध्यक्ष,
आर.सी.पटेल कला, वाणिज्य एवं विज्ञान महाविद्यालय
शिरपूर, जिला धुलियाँ

आज के कविता के सामने का सबसे बडा संकट यह है कि कविता की मान-प्रतिष्ठा तेजी से घट रही है। कविता का यह समकालीन संकट वस्तुत: मनुष्यता का संकट है। आज कविता का परिदृश्य संकटग्रस्त नजर आता है। कविता के मर जाने से मनुष्य को क्या क्या खोना पडता है। बल्कि मानव की आत्मिक संस्कृति अभिव्यक्ति है। वह जन मन की वाणी है। जीवंत कविता हमेशा मानवीय और संभावनापूर्ण होती है। मनुष्यता का संरक्षण संवर्द्धन करना तथा जीवन को अर्थपूर्ण बनाना कविता का मुख्य सरोकार रहा है।

कविता का जैविक संबंध मानव के जीवन से ही होता है। उसके जीवन से ऊर्जा पाकर ही कोई भी महान रचना प्रणीत होती है। मानव जीवन जितना पेचीदार बनता जा रहा है, उतना ही उसकी कविता भी संवेदना एवं संरचना दोनों स्तरोंपर संकीर्ण होती जा रहीहै। आज कविता का भाव बोध बिल्कुल बदल चुका है और कविता रसानुभूति की अपेक्षा ज्ञानात्मक संवेदना प्रदान करती आ रही है। समकालीन कविता में हमारे सामाजिक जीवन की अनेक स्थितियों की अभिव्यक्ति हुई है। अन्य विषयों के साथ किसान विमर्श, स्त्री विमर्श और पर्यावरण विमर्श भी समकालीन कविता के विषय बन रहे है।

पर्यावरण भी समकालीन कविता की केन्द्रीय चिंता का एक विषय रहा है। अत: यह आकस्मिक नही है कि समकालीन कविता में पर्यावरण प्रदुषण से उत्पन्न चिंताएँ भी जहाँ तहाँ झाँकती है। आज की अनेक समस्याएँ प्राकृतिक संतुलन के बिगडने से पैदा हुई है। औद्योगिक और नागरीकरण की अंधी दौड ने प्रकृति को इतना क्षत्त-विक्षत्त किया है उसका खामियाजा हमें कई स्तरों पर भुगतना पड रहा है। मौसम चक्र के गडबडाने से लेकर ओजोन

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प्रा. डॉ. रमेश धनराज जाधव

[illegible] विभाग प्रमुख, आर.सी.पटेल कला, वाणिज्य व विज्ञान, महाविद्यालय, शिरपूर जि.धुळे

प्रस्तावना :

दि. 14,15 व 16 फेब्रुवारी 1930 रोजी साबरमती या ठिकाणी काँग्रेस कार्यकरणीची बैठक झाली. या बैठकीत सविनय कायदेभंग [illegible] चळवळीचे सर्व अधिकार म. गांधींना बहाल करण्यात आले.1 त्यानंतर मा. गांधींनी ब्रिटीश सरकारशी शांततेच्या मार्गाने तडजोड [illegible] प्रयत्न केला त्यांनी 2 मार्च 1930 रोजी व्हाईसरॉय लार्ड आयर्विन यास पत्र लिहून आपल्या 11 मागण्या मान्य करण्यास [illegible]2 त्या 11 मागण्यांमध्ये ब्रिटीश सरकारने संपूर्ण दारुबंदी करावी या गोष्टीचा समावेश करण्यात आला होता. परंतु या मागण्यांकडे [illegible] आयर्विन यांनी दुर्लक्ष केले. त्यामुळे म. गांधीजी समोर सविनय कायदेभंगाची चळवळ सुरु करण्याशिवाय पर्याय नव्हता. 14 फेब्रुवारी [illegible] रोजी म. गांधींनी भारतीयांना मिठाचा कायदा मोडून सविनय कायदेभंगाचा आदेश दिला.3 त्या आदेशानुसार पुर्व खान्देशातील [illegible] कायदा मोडून काढण्याचे ठरविले. जनतेने उत्फुर्तपणे पाठींबा दिला. म. गांधीजींनी या चळवळीत मिठाचा कायदा मोडून [illegible]सत्याग्रह करण्याचे ठरविले. दारुच्या दुकानासमोर पिकेटींग यातही सहभाग घेतलेला दिसतो. म. गांधींनी 6 एप्रिल 1930 रोजी [illegible]तील दांडी येथे मिठाचा कायदा मोडून या चळवळीचा प्रारंभ केला.

[illegible] सविनय कायदेभंगाच्या चळवळीतील पूर्व खान्देशाच्या सहभागाबाबत माहिती मिळविणे.

पूर्व खान्देशातील दारुबंदी व त्यात सहभाग घेतलेल्या व्यक्तींची माहिती मिळविणे.

[illegible]विवेचन :

या घटनेचा प्रभाव महाराष्ट्रासह पूर्व खान्देशवर ही पडलेला दिसतो आणि त्यातून पर्व खान्देशातील स्वयंसेवकांनी व कार्यकर्त्यांनी [illegible] सत्याग्रह, मिठाचा सत्याग्रह, मोर्चे, निर्दशने इत्यादी कार्यक्रमात आणि दारु पिकेटिंग मध्ये सक्रिय सहभाग घेतला.4

जळगाव जिल्हा स्वतंत्रपणे निर्माण होण्यापूर्वी जळगाव, धुळे आणि नंदूरबार या तिन्ही जिल्ह्यांना संयूक्त खानदेश असे म्हटले जात [illegible]

इ.स. 1906 मध्ये खानदेश जिल्ह्याचे पूर्व खानदेश आणि पश्चिम खानदेश म्हणून विभाजन करण्यात आले. पूर्व खानदेशचे मुख्यालय [illegible] पश्चिम खानदेशचे मुख्यालय धुळे येथे करण्यात आली०. इ.स. 1960 मध्ये पूर्व खानदेश ऐवजी जळगाव जिल्हा व पश्चिम [illegible]ऐवजी धुळे जिल्हा असे नामकरण करण्यात आले.

स्वातंत्र्य चळवळीच्या आंदोलनात पूर्व खानदेश म्हणजे जळगाव जिल्ह्याचाही सहभाग मोठ्या प्रमाणावर होता. लोकमान्य टिळक, [illegible] गांधी, पंडीत जवाहरलाल नेहरु, सरदार वल्लभभाई पटेल यांचा प्रभाव पडून पूर्व खान्देशात सानेगुरुजी, श्री शंकरराव देव, श्री. [illegible]साहेब दास्ताने, धनाजी नाना चौधरी, श्री. मीर शुक्ला, देवकीनंदन नारायण यासारख्या थोर क्रांतीकारक व विचारवंताच्या [illegible]मुळे व त्यागामुळे भारतीय स्वातंत्र्य चळवळ पूर्व खान्देशात (जळगाव जिल्ह्यात) खेड्यापाड्यापर्यंत पोहचली. त्यांचाच महत्त्वाचा [illegible] म्हणजे खानदेशात राष्ट्रीय काँग्रेसचे अधिवेशन फैजपूर येथे भरले.5

राजकीय हक्कांबरोबरच सामाजिक स्वास्थ्य बिघडू नये व भारतीय लोकांच्या दारिद्र्यात वाढ होवू नये. यासाठी मा. गांधीजींनी [illegible] चळवळीच्या कार्यक्रमात मद्यपान निषेध चळवळ सुरु केली होती. दारुच्या दुकानांसमोर पिकेटींग करणे व लोकांमध्ये जागृती [illegible] करुन या व्यसनापासून त्यांना परावृत्त करणे या गोष्टीचाही समावेश करण्यात आला होता.

सविनय कायदेभंग चळवळीस सुरुवात होण्यापूर्वी या चळवळी संबंधी व सत्याग्रहाविषयी प्रचार करण्यात आला. प्रिंपाळे येथील [illegible] शाळेत श्री. बाबासाहेब देशमुख यांच्या अध्यक्षतेखाली दि. 26/3/1930 रोजी झालेल्या सभेत पूर्व खान्देशातून पाचशे स्वयंसेवक [illegible]ग्रहासाठी देण्याचा ठराव संमत करण्यात आला. त्यासाठी 8 तुकड्या जिल्ह्यातून प्रचारासाठी निघाल्या. त्यांनी खेड्यापाड्यातून पायी [illegible] केला. सत्याग्रहाविषयी जनजागृती करणाऱ्यांमध्ये सानेगुरुजींचाही समावेश होता.6

सविनय कायदेभंग चळवळीचा पूर्व तयारीसाठी पुणे येथे भरलेल्या महाराष्ट्र कायदेभंगाच्या बैठकीला पूर्व खान्देशातून श्री. [illegible]साहेब दास्ताने व श्री. ठाकर यांची उपस्थिती होती. सविनय कायदेभंग चळवळीचे महाराष्ट्रातील आंदोलनाचे मुख्य केंद्र [illegible] [illegible] स्थापन करुन प्रांतिक काँग्रेसने कायदेभंग मंडळास सर्व अधिकार दिले होते. त्याचबरोबर जिल्हावार युद्धमंडळे नेमण्यात आली होती.7 [illegible] पूर्व खान्देशाच्या युद्धमंडळाचे (कायदेभंग मंडळाचे जिल्हाधिकारी म्हणून श्री. गोखले यांची नियुक्ती केली होती. पूर्व खानदेश [illegible] [illegible] कमेटीचे अध्यक्ष आण्णासाहेब दास्ताने यांनी विदर्भातील प्रसिद्ध पुढारी श्री. बाबासाहेब देशमुख व श्री. [illegible] [illegible] राका जनजागृतीसाठी व्याख्याने आयोजित करण्यात आली होती.

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R.C.Patel Arts, Commerce & [illegible] College, Shirpur (Dhule)

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छत्रपती शाहू महाराजांची इनामे - एक दृष्टीक्षेप

प्रा. डॉ. रमेश धनराज जाधव
इतिहास विभाग प्रमुख, आर.सी.पटेल कला, वाणिज्य व विज्ञान महाविद्यालय, शिरपूर जि.धुळे.

प्रस्तावना :

शाहु महाराजांची ८ मे १७०७ मोगलांच्या कैदेतून सुटका झाली स्वराज्यात आल्यामुळे महाराणी ताराबाई-शाहू महाराज यांच्यामध्ये सत्तेसाठी संघर्ष निर्माण झाला आणि त्यातूनच खेडची लढाई झाली त्यात महाराणी ताराबाईंचा पराभव झाला. त्यामुळे शाहू महाराजांनी आपला मोर्चा साताऱ्याकडे वळविला. शाहूंची बाजू भक्कम झालेली पाहून सातारा लढविण्याची कामगिरी प्रतिनिधींकडे सोपवून महाराणी ताराबाई पन्हाळ्याकडे निघून गेल्या आणि शाहूमहाराजांनी सातारा राजधानी आपल्या ताब्यात घेवून १२ जानेवारी १७०८ रोजी स्वत:स राज्याभिषेक करुन मराठा साम्राज्याचा वारस घोषित केले.[१]

छत्रपती राजारामाच्या काळात तत्कालीन राजकीय परिस्थितीनुसार राजकीय व लष्करी अनुषंगाने वतने देण्यास सुरुवात केली. छत्रपती शाहू महाराजांनी सत्ता प्राप्तीनंतर (१७०८) मराठा राज्यातील विविध ठिकाणी असलेले सरदार, सरंजामदार, दिमतीस असलेले कारभारी यांना मोकासे,इनामे देण्यास सुरुवात केली. मोल्वर्थ मराठी-इंग्रजी शब्दकोषात पुढीलप्रमाणे आहे.

१. Village or lands, or a share in the rule over than and revenue arising from then, granted on condition of Millitary Service or in India. २. The share of the state or government in the rule over a village and in the revenue.[२] लष्करी सेवेबद्दल व त्या खर्चासाठी विशिष्ट गावातील महसुल वसुलीचा तो अधिकार होता.

उद्देश :

१) छत्रपती शाहू महाराजांच्या काळातील इनामे यांची माहिती मिळविणे.
२) इनामे देण्याच्या उद्देशाची माहिती मिळविणे. इनामे कोणकोणत्या व्यक्तीस दिली होती यांची माहिती मिळविणे.

संशोधन पद्धती :

प्रस्तुत विषयासाठी विश्लेषणात्मक संशोधन पद्धतीचा वापर केला असून उपलब्ध असणारी संदर्भग्रंथे त्यांत प्रामुख्याने मराठी रियासत, वैद्य दप्तरातून निवडलेले कागद- खंड-२, शाहू महाराजांची रोजनिशी, पेशवेदप्तरातील सनदा पत्रातील माहिती या संदर्भग्रंथाचा उपयोग करुन प्रस्तुत शोधनिबंध मांडण्याचा प्रयत्न केला आहे.

विषय विवेचन :

सनदा व आज्ञापत्रे : सनद याचा अर्थ अधिकारपत्र किंवा देणगीपत्र असा होत असला तरी त्यापेक्षाही व्यापक असल्याने त्याचे स्पष्टीकरण करणे जरुरीचे असून योग्यही आहे.[३] छत्रपती शिवाजी महाराजांना अष्टप्रधान मंडळाची नेमणूक का करावी लागली. याचे महत्वाचे कारण म्हणजे राज्यकारभार चालविण्यास लागणाऱ्या मनुष्यबलाची व ज्ञानबलाची योग्य ती तजवीज केलेली दिसते. कोणाला लढाईचे तर कोणाला न्यायाचे, कोणाला फडणविशीचे तर कोणास चिटणिसीचे व मुजूमदारीचे वैगेरे कामे करता येतील हे पाहून योग्य व्यक्तीची निवड केली व अंगी असलेल्या बुद्धी चातुर्य दाखविण्यासाठी आणि राष्ट्रहिताचे कामे करण्यास संधी देवून त्या त्या कामाची जबाबदारी त्यांच्यावर सोपविली.[४] त्या कामाच्या बदल्यात एखाद्यास गावाचे उत्पन्न इनाम करुन दिले तर, एखाद्यास खजिन्यातून नगद नेमणूक करुन दिली. काही बाबतीत धार्मिक वृत्तीनेही देवस्थानास किंवा ब्राह्मणास काही गावे व जमिनी इनाम करुन दिल्या. यासंबंधीची जी पत्रे त्यांनी करुन दिली त्यासच 'इनामपत्र' असे म्हणतात.[५]

डॉ. बाबासाहेब आंबेडकरांचे निष्ठावान सहकारी गणपत महादेव जाधव तथा मडकेबुवा

प्रा. डॉ. रमेश धनराज जाधव (इतिहास विभाग प्रमुख)
आर.सी.पटेल कला, वाणिज्य व विज्ञान महाविद्यालय, शिरपूर जि.धुळे

- प्रास्ताविक :

इ. स. १९१९ पासून डॉ. बाबासाहेब आंबेडकरांच्या दलित मुक्तिच्या अस्पृश्य वर्गाच्या दु:खाला वाचा, फोडण्यासाठीच्या कार्याला इ.स. १९२० मध्ये 'मूकनायक' हे साप्ताहिक सुरु करुन केले आणि माणगाव परिषद भरविली. तेव्हापासून ते दलीत जनतेचे पुढारी म्हणून ओळखले जावू लागले.[१] अस्पृश्यांना गुलामगिरीच्या जोखडातून मूक्त करण्यासाठी दलित मूक्तीच्या या चळवळीत डॉ. बाबासाहेब आंबेडकर यांना अनेक सहकारी लाभले या सहकाऱ्यात अस्पृश्यांप्रमाणे सवर्ण देखील होते. या सर्व सहकाऱ्यांचे दलित-मूक्तीच्या चळवळीतील योगदान महत्त्वाचे आहे. मूकनायक, बहिष्कृत भारत, जनता, समता, प्रबुद्धभारत यांच्या संपादन आणि प्रकाशनाच्या दृष्टीने त्याचप्रमाणे बहिष्कृत हितकारणी सभा, समाज समता संघ, स्वतंत्र मजूर संघ, शेड्यल कास्ट फेडरेशन, पिपल एज्युकेशन सोसायटी इत्यादी संघटनांच्या उभारणीत महाड येथील चवदार तळ्याचा सत्याग्रह, जळाराम मंदीर सत्याग्रह अशा प्रकारच्या अनेक सामाजिक परिवर्तनाच्या चळवळीत गंगाराम सवादकर, कमलाकांत वासुदेव चित्ते, संभाजी तुकाराम गायकवाड, कर्मवीर भाऊराव गायकवाड, पांडुरंग राजभोग बॅरीस्टर खोब्रागडे , गणपत महादेव जाधव तथा मडकेबुवा असे अनेक कार्यकर्ते लाभले.[२]

उद्देश :१) डॉ. बाबासाहेब आंबेडकराचे सहकारी गणपत महादेव जाधव उर्फ मडकेबुवा यांच्या कार्याची माहिती मिळविणे.
२) त्यांनी डॉ. बाबासाहेब आंबेडकरांच्या कार्यास कसा प्रकारच्या सहभाग नोंदविला याची माहिती मिळविणे.

- संशोधन पद्धती : हा शोधनिबंध तयार करतांना विश्लेषणात्मक संशोधन पद्धतीचा वापर केलेला असून उपलब्ध असलेल्या प्राथमिक व दुय्यम दर्जाच्या साधनाद्वारे हा शोधनिबंध पूर्ण केलेला आपणांस दिसून येईल.

- विषय विवेचन :

मडकेबुवा तथा गणपत महादेव जाधव यांचा जन्म इ.स. १८८५ मध्ये पनवेल तालूक्यात झाला. मडकेबुवा हे उत्कृष्ठ मॅकेनिक होते. इ.स. १९२८ मध्ये ते अफ्रिकेत गेले. तेथे बॉयलर मेकर म्हणून ४०० रु. पगारावर काम केले. परंतु दुसऱ्याच वर्षी म्हणजे इ.स. १९२९ मध्ये ते भारतात परत आले. त्यानंतर त्यांनी काही काळ त्यांनी मडकी विकण्याचा व्यवसाय केला. म्हणून त्यांना मडकेबुवा असे म्हणत. मुंबई प्रदेश शेड्यल कॉस्टचे फेडरेशनचे अध्यक्षपद त्यांनी बरीच वर्षे भूषविली. त्याशिवाय डॉ. बाबासाहेब आंबेडकरांनी इ.स. १९३४ मध्ये स्थापन केलेल्या. म्यूनिसिपल कामगार संघाचे ते सरचिटणीस म्हणूनही त्यांनी काम पाहीले होते. मडकेबुवा हे डॉ. बाबासाहेब आंबेडकरांचे अंगरक्षक म्हणूनही ते ओळखले जात असत. त्यांनी बाबासाहेबांच्या प्रत्येक कार्यात कृतीमय सहभाग दर्शविला. अशा कृतिमय कार्यकर्त्याचा मृत्यू २८ मार्च १९४८ रोजी मुंबई येथे झाला.

- कार्यसहभाग : <u>बदलापूर जिल्हा ठाणे श्री. शिवाजी उत्सवात सहभाग</u>

डॉ. बाबासाहेब आंबेडकरांना उत्सव कमिटीच्या सदस्यांनी श्री. शिवाजी उत्सवाच्या कार्यक्रमाचे अध्यक्षस्थान स्विकारावे अशी विनंती केली असता. त्यांच्या विनंतीला मान देवून डॉ. बाबासाहेब मुंबईहून उत्सवाच्या दिवशी दि. ३ मे १९२७ रोजी ४ वाजता मुंबईहून सिताराम नामदेव शिवतरकर रा. नाईक आणि रा. गणपत महादू जाधव या मंडळीवर बदलापूर येथे झाले.[५]

<u>मुंबई जाहीर सभेतील भाषण- ता. २३/५/१९२७</u>

रविवार रोजी संध्याकाळी ५ वाजता परळ पायबावडी येथे दामोदर हॉलच्या मागील गोविंद मोकाशी येथील गावकऱ्यामार्फत महाड प्रकरणाचा विचार विनिमय करण्यासाठी सर्व अस्पृश्य वर्गाची जाहिर सभा सोसल सर्व्हिस लिगचे प्रमुख कार्यकर्ते श्री. गंगाधर निळकंठ यांच्या अध्यक्षतेखाली भरली होती. या सभेत गणपत बुवा जाधव यांनी प्रसंगाला अनुसरुन परिणामकारक भाषण दिले.[६]

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[illegible] घराण्यातील स्त्रियाचे लोकोपयोगी व [illegible]जनिक हिताची कामे - एक दृष्टिक्षेप

प्रा. डॉ. रमेश धनराज जाधव
इतिहास विभाग प्रमुख,
[illegible] पटेल कला, वाणिज्य व विज्ञान महाविद्यालय शिरपूर,
जि. धुळे

****

[illegible]

[मराठा] घराण्यातील स्त्रियांनी अनेक लोकोपयोगी व [illegible] हिताची कामे केलेली दिसून येतात. त्यांनी देखील मंदीर [illegible] मंदीराची डाकडूगी करणे यासाठी खर्च केलेला दिसून [illegible] सरदारांनी देखील अशा स्वरूपाची मंदीरे बांधलेली [illegible] येतात. देवालये, घाट इत्यादी बांधण्यावर पेशवे, त्यांचे [illegible] यांनी बराच खर्च केलेला आढळतात. मराठा सरदारांच्या [illegible] शिंदे, होळकर व भोसले घराण्यातील स्त्रियांनी मंदीरे [illegible] बांधण्यात त्यांनी मोठा सहभाग घेतल्याचे दिसून येते.१

[illegible] -

१. मराठा घराण्यातील स्त्रियांच्या धार्मिक जीवनावर प्रकाश [illegible].

२. मराठा घराण्यातील स्त्रियांच्या लोकोपयोगगी कार्याचा [illegible] घेणे.

३. मराठी कालीन सार्वजनिक हिताच्या कार्यात मराठा [illegible]या योगदानावर प्रकाश टाकणे.

[illegible] विवेचन -

छत्रपती शाहू महाराजांनीही राज्यकारभार करतांना [लोको]पयोगी कार्याला त्यांनी प्राधान्य दिलेले दिसून येते. छत्रपती [शाहू म]हाराजांनी आपल्या राज्यात देवालय, वापीकूप, तयार केलेले [दि]सून येतात. तसेच ठिकठिकाणी झाडी लावून फुले झाडे लावण्याची [शाहू] महाराजांनी खास करून आवड होती. त्यांनी विविध ठिकाणी [फु]ल झाड्यांची रोपे लावण्यासाठी मागविलेली दिसून येतात. त्यावरून [त्यां]ची फुलझाडे लावण्याची त्यांची आवड लक्षात येते.२ [शाहू]महाराजांनी त्यांच्या कारकिर्दीत ब्रम्हेंद्रस्वामींचे म्हणणे त्यांना मनापासून पसंत होते. त्यांनी जागोजागी देवालये बांधली आणि जवळजवळ साडे आठ लक्ष रुपये खर्च केला होता. देवालयाप्रमाणेच घाट, तळी बांधणे, तलाव बांधणे यासाठीही मराठा सरदारांच्या स्त्रियांनीही खास लक्ष दिलेले दिसते. करवीरकर राजमाता जिजाबाई यांनी कसबा पेठेतील गणपतीचे मंदीर बांधल्याचे कागदोपत्री दिसते.३ राजमाता जिजाबाईची संस्कृती जोपासण्याची परंपरा [illegible] घराण्यातील स्त्रियांनी पुढे चालवलेली आढळून येते. महाराणी ताराबाई यांच्या कारिकिर्दीत त्यांनी अशी खबरदारी घेतली होती की, धार्मिक स्थळांना सैन्याकडून कोणत्याही स्तराचा उपद्रव पोहचू नये. लोकांच्या धार्मिक भावनांचा आदर राखून त्यांनी अशी खबरदारी घेतली होती की, कोणत्याही देवस्थानास कोणताही उपसर्ग होऊ नये मराठ्यांच्या काळात अशा कर्तबगार मराठा स्त्रियां आणि त्यांचे मालीकाच होऊन गेलेली दिसते. त्यात राजमाता जिजाबाई, महाराणी ताराबाई, करवीरची जिजाबाई अशा अनेक स्त्रिया धार्मिक वृत्तीच्या होत्या. त्यात अहिल्याबाई होळकरांचे स्थान [illegible] आहे. मराठा घराण्यातील अनेक स्त्रियांनी समाधी, वृंदावन व देवालय यांची देखरेख करुन पूजा-अर्चा करण्यासाठी त्या देवस्थानांना [illegible] आढळून येते. शाहू महाराजांची राणी सगुणाबाई हिने मौजे माहुली समंतनिबे येथे शाहू महाराजांच्या समाधीची देखरेख व पूजा करण्यासाठी काही जमीन इनाम दिली होती.४ करवीरकर जिजाबाईचा अशा धार्मिक कार्यात बराच सहभाग असल्याचे [illegible] त्यांनी छत्रपती संभाजी महाराजांची समाधी [illegible] व तेथे मठाचीही स्थापना केली होती. त्या मठाच्या परिसरात साधु, संन्यासांना आपले कार्य [illegible] यासाठी जिजाबाईनी त्यांच्या निवासाची व भोजनाची व्यवस्था केलेली दिसून येते.५

मंदीरांचा जीर्णोध्दार करण्यात मराठा सरदार घराण्यातील स्त्रिया या अग्रेसरच राहिल्या आहेत. त्यांनी अनेक मंदीरांचा जीर्णोध्दार केल्याची नोंद ऐतिहासिक कागदपत्रावरून दिसून येते. महाराणी ताराबाई हिने तर, [illegible] येथील मंदीराचा जिर्णोध्दार केलेला दिसतो ६ अशा मंदीरांचा जिर्णोध्दार [illegible] कारवाया व लष्करीकृत्य या काळात लोकांच्या धार्मिक भावनांची जोपासना करणे अधिक महत्वाचे होते. त्यांची धार्मिक श्रध्दास्थाने जोपासले जाणे गरजेचे होते.

वाहतुकींच्या साधनांसाठी उत्तेजन :

मराठा घराण्यातील स्त्रियानी धार्मिककृत्याबरोबरच त्यांनी तत्कालीन वाहतूकीची साधने यांच्यासाठी लोकांना उत्तेजन दिलेले दिसते. छत्रपती शाहु महाराजांची राणी विरुबाई हिने साताऱ्याकडून

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महाराष्ट्रातील वृत्तपत्रांचा उदय आणि स्वातंत्र्य आंदोलन काळातील मराठी वृत्तपत्रे

प्रा. डॉ. रमेश धनराज जाधव
इतिहास विभाग प्रमुख,
आर.सी.पटेल कला, वाणिज्य व विज्ञान
महाविद्यालय, शिरपूर जि.धुळे
jadhavramesh1969@gmail.com

प्रस्तावना :

वृत्तपत्रांना लोकशाहीचा चौथा स्तंभ म्हणून ओळखला जातो. मुद्रणकलेचा शोध 1439 मध्ये गटेनबर्ग याने लावला. भारतीय वृत्तपत्रांचा प्रारंभ युरोपियनांच्या आगमनाबरोबर झालेला आपणास दिसून येतो. भारतात मुद्रणाची सुरुवात गोव्यात झाली. भारतात वृत्तपत्रांचा प्रारंभ इंग्रजाच्या राजवटीत झाला. भारताप्रमाणे मुंबई प्रांतातील वृत्तपत्रांनी अत्यंत प्रतिकुल परिस्थितीतून वाटचाल केली आणि 19 व्या शतकात जी सामाजिक, राजकीय व सांस्कृतिक चळवळी उदयास आल्या. त्यात वृत्तपत्रांची भूमिका अत्यंत महत्त्वाची असलेली आपणास दिसून येते.1

उद्देश : 1) भारतातील वृत्तपत्रांच्या उदयासंबंधी माहिती मिळविणे.

2) मराठी वृत्तपत्रांच्या उदयासंबंधी माहिती मिळविणे.

3) स्वातंत्र्यआंदोलन काळातील मराठी वृत्तपत्रांची माहिती मिळविणे.

संशोधन पद्धती :

या शोधनिबंधाकरिता विश्लेषणात्मक संशोधन पद्धतीचा वापर केला असून उपलब्ध असणाऱ्या ग्रंथावरुन हा शोधनिबंध पूर्ण करण्याचा प्रयत्न केला आहे.

भारतात पहिले वृत्तपत्र सुरु करण्याच्या प्रयत्न ऑगस्टस हिकी याने इ.स. 1780 मध्ये The Bangal Gazette नावाचे वृत्तपत्र सुरु करुन ऑगस्टस हिलीने भारतीय वृत्तपत्र सृष्टीचा पाया रचला. परतु हिकीने ब्रिटीश अधिकारी आणि सरकारी यंत्रणेवर टिका केल्यामुळे इ.स. 1782 मध्ये त्याचा छापखाना जप्त करण्यात आला.2

त्यानंतर 1784 मध्ये Calcutta Gazette, 1785 मध्ये Bengal Journal अशा प्रकारे कलकत्ता, मद्रास आणि मुंबई अशा विविध शहरांमधून वृत्तपत्रे निघू लागली.3

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लोकशाहीत प्रसार माध्यमाची भूमिका

प्रा.रामसिंग आर.वसावे
राज्यशास्त्र विभाग,
आर.सी.पटेल कला, वाणिज्य व विज्ञान महाविद्यालय, शिरपूर जि.धुळे

प्रस्तावना :

लोकशाही आणि प्रसार माध्यमांचा जवळचा संबंध आहे अथवा परस्परपूरक आहे. प्राचीन काळापासून आधुनिक काळापर्यंत समाजात प्रसार माध्यमांनी स्वत:ची वेगळी अशी छाप उमटवली आहे. फरक एवढाच आहे की, प्रत्येक कालखंडात प्रसार माध्यमामध्ये बदल होत राहिला. जनसंवादाची भूमिका मात्र सारखी दिसून येते. आधुनिक काळात वैज्ञानिक प्रगतीने प्रसार माध्यमात क्रांतीकारक बदल घडवून आणले आहे. त्यामुळे जगातील सर्व देश जवळ आल्याचे जाणीव होते. राजकीय दृष्टीने विचार केल्यास असे दिसून येते की, प्रसार माध्यमानी लोकशाहीत जनमत तयार करण्यासाठी महत्वाची भूमिका बजावली असल्याचे दिसून येते. कोणत्याही देशात ज्यावेळी शासनसंस्थेनी व्यक्तीच्या जीवनात अथवा अधिकारावर आक्रमण करण्याचा प्रयत्न केला आहे अशा वेळी शासनाच्या विरोधी प्रसारमाध्यमांनी जनमत संग्रहीत करून शासनाला चांगल्या मार्गावर चालण्यास भाग पाडले आहे. म्हणूनच प्रसार माध्यमांना बर्क चौथी सत्ता म्हणून उल्लेख करतात.

संशोधनाचे महत्त्व :

लोकांच्या तंत्रानुसार काम करणारी व्यवस्था म्हणजे लोकतंत्र अथवा लोकशाही होय. लोकशाहीचे लोकांच्या अभ्यासपूर्ण सहभागावर अवलंबून असते. लोकांपासून माहिती हेतूत: लपवून ठेवली जात असेल तर राजकीय प्रक्रियेच्या संदर्भात लोक उदासीन होऊन त्याचा विपरीत परिणाम लोकशाहीवर होतो. ज्या देशात प्रसार माध्यमाची साधने मुक्त असतात आणि विचार व अभिव्यक्ती स्वातंत्र्य असते. त्याठिकाणी लोकसहभाग मोठ्याप्रमाणात वाढतो परिणामत: लोकशाही यशस्वती होते. म्हणूनच लोकशाहीत प्रसार माध्यमाची भूमिका महत्वाची ठरते. आधुनिक काळात लोकशाहीमध्ये श्राव्यमाध्यम, दृक-माध्यम, लिखीत माध्यम, दृक-श्राव्य माध्यमांचा जनतेवर जास्त प्रभाव दिसून येतो. प्रसारमाध्यमे कमी वेळात जास्त क्षेत्रात जनतेला प्रभावीत करीत असततात. प्रसारमाध्यमांमुळे साक्षर-निरक्षर, युवापिढी-वयस्क, महिला-पुरूष, शहरी-ग्रामीण हे सर्व वैचारिकतेने प्रभावीत होतात. अमेरिकासारख्या देशात प्रसार माध्यमांवर शासनाचे नियंत्रण कमी आहे. अशा ठिकाणी लोकशाहीत स्वास्थ लोकमत निर्माण होण्यास मदत होते.

संशोधनाचा उद्देश :

१) लोकशाहीत राजकीय सामाजिकरण प्रसार प्रसार माध्यमाचे स्वरूप स्पष्ट करणे.
२) लोकशाहीत लोकमत निर्मितीत प्रसारमाध्यमाचे विश्लेषण करणे.

गृहीतके :

१) लोकशाहीत प्रसार माध्यमे लोकमत घडविण्यात महत्त्वाची भूमिका बजावली आहे.
२) लोकशाहीत राजकीय सामाजिकरणात प्रसार माध्यमाची भूमिका महत्वाची आहे.

संशोधन पद्धती :

प्रस्तुत शोधनिबंधासाठी दुय्यम साधनाचा वापर केला असून विश्लेषणात्मक पध्दतीचा वापर केला आहे.

ऐतिहासिक पार्श्वभूमि :

भारतीय स्वतंत्र संग्रामात ब्रिटीश राजवटीविरूध्द भारतीय जनतेस स्फूर्ती व उत्साह निर्माण करण्यात प्रसार माध्यमाची भूमिका निर्णायक राहिली आहे. जी.सुब्रमण्यम अय्यर संपादित 'हिंदू', बाल गंगाधर टिळक संपादित 'केसरी व मराठा', सरेंद्रनाथ बॅनर्जी संपादित 'बंगाली', शिशिर कुभार घोष संपादित 'अमृत बाजार पत्रिका', एन.एन. सेन संपादित 'इंडियन मिरर', दादाभाई नौरोनी संपादित हिंदूस्थानी तसेच पंजाबमध्ये दि ट्रिब्यून व अखबार-ए-आम तर बंगालमध्ये 'इंद्रप्रकाश', 'बंगवासी' आदि प्रसार माध्यमानी ब्रिटिश राजवटी विरूध्द भारतीय जनतेचा आवाज बुलंद केला. या प्रसार माध्यमाचा वाढता प्रभाव पाहून ब्रिटिश राजवटीने १८७० मध्ये भारतीय दंड संहिता धारा १२४ नुसार भारतात या कायद्याद्वारे स्थापीत ब्रिटिश राजवटी विरोधी भावना भडकविणाऱ्या व्यक्तीला तीन वर्षे कैद शिक्षेपासून आजीवन देशातून बाहेर हाकलण्याची शिक्षेची तरतुद केली. १८७४ मध्ये ब्रिटिश सरकारने वर्नाकुलर प्रेस ॲक्ट पास करून या कायद्याद्वारे सरकारला वर्तमानपत्र व प्रेस साधनसामग्री जप्त करण्याचा अधिकार मिळाला. टिळकानी ब्रिटिश राजवटीच्या या कायद्याविरोधी जोरदार विरोध केला तर दादाभाई नौरोजीने ब्रिटिश प्रशासनाची निर्दयी पध्दत्तीने प्रेसचा गोळा दाबण्याची ही पद्धत आत्मघाती ठरेल असे स्पष्ट केले.

स्वातंत्र्योत्तर काळानंतर सर्व देशवासीयानी प्रसर माध्यमाचे महत्त्व ओळखून आपल्या जीवनात महत्त्वपूर्ण स्थान दिले. संविधानाच्या मूलभत हक्कांमध्ये अप्रत्यक्ष व्यवस्था करून संविधानाच्या कलम १९(१) नुसार प्रत्येक भारतीय नागरिकाला विचार तथा अभिव्यक्ती स्वातंत्र्य दिले असून त्याला संरक्षणही दिले आहे. त्यामुळे भारतात प्रसारमाध्यमाचे स्थान, नागरिकांचे अधिकार अधिक मजबूत होण्यास मदत झाली आहे. आधुनिक युगात ज्ञान, माहिती, संपर्क आणि प्रचार प्रसार माध्यमातून जास्तीत जास्त कल्याण साधण्यासाठी, सर्व समुहातील घटकाना परस्पर जोडून परस्परांमध्ये विश्वासर्हता निर्माण करण्याबरोबरच सामुहिक विकासाला योजना शेवटच्या घटकांपर्यत पोहचविण्यात आणि सामाजिक शिक्षण देण्यास लोकशाही शासनप्रणाली अधिक बळकट करण्यासाठी प्रसार माध्यमांनी भूमिका

महत्त्वपूर्ण राहिली आहे.

लोकशाहीत लोकमत निर्मितीत प्रसार माध्यमांचे महत्त्व :

आजच्या आधुनिक काळात लोकमत घडविणारे अत्यंत प्रभावी माधने म्हणून प्रसार माध्यमांचा उल्लेख केला जातो. कागदाचा शोध लागल्यापासून वृत्तपत्रे हे लोकशाही राजकीय व्यवस्थेमध्ये अत्यंत महत्त्वाचे घटक म्हणून मान्य पावल्यामुळे ते एक प्रभावी माध्यम ठरले आहे. त्याचबरोबर आधुनिक वैज्ञानिक तंत्रज्ञान सामाजिक प्रसार माध्यमांचा प्रभावही लोकमत निर्मितीत महत्त्वपूर्ण ठरत आहे. व्यक्ती स्वातंत्र्याचा संकल्पनेला मूर्त स्वरूप देण्यामागे प्रसार माध्यमांनी बजावलेली भूमिका अभूतपूर्व अशी आहे. सामान्य माणसापर्यंत जलदगतीने सर्वदूरपर्यंत व स्वस्त दराने घटना, घाडामोडी, माहिती आणि विचार पोहचवणारे महत्त्वाचे माध्यम आहे. गुलामगिरी आणि पारतंत्र्यातून स्वातंत्र्य मिळविण्याची चळवळ असो की, सामाजिक परिवर्तनाचा लढा असो. आजच्या मानवाच्या सर्वांगीण जीवनाला दिशा देणारे, वैयक्तीक आणि सामुहिक प्रगतीसाठी उपयुक्त ठरणारे प्रसारमध्यमे अतिशय महत्त्वाचे ठरलेले आहे. स्थानिक घडामोडीपासून ते आंतरराष्ट्रीय पातळीपर्यंत सर्व प्रकारच्या माहितीचे केंद्र म्हणून प्रसार माध्यमे उपयोगी पडतात. प्रसारमाध्यमे केवळ माहितीच देतात असे नाही तर विचारही देतात. त्यामुळे आपले मत बनू शकते व लोकशाहीला पोषक वातावरणाची निर्मिती होते.

लोकशाहीत राजकीय समाजिकरणास प्रसार माध्यमांचे महत्त्व:

लोकशाहीत राजकीय सामाजिककरणाच्या प्रक्रियेत प्रसार माध्यमांची म्हणजेच वृत्तपत्रे, आकाशवाणी, टि.व्ही. व अन्य माध्यमे याची भूमिका महत्वाची आहे. जनमतावर या माध्यमाचा सतत प्रभाव पडत असतो. सर्व माध्यमातून निरनिराळे कार्यक्रम, बातम्या या सर्वांना बहुतेकवेळी राजकीय संदर्भ असतो. या संदेशातून जनतेचे राजकीय सामाजिकरण होत असते. आधुनिक काळात लहान मुले व युवापिढी यांच्या जीवनाचा प्रसार माध्यमे अविभाज्य भाग बनला आहे. दृक-श्राव्य माध्यमाच्या कार्यक्रमातून अनेक प्रकारची माहिती त्यांना मिळते. या माध्यमाचा परिणाम फार मोठा असतो. कारण पाहिलेले आणि त्यावेळी एकलेले सत्य मानण्याची सर्वसामान्यपणे प्रवृत्ती असते. भारतात दूरदर्शन आणि आकाशवाणी ही माध्यमे सरकारी मालकीची आणि नियंत्रणाखाली आहे. त्यामुळे केंद्रात सत्तेवर असलेल्या पक्षाला झुकते माप मिळते. सत्ताधारी पक्षाविषयी अधिक बातम्या, कार्यक्रम इत्यादींची रेलचेल असते. वृत्तपत्रे ही फक्त साक्षर जनतेपुरतीच मर्यादित असते. त्याचा खप समाजाच्या मध्यम व वरच्या वर्गापुरताच असतो. पाश्चिमात्य वृत्तपत्राप्रमाणेच भारतीय वृत्तपत्रे मत घडवीत असतात. वाचकाच्या राजकीय मते व दृष्टीकोण वृत्तपत्राच्या प्रभावाखाली व बातम्याच्या ब्रकींग न्युज ज्या प्रभावाखाली बदलत असतात. सर्वच राजकीय पक्ष व त्यांचे नेते वृत्तपत्रे वाचकाना नवी दृष्टी देतात. यात अग्रलेख विशिष्ट लेख, छायाचित्रे, व्यंगचित्रे याचा परिणामकारक वापर केला जातो. नेत्याना मोठे करणे अथवा त्यांची कुंडली बाहेर काढून त्यांना नामोहरण करणे हे प्रसारमाध्यमे करू शकतात. नेत्याची राजकीय उन्नती वा अवनती अनेकदा प्रसार माध्यमावर अवलंबून असते. भारतात स्वातंत्र्यापूर्वी वृत्तपत्र या प्रसार माध्यमांनी स्वातंत्र्य चळवळीला सतत पाठिंबा दिला. स्वातंत्र्योत्तर काळातही प्रसार माध्यमानी लोकशाही रक्षणाचे काम चोखपणे पार पाडले आहे. आपल्या राजकीय लिखाणात भारतीय प्रसार माध्यमांनी सत्ताधीश नेत्याना उघडे पाडले आहे. केंद्रीय व राज्यशासनाच्या चुकीच्या धोरणावर कडाडून हल्ले चढविले आहेत. या त्यांच्या कार्यमुळेच केवळ निर्भीड, लढाऊ प्रसारमाध्यमांचे दर्शन घडतेच असे नाही तर भारतीय लोकशाही सुदृढ व सुयोग्य होण्यासाठी मदतही झाली आहे. प्रस्थापितांच्या व सत्ताधीशांच्या विरोधात प्रसार माध्यमांनी निर्भीयपणे कामे केली आहे.

लोकशाहीत प्रसार माध्यमे जनसंपर्काची महत्त्वाची साधने :

आधुनिक काळात शासन व प्रशासन आणि जनता यामध्ये प्रसार माध्यमे जनसंपर्काची महत्त्वाची साधने म्हणून उल्लेख केला जातो. प्रशासकीय कार्याबद्दल जनतेला माहिती देणे व जनतेच्या त्या विषयी असणाऱ्या भावना, मन विचार समजून घेणे हे आधुनिक प्रशासनाचे लक्ष्मण मानले जाते. जनतेला शासकीय ध्येयधोरण, निर्णय व कार्यक्रमाची माहिती टिव्ही, रेडिओ, वृत्तपत्रे इंटरनेट, जाहिरात या संसूचन माध्यमाद्वारे दिली जाते तसेच जनतेच्या अडचणी समस्या शासनाला प्रसार माध्यमाद्वारे कळतात. त्यामुळे जनतेची नाराजी दूर करून विश्वास संपादन करण्याचे कार्य प्रसार माध्यमे करीत असतात. लोकशाही राज्यात जनहिताच्या दृष्टीने प्रसार माध्यमे महत्त्वाची भूमिका बजावत असते.

समारोप :

प्रसार माध्यमे ही लोकशाही शासनप्रणालीचे अविभाज्य घटक आहे. म्हणूनच लोकशाहीची चौथी सत्ता म्हणून प्रसार माध्यमांकडे लक्ष वेधले जाते. फक्त प्रसार माध्यमांनी स्वतंत्र राहून लोकशाहीत आपली भूमिका पार पाडली पाहिजे. विशिष्ट पक्ष अथवा सरकारची प्रतिमा बनून प्रसार माध्यमे काम करू लागलीतर लोकशाहीत प्रसार माध्यमाची भूमिका नाकारली जाऊ शकते म्हणूनच प्रसार माध्यमाच्या अभावामुळे कोणत्याही समाजाला आधुनिक समाज अथवा लोकशाही समाज सांगणे कठीण आहे. आधुनिक काळात प्रेस, रेडिओ, टि. व्ही.व इतर अन्य प्रसार माध्यमे हेच समाजाला लोकशाही समाजाकडे घेऊन जात आहे.

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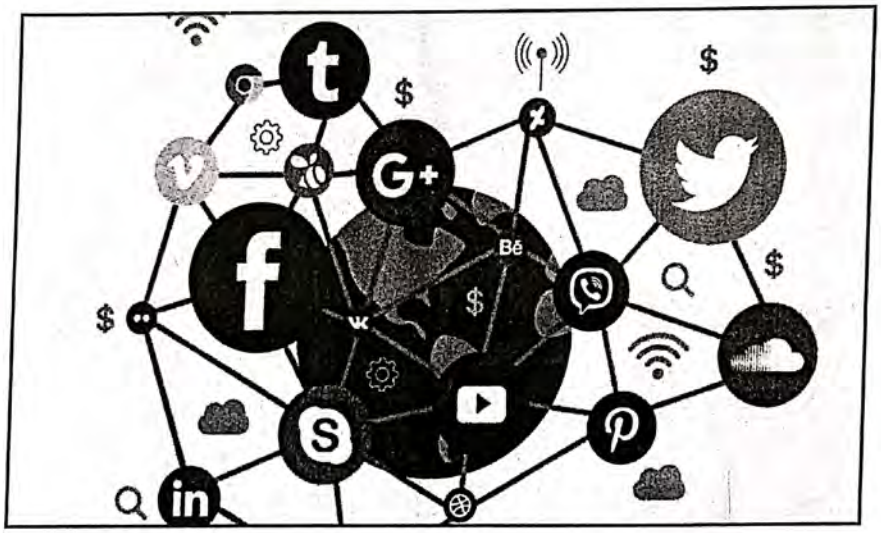

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A Study on Impact of Social Media inTourism Business Development

Dr. Anil Gambhirrao Sonawane
Associate Professor,
R. C. Patel Arts, Commerce & Science College,
Shirpur, Dist. Dhule

Mr. Yogesh C. Shethiya
Assistant Professor,
R. C. Patel's I.M.R.D.,
Shirpur, Dist. Dhule

Abstract:

The media are playing in the variety of feature of life is becoming progressively more greater day by day, mainly in subject like social interaction, and cultural and educational feature of our life. The significance of social media is upward in the area of the tourism industry. To a greater extent researchers are undertaking studies in the areas of the impact of social media on the tourism industry. Aspire of this study is to recognize this upward importance media in the tourism business and to appreciate the impact of media in the tourism. The rationale is to understand the future role of media in the years to come on the tourism business so that it benefits the tourism business and the tourists internationally. The leveraging of media to the tourism products has show to be a good strategy in improving not only the quality of the trade but also the revenues of the tourism business at large. In this world of steady technological development, tourists are varying their behaviour patterns seem to be for more "tourist-friendly" resources of information. Thus this research paper focuses on the collision of media in promoting tourism business globally.

Keywords : Social Media, Tourism, Business, GDP, Development.

Introduction :

UNWTO defines tourism as "a social, cultural and economic phenomenon, which entails the movement of people to countries or places outside their usual environment for personal or business/professional purposes" The tourism business is one of the fastest increasing sectors in the world. In reference to Pforr and Hosie (2009), the tourism business is the major in the world with a significant annual growth rate of approximately 25 percent. In this look upon, Alsos, Eide and Madsen (2014) study that the growth rate of the tourism business in Organization for Economic Co-ration and Development (OECD) nation has go over the enlargement rate of their GDP.

Social media pass on to the resources of communications among community in which they share, make, or swap over information and thoughts in virtual group of people and association. In today's times social media plays an extremely significant role in almost every section. Platforms such as Facebook, Whatsapp, Twitter, Instagram etc. have become vital both from individual and trade point of view. Social media has made a massive impact on the tourism business. Tourist engages with social sites in order to make up to date decisions regarding their travels and share their own experiences which they had at a particular hotel, restaurant or airline. The tourism business is in position to take benefit of social media channel, as the business has long relied for the most part on target repute, tourist opinion, spread of information, and positive word-of-mouth publicity. In many examples, for example the case of the 'Bharat Darshan' campaign and 'Incredible India' campaign, incorporation of social media into the marketing approach of Indian Tourism has shown incredible, considerable outcome in greater than before rates of visits as well as visitor happiness. As a outcome, a variety of states around the nation are appropriate more dependent on social media as a cost-efficient and successful tool for visiting the attractions promotion for their particular state.

Need for the Study :

Global and domestic tourism business contributes more to India's GDP. Foreign exchange earnings from tourism stood at $16.757 billion between January and July 2019, as against $17.059 billion in the corresponding period last year, posting a -1.8% growth vis-à-vis a 12.1% surge last year, according to data from the ministry. In this competitive world media plays a vital role in all business. There is main purpose that this study will take in hand to the extent that the role of social media in the tourism business is concerned. To start with, the study will assess how both existing and probable tourists use social media stage to make travel decisions. In this study will seek to understand how tourists utilize diverse types of social media to research and plan their travel behavior.

Objectives :

1. To know the understanding of social media approach in tourism business.
2. To observe the role and impact of social media promotion approach in tourism business.
3. To understand the increase in revenues of the tourism business.

Research Methodology :

To enter at research result that strictly answer the research questions and as a result, meet the objectives of the study, there is a need to make use of a precise methodology. Speaking from this viewpoint, the study first explores the past research and study findings on how social media has been used in the past in tourism promotion. Likewise, the research use primary data to either affirm or dispute the secondary research findings. In this study will carry out an observation and discussion to collect primary data. This data will be prearranged and analyzed using different statistical tools to conclude whether it supports or be against the secondary research findings.

Review of Literature :

Tourism business plays an incredibly vital role in economic growth and structural revolution of the world. Indian tourism is based on the concept of 'Atithi Devo Bhav' and 'Vasudev Kutumbakam'. It means the guests will be treated as equal as god and it also means that welcome tourist friendly and send back a friend.

The literature on different aspect of blow of tourism on financial system a brief review of existing literature on diverse aspects of tourism will be made in this section. Sethi A S, B P Singhal (2016) in a research paper entitled "Identification of factors affecting Tourism destination competitiveness: A Study in Uttarakhand" made an attempt to classify the factors that affect tourism destination competitiveness for the state of Uttarakhand. In the recent year's tourism as an business has developed many fold up in terms of employment prospect and income generation. Uttara Khand as a tourism destination has received its share of domestic and internationals guests but still a long way to go before suitable a priority tourism destination.

Zach F (2016) in a research paper "Collaboration for Innovation in Tourism Organizations" aimed to tackle the gap by examining the role and effect of key drivers of managerial surroundings for innovation (leadership support, innovation formality) and inter managerial relations (leadership support, communication) on association for innovation. The value added by the study was twofold: First, it has evaluated the organizational settings simultaneously and accounts for their interdependencies; and second, it has investigated the largest group of tourism organizations.

Sahin & Sengün (2015) did a study and investigated the importance of social media in tourism marketing. The study they did was based on a survey implemented on the students of Atilim University evaluating the effects of social media among young generation. Results of the survey showed that social media has a significant influence in tourism sector both in positive and negative ways. The results also showed that the the tourism decisions of young generation gets strongly affected by personal experiences and comments of other users on social media

Gupta D, Thind S (2014) in the research paper entitled "Changing Geographies of International Tourist Patterns" has converse regarding the distraction in tourist geographical area with change in income. Tourism has appeared as one of the strongest and the most responsive mechanism in the service business in the last two decades. New destinations have emerged on the map of the world whereas, old has been unable to keep hold of their position. The share of income generated by the tourism sector has changed not only temporally but spatially as well. Central Eastern Europe and North China has emerged as new destinations for global tourists while Northern Europe has lost its share of international tourists. Therefore, looking at the spatio-temporal changes in the share of international tourist arrivals the paper attempted to analyse the spatio-temporal variations in international tourist arrivals internationally and regionally.

(Hvass & Munar, 2012) Online promotion has developed in significance in the tourism business over the years. Social media allows companies to interact directly with tourist via various online platforms. It also allows companies to monitor and interact with tourist. But when we talk of Airlines, It is shown that there is a lack of strategic viewpoint of social media as it is being used with limited uniformity.

Analysis of Study :

Table 1 showing the Foreign Tourist Arrivals in India

Year	Foreign Tourist Arrivals (in Millions)	Year	Foreign Tourist Arrivals (in Millions)
2001	2.54	2010	5.78

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2002	2.38	2011	6.31
2003	2.73	2012	6.58
2004	3.46	2013	6.97
2005	3.92	2014	7.68
2006	4.45	2015	8.03
2007	5.08	2016	8.80
2008	5.28	2017	10.04
2009	5.17	2018	10.56(P)

(P) Provisional, Figures updated as in August, 2019 R: Revised,
Source: Bureau of Immigration, Govt. of India

Table 2 showing the growth of tourism in India on 2018

Sr.No.	Particular	Result
1	No. of Foreign Tourist Arrivals in India	10.56 Million (P)
	Annual Growth Rate	5.2%
2	No. of Indian Nationals Departures from India	26.30 Million (P)
	Annual Growth Rate	9.8%
3	No. of Domestic Tourist Visits to all States/UTs	1854.9 Million(R
	Annual Growth Rate	11.9%
4	Estimated Foreign Exchange Earnings from Tourism In INR terms	`1,94,892 Crore
	Annual Growth Rate	9.6%
5	Share of India in International Tourist Arrivals	1.24%
6	India's rank in World Tourist Arrivals	25th
7	India's rank in World Tourism Receipts	13th

(P) Provisional, Figures updated as in August, 2019 R: Revised,
Source: Bureau of Immigration, Govt. of India

The role of social media in tourism has been progressively more prominent and investigates as a rising subject. Over the years Social media have contributed towards significant tourism into a responsible business .Social media plays a progressively more vital role in many features of tourism, particularly in information investigate and decision-making behaviours and tourism advertising spotlight on most excellent apply for cooperate with tourist via social media channels. A social media to market tourism products has proved to be an admirable policy. Many nations observe social media as a vital means to encourage for their tourism business.

Conclusion :

Based on research study and the literature review, it can be conclude that, the social media phenomenon represents an ongoing trend. The social media plays an important role in Tourism business. From information investigate to decision making behaviors social media plays a vital role in many characteristic of tourism business. Social media also plays a significant role in tourism advertising and facilitates the tourism service suppliers in spotlight on best practices during the response they obtain from tourists and community via social media. Social Media has been commonly acknowledged as a resource of advance tourism goal and products by popular target promotion organizations. As a result of the studies on the subject of social media it is expanding tool for the upgrading the tourism business and also for the benefits of the country's GDP.

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