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Tapping the Potential of Traditional Knowledge Associated with Medicinal Plants of Tribal Communities in Central India: Perspective and Avenues

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Summary

India is known to have over 700 scheduled tribes which are native to five different regions viz., Himalayan, Central, Western, Dravidian and islands, each having its own primitive trait and cultural distinction. Out of these diverse territories, Central Indian region has the distinction of hosting 55% of the total tribal population of India which provides diverse region for bioprospecting. This region provides a natural, invaluable store house of indigenous medicinal plant diversity that is of great importance for mankind. Protection of traditional knowledge of these tribal communities residing in central India is the need of hour as overexploitation of natural resources due to increase in population may lead to extinction of important medicinal plant species. With careful management of the natural resources a sustainable balance can be achieved. The review envisages providing baseline data on important tribal communities and their status, traditional knowledge, medicinal properties of native plants of tribals and gives an insight for exploitation of these plants by pharmaceutical industry as well as insilico approach for screening new active compounds and drug designing.

Key Words: Tribes, Traditional Knowledge, Antimicrobial activity, Insilico approach

Introduction

Tribals are the native inhabitants of a geographically isolated region living close to nature. They are economically backward and culturally isolated and cater their basic necessities from the forests. They have distinct religious practices and cultural belief systems that demonstrate an immense knowledge and regulate the use of natural resources. According to 2001 census, India is known to have over 700 scheduled tribes (STs), each having its own primitive trait and cultural distinction [1]. Tribals in India live in the following five territories: (i) The Himalayan belt: (Assam, Meghalaya, Arunachal Pradesh, Nagaland, Manipur, Mizoram, Tripura, hills of Uttar Pradesh and Himachal Pradesh) (ii) Central India: Bihar, West Bengal, Orissa, and Madhya Pradesh (iii) Western India: Rajasthan, Maharashtra, Gujarat, Goa, Dadra and Nagar Haveli. (iv) The Dravidian region: Karnataka, Andhra Pradesh, Kerala and Tamil Nadu. (v) Andaman, Nicobar and Lakshadweep islands [2]. 55% of the total tribal population of India lives in Central region. Certain primitive tribal region of central India are still beyond reach providing undisturbed natural niches where tapping of various medicinal plants can offer new insights for development of natural products. In India, about 95% of medicinal plants are obtained from wild sources and only 150 species are commercially utilized [3]. The indigenous knowledge of the tribal people of these medicinal plants are only identified, catalogued and documented, ie., only ethnobotanical studies are carried out for tribal regions. Medicinal plants are now being used as an alternative source to derive new antimicrobial compounds. The bioactive constituents of these medicinal plants that are of chemical nature can be studied and the chemical structure of a these bioactive compound and its biological properties can help in rational drug design. Different computational approaches have enhanced our understanding of interaction between proteins and chemical compounds which has facilitated the development of drug design [5]. Hence, the present review aims to discuss about various tribal communities of Central India, its status, their traditional knowledge, important novel medicinal plants of tribal region and their uses by validation of its pharmacological effects to produce novel drug entities.

Demographic Status of Tribals in India

According to the 1991 census, the population of STs in the country was 67.8 million constituting around 8% of the total population, whereas according to 2001 census the population of schedule tribes in the country was 84.3 million constituting around 8.2% of the total population. Decadal growth of 24.45 % of tribal population had been observed.

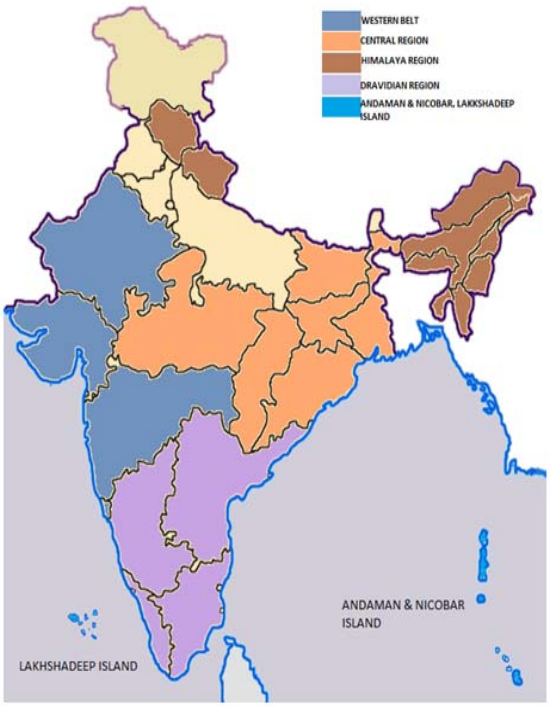

Figure 1: Tribals residing in five territories of India

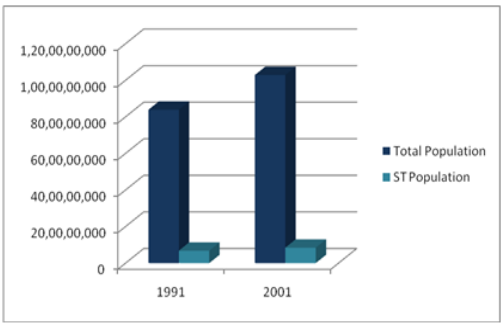

Figure 2: ST Population with respect to Total Population according to 1991 and 2001 Consensus

Status of Tribals in Central India

Largest tribes are found in central region belt, over half the tribal population is concentrated in five states shown in table 1. In the year 1991, Madhya Pradesh accounted for 23% and Bihar 9.7% of the total tribal population in the country but in the year 2001 Madhya Pradesh along with Chhattisgarh accounts for 22.36% and Bihar along with Jharkhand 9.3% of the total tribal population in the country.

Table 1. ST Population in Different States of Central India

ST Population in different states of Central India	1991	2001
Madhya Pradesh (Madhya Pradesh + Chhattisgarh)	15.4 million	18.8 million
Bihar (Bihar + Jharkhand)	6.6 million	7.8 million
Orissa	7.0 million	8.1 million
Andhra Pradesh	4.2 million	5.0 million
West Bengal	3.8 million	4.4 million

The sex ratio among Scheduled Tribes is more favorable than general population, at 977 females per thousand males. Literacy rate has also increased from 8.53 percent in 1961 to 47.10 percent in 2001 for STs while the corresponding increase for total population was from 28.30 percent in 1961 to 64.84 percent in 2001, a significant increase in STs literacy rate can be observed. According to the 2001 Census figures, 44.70% of the ST population were cultivators, 36.9% agricultural laborers, 2.1% house hold industry workers and 16.3% were other occupation workers.

However there are still some tribals residing in about 2,474 identified forest villages in 12 States whose level of development is not at par with rest of the tribal villages. These states include Madhya Pradesh, Chhattisgarh, Jharkhand and Orissa of Central India consisting of 1362 forest villages. These also include particularly vulnerable tribal groups or primitive tribal groups characterized by a low rate of growth of population, pre-agricultural level of technology and extremely low level of literacy [1]. These communities are declining or stagnant and are economically backward and 75 such groups are recognized. List of primitive tribal of Central India is given in Table 2.

Table 2: Primitive Tribal Groups of Central India

State	Primitive Tribal Communities
A. Andhra Pradesh	Bodo Gadaba
	Bondo Poroja
	Chenchu
	Dongria Khond
	Gutob Gadaba
	Khond Poroja
	Kolam
	Kondareddi
	Konda Savaras
	Kutia Khond
	Parengi Poroja
	Thoti
B. Bihar (including Jharkhand)	Asurs
	Birhor
	Birjia
	Hill Kharia
	Korwas
	Mal Paharia
	Parhaiyas
	Sauria Paharia
	Savar
C. Madhya Pradesh (including Chhattisgarh)	Abujh Marias
	Baigas
	Bharias
	Hill Korbas
	Kamars
	Saharias
	Birhor
D. Orissa	Birhor
	Bondo
	Didayi
	Dongria-Khond
	Juangs
	Kharias
	Kutia Kondh
	Lanjia Sauras
	Lodhas
	Mankidias
	Paudi Bhuyans
	Soura
	Chuktia Bhunjia
E. West Bengal	Birhor
	Lodhas
	Totos

The Ministry of Tribal Affairs was constituted in October 1999 with the objective of providing more focused attention on the integrated socio-economic development of the most under-privileged sections of the Indian society, the Scheduled Tribes (STs), in a coordinated and planned manner [1]. The tribal majority areas, which overlap with the country's major forest areas, are also areas with the highest concentrations of poverty [6]. The most common diseases among tribal communities are parasitic infections, diarrhoea, dysentery, skin diseases, respiratory infections, whooping cough and measles.

Serious diseases such as tuberculosis, leprosy and malaria are also common [6].

Traditional Knowledge

Primitive forest dwellers with good forest cover, rely on their traditional herbal medicine practices and indigenous knowledge. Indigenous Knowledge (IK) can be broadly defined as the knowledge that an indigenous (local) community accumulates over generations of living in a particular environment. This definition encompasses all forms of knowledge – technologies, know-how skills, practices and beliefs – that enable the community to achieve stable livelihoods in their environment [2]. The term 'traditional knowledge' has been defined by the World Intellectual Property Office Inter- Governmental Committee (WIPO- IGC) as including 'indigenous knowledge relating to categories such as agricultural knowledge, medicinal knowledge, biodiversity-related knowledge, and expressions of folklore in the form of music, dance, song, handicraft, designs, stories and artwork which have generally been transmitted from generation to generation; are generally regarded as pertaining to particular people or their territory; and are constantly evolving in response to a changing environment [8, 9]. Traditional knowledge of the tribals is based on years of experience and provides guidance and solution for not only sustainable environment but also use of medicinal plants for the treatment of various diseases. According to the World Health Organization more than 80% of the world's population relies on traditional medicine for their primary healthcare needs [10, 11]. India is rich in medicinal plant diversity. All known types of agro-climatic, ecologic and edaphic conditions are met within India [12, 13]. India is rich in all three levels of biodiversity, as species diversity, genetic diversity and habitat diversity [12, 13]. These conditions enables the growth of almost 20,000 plant species, of which 2,500 are of medicinal value [14]. Humans largely depend on less than 9000 plant species for food, clothing, shelter, medicines, forages and industry, and around 1,200 herbal plants are mentioned in ancient Indian texts.[15, 16] Of these, about 900 species have been domesticated for agriculture and from these about 168 species are specifically cultivated for food and agriculture [17]. The indigenous knowledge is not only confine to its use and collection but also about their specific characteristics (toxicity palatability), their spatial distribution, seasonal availability and ecological relationship etc. [17]. Through indiscriminate exploitation, destruction of habitats a number of medicinal legumes have already disappeared while others await a similar fate, at times even without our being aware of their existence. The excessive exploitation from the nature has resulted in shrinkage of these plant species, while few are facing the threat of extinction. Their regeneration, protection and preservation in nature are a challenge today to restore our biological heritage [18]. Still the conservation and protection of these wildly growing medicinal legumes of tribal region has been overlooked. The Botanical Survey of India (established in 1890) and the Zoological Survey of India (established in 1916) are primarily responsible for survey of flora and fauna [16]. As suggested by Mairh et al, proper documentation of traditional ethnobotanical knowledge has not been done properly and the present era of globalization, traditional ethnobotanical information of the tribe is at stake of bio-piracy [17]. The most complex set of problems facing the future of traditional knowledge comes from the misappropriation of this knowledge from the local communities and tribal people who should be its rightful owners [16, 19]. Venkateraman in his review suggested that introduction of modern technologies and industrialization has lead to a gradual decline in these traditional knowledge, with key component being the introduction of intellectual property right (IPR) which was meant to protect innovators for novel product. However after being extended to the biological resources it does not provide protection for the traditional knowledge of the communities [16, 20]. The TRIPS Agreement also does not provide any specific mention about the traditional knowledge and innovations which are in the public domain. The grant of patents on non-original innovations (particularly, those linked to traditional medicines), which are based on what is already a part of the traditional knowledge of most of the developing and mega-biodiverse countries without their consent have been causing a great concern [16, 21]. Traditional knowledge is one of the most important source for sustainable development of developing countries in various fields like agriculture, food and medicine where biological resources are the main components. A wide array of natural products from botanicals are traditionally in use over several years [22]. According to World Health Organisation (WHO, 2000), medicinal plants would be the best source to obtain a variety of drugs and hence its important to study their properties, safety and efficacy [11, 23]. Government of Tribal Affairs has set up Multi-State Cooperative Society in 1987 under the Multi State Cooperative Societies Act, 1984 (now the Multi State Cooperative Societies Act, 2002) known as The Tribal Cooperative Marketing Development Federation of India Limited (TRIFED). TRIFED is now functioning both as a service provider and market developer for tribal products and it also looks after Research & Development / Intellectual Property Rights (IPR) of traditional knowledge.

Ethnobotanical Studies of Medicinal Plants of Tribals from Central India

Primitive tribals still residing in dense forest which are inaccessible and still not surveyed are expected to be rich repositories of endemic and other species [16]. Medicinal Plants are studied from these tribal region in more intensified way to promote the proper uses of herbal medicines and to determine their potential as source of new drugs, which have folklore reputation [24-28].

Ethnobotanical study attempts to underline intimate relationship between plants and ethnic tribes [17, 29]. There is a rich local ethnobotanical knowledge and bibliography describing the species most frequently used by population to cure various diseases [29]. It is also not associated with many side effects and have an enormous therapeutic potential to heal many infectious diseases [30, 31].

Many researchers have reported different medicinal plants from various regions which are being used by tribal communities for various therapeutic purposes. Ethnobotanical studies carried out on Birhore tribes of Bihar have reported varied plant species used by them depending on their day to day need. The description includes plant names, local name, family and usage [17]. Similarly documentation of 500 medicinal plant species from Gond and Bharias of Madhya pradesh have been carried out by Acharya and Rai [43].

Studies on khamptis tribe of Arunachal Pradesh recorded 37 plant species of ethnomedicinal value belonging to 29 families. However researchers have only provided information of various plants found in different regions without confirming its medicinal activities, hence there is no scientific basis of use of traditional and herbal medicines [15].

Antimicrobial Activity of Medicinal Plants

Many researchers have reported antimicrobial activity of various medicinal plants from various regions which is now being used as an alternative source for drugs. Bioactive compounds are normally accumulated as secondary metabolites in all plant cells but their concentration varies according to the plant parts, season, climate and particular growth phase. Leaf is one of the highest accumulatory plant parts of such compounds and people are generally preferred it for therapeutic purposes. Some of the active compounds inhibit the growth of disease causing microbes either singly or in combination [32]. They can inhibit the growth of microbes by binding their surface proteins, breaking the peptide bonds, acting as chelating agents, altering their biochemical systematics or by preventing utilization of available nutrients to the microorganisms. Some compounds also cause lyses of microbial cells [32]. In studies carried out by Sharma et al it is observed that plant produce a wide variety of secondary metabolites which are used either directly as precursors or as lead compounds in the pharmaceutical industry and it is expected that plant extracts showing target sites other than those used by antibiotics will be active against drug resistant microbial pathogens [33]. Though the screening of Indian medicinal plants has revealed varying degrees of antimicrobial activity against pathogenic microorganisms but due to lack of experimental scientific studies, confirmation of the antimicrobial properties of a great number of these remedies is not possible [33, 34].

The most important bioactive constituents of plants are alkaloids, tannin, flavonoid and phenolic compounds [35]. Various industries are now looking into sources of alternative, more natural and environmentally friendly antimicrobials, antibiotics, antioxidants and crop protection agents hence various plant species are being investigated in detail and are being thoroughly tested for their pharmacological properties They are mainly interested in the discovery of active chemical structures from which they can develop and prepare synthetic analogues which are more controllable from the point of reproducibility, patentability, safety, and are more economically viable [36]. Some researchers have observed that volatile oils of many plants are known to have antimicrobial activity [37]. Plant essential oils also act as antioxidants which have been researched in detail with the view to investigate their protective role for highly unsaturated lipids in animal tissues [38]. The multidrug resistant strain of many microorganisms has revealed exploration of alternative antimicrobial agent. As reported by Bhaskarwar et al *Jatropha podagrica* of family Euphorbiaceae is known for many biological activities such as antitumour, antimicrobial, molluscicidal and anti-insect [39- 41]. This plant is also used as an antipyretic, diuretic, choleretic and purgative [39]. Hundreds of new natural substances which are being isolated and identified every year are effective antimicrobial substances against a wide array of microorganisms, but data concerning their biological activities are known for only some [36]. Medicinal plants have become the focus of intense study in terms of validation of their traditional uses through the determination of their actual pharmacological effects [39]. This can be brought about by using different computational approaches for identifying promising lead candidates for the development and study of the bioactive substances of medicinal plants.

Insilico Approach

The pace of new discoveries, drug and vaccine design and the design of anti-microbial agents have been enhanced with the advent of various bioinformatics tools and techniques. It has made data analysis time and cost effective which was earlier unmanageable due to vast amount [42]. Various bioinformatics techniques and tools have been developed to identify and analyze metabolic and regulatory pathways of cells in the last decade. With the help of various bioinformatics techniques identification and analysis of various components of cells such as gene and protein function has become effortless. Using the combination of bioinformatics, wet lab, and cell simulation techniques, understanding of cellular mechanism and cellular manipulation will be less strenuous [43-45]. Bioinformatics has enabled in-silico associated molecular tools aiming to screen and identify genes coding for antimicrobial peptides from various cultivated or wild plants [46, 47]. Many researchers have reported that bioinformatics analysis will facilitate and quicken the analysis of systemic level behavior of cellular processes. It can be used for the microbial biotechnology in many ways:(i) the wet-lab data can be easily analyzed by computational approaches, (ii) genome sequencing, (iii) identification of protein coding segments and genome comparison to identify the gene function (iv) the development of genomic and proteomics databases and (v) inference of phenotypes (higher level functions) from genotypes (gene level functions) [45, 51-61, 66].

Various researchers have undertaken some important studies to understand higher level cellular functions which include study of protein-protein and protein-DNA interactions to understand regulatory pathways. Studies are also carried out on automated reconstruction and comparison of metabolic pathways. Lots of research is being carried out on modeling 2D and 3D structure of proteins as well as modeling the docking of 3D models of proteins with drugs for development of drug design [63]. Studies on interactions between chemical compounds and proteins has already enabled the development of drug design [63-66].

Approaches that are being used in bioinformatics are (i) use of computational search and alignment techniques to compare new genome against the set of known genes to annotate the structure and function of genes in a newly sequence genome, (ii) the use of mathematical modeling techniques such as data mining, statistical analysis, neural networks, genetic algorithm, and graph matching techniques to identify common patterns, features and high level functions, and (iii) an integrated approach that integrates search techniques with mathematical modeling [67, 68].

3D structure modeling and docking

Antimicrobial drug researches rely on databases and chemo and bioinformatics tools that contain genomic, proteomic and functional information. The combination of

chemoinformatics tools, bioinformatics tools and relational databases provides means of analyzing, linking and comparing online search results [69]. A protein is known to exist under one or more low free-energy conformational states depending upon its interaction with other proteins. Under a stable conformational state certain regions of the protein are exposed for protein-protein or protein-DNA interactions. Function of a protein is dependent upon exposed active sites and hence it can be predicted by matching the 3D structure of an unknown protein with the 3D structure of a known protein [42, 57, 66]. 3D structures of various proteins have been identified and submitted to databases with the help of X-ray crystallography and NMR spectroscopy but information is still limited hence alternate mechanism is required to relate a gene, its function and its 3D structure. Sequences matching is sufficient for function annotation but many times multiple sequences map to the same 3D structure and in such cases 2D structure matching can help to verify the function of newly sequenced protein [57, 71].

Two major approaches to model 3D structure of a protein suggested are: (i) sequence homology based prediction and (ii) *ab initio* (or *de novo*) method. The sequence homology approach uses sequence alignment to identify the best matching 3D structure for different components: conserved portion, loop portion and side chains from the database, and threads them to predict the overall 3D structure. The *ab initio* method is based upon energy minimization principle, and predicts the structure from the sequence alone [66]. Docking is a term used to identify best matches between 3D structures of two molecules (receptor and ligand) that bind to each other by simulating interacting surfaces and free energy minimization at the domain level [63]. Docking problem requires modeling of surfaces using spheres (or grids) and identifying the best match that will fit two surfaces without excessive intersection. Many times biochemical information such as binding sites is provided. There are three major problems in docking: (i) for multidomain proteins conformation may change during docking, (ii) docking algorithms have high computational overhead that makes large-scale modeling quite slow, and (iii) docking algorithms suffer from over prediction that results in a high number of false positives [72]. As suggested by Bansal in his review the mathematical modeling approaches are suitable for new discoveries to derive candidate genes for vaccine and rational drug design, metabolic pathways, metabolic pathway variations, and transcription factors for regulatory pathways [73]. Most researchers have emphasized that bioinformatics techniques are critically dependent upon the knowledge derived from wet laboratories and the available computational algorithms and tools [4]. The validation of the results had to done by wet lab experiments as they are known to contain false positive and false negative. One of the methodology which allow cost saving, by reducing the required laboratory resources and time, for designing new drugs with specific biological activity is Quantitative structure activity relationships (QSAR). It establishes a correlation between trends in chemical structure modification and respective changes of biological activity [72,73]. There are various methods for using available evolutionary and structure-activity information to find new drug entities with high specificity and low toxicity. But these in silico methods must be followed by validating experiments for defining activity, selectivity, toxicity and mechanism of action of chemically synthesized versions of the identified drug entities from natural resources. [74].

Future Prospects

Tribal communities having distinct culture, values and practices hold on to their traditional knowledge which is transmitted only to people belonging to their clan. The specialized traditional knowledge consists of medicinal plant remedies and community healthcare. Deriving indigenous knowledge from these communities of their traditions, and then exploring for medicinal plant diversity in a systematic manner, benefits through their commercial exploitation in future. Hence documentation and developing a database on existing knowledge is very important to ensure its proper use. Although Indian government has made effort to protect the biodiversity and counter the problem of biopiracy by enacting legislations like the Biological Diversity Act 2002 and Patents Amendment Act 2005, a wide range of approaches are required for sustainable and effective protection of tribal traditional knowledge. It is also very important to carry out future investigations on the diversity of the medicinal plants as well as its scientific function with respect to the tribal communities and its diversity-function relationship. Studies on bioactive rhizospheric microflora associated with rhizosphere of medicinal plants of the tribal community has not been considered as research target, therefore, evaluation of the differences of rhizo-bacterial diversity and the bioactive component of selected medicinal plants among different habitats is also important and will lead to exploration of the relationship between microorganism diversity and the quality of genuine authentic crude drug. Hence, these plants should be investigated for novel antimicrobial compounds that lead to rational drug design. Conventionally drug development was carried out by a hit and miss approach. But with the advent of computational approach or in-silico approach of drug designing, it has led to discovery of various novel chemical entities with promising activity against a particular biological target. The integration of bioinformatics and wet lab will lead to formulation of more effective natural therapeutic products from the medicinal plants of the tribal community and will be helpful for sustainable management.

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References

[1] Ministry of tribal affairs: Government of India. Annual Report 2009-2010.

[2] FAO Investment Centre Socio-economic and Production Systems Studies. [http://www.scribd.com/doc/35346480/Tribal-Development-in-MP-FAO].

[3] Pulliah, T. 2002. Medicinal Plants in India, Regency Publication, New Delhi.

[4] Bansal, A.K. 2005. Bioinformatics in microbial biotechnology–a mini review. Microbial Cell Factories. 4:19.

[5] Ushimaru, P.I., Nogueira da Silva, M.T., Di Stasi, L.C., L. Barbosa and A.F. Junior. 2007. Antibacterial activity of medicinal plant extracts. Braz. J. Micro. 38:717-719.

[6] ITKs (Indigenous Traditional Knowledge), National Tribal Policy. [http://www.sociologyguide.com/types-of-society/Profiles-of-tribes. php]

[7] D.K. Dahare and A. Jain. 2010. Ethnobotanical Studies on Plant Resources of Tahsil Multai, District Betul, Madhya Pradesh, India. Ethnobotanical Leaflets 14:694-705.

[8] WIPO [http://www.wipo.int/tk/en/consultations/draft_provisions/pdf/draft-provisions-booklet-tk.pdf].

[9] R. Gopalan and S. Sivakumar. 2007. Keeping cashmere in Kashmir− the interface between GI and TK. J. Intellec. Prop. Rights. 12: 581-588.

[10] Diallo, D., Hveem, B., Mahmoud, M.A., Betge, G., B.S. Paulsen and A. Maiga. 1999 An ethanobotanical survey of herbal drugs of Gourma district. Mali. Pharma. Biol. 37:80-91.

[11] Sharma, A., V.K. Patel and A.N. Chaturvedi. 2009 Vibriocidal activity of certain medicinal plants used in Indian folklore medicine by tribals of Mahakoshal region of central India. India. J. Pharmacol. 41:129-33.

[12] R. Nair and S.V. Chanda. 2007. Antibacterial activities of some medicinal plants of the western region of India. Turk. J. Biol. 31: 231-236.

[13] Zafar, M., A. Iqbal and M. Faiz. 1999. Indian medicinal plants: a potential source for anticandidal drugs. J. Ethnopharmacol. 37: 237-242.

[14] Manjamalai, A., Sardar, R., Singh, S., C. Guruvayoorappan and V.M.B. Grace. 2010. Analysis of phytochemical constituents and anti-microbial activity of some medicinal plants in Tamil Naidu, India. Global J. Biotech. & Biochem. 5(2): 120-128.

[15] Sen, P., Dollo, M., M.D. Choudhury and D. Choudhury. 2008. Documentation of traditional herbal knowledge of khamptis of Arunachal Pradesh. India. J. Trad. Know. 7(3): 438-442.

[16] Venkataraman, K. 2010. IPR, TK and Biodiversity of India. J. Intellec. Prop. Rights. 13:326-335.

[17] Mairh, A.K., Mishra, P.K., J. Kumar and A. Mairh. 2010. Traditional botanical wisdom of birhore tribes of Jharkhand. Ind. J. of Trad. Know. 9(3):467-470.

[18] Abbasi, A.M., Khan, M.A., Ahmad, M., Qureshi, R., Arshad, M., Jahan, S., M. Zafar and S. Sultana. 2010. Ethnobotanical study of wound healing herbs among the tribal communities in northern himalaya ranges district Abbottabad, Pakistan. Pak. J. Bot. 42(6): 3747-3753.

[19] S.G.V. Babu and S. Arora. 1999. Hot Spots of Biodiversity. [http://envfor.nic.in/news/aug99/biodiv.html].

[20] Hegde, V.G. 2007. IPRs and Asian African States. In: AALCO: Fifty Years of AALCO Commemorative Essays in International Law, New Delhi: AALCO, pp. 124-147.

[21] Farhana Y. Intellectual Property Rights, Biotechnology and Food Security, IDS Working Paper. [http://www.ids.ac.uk/ids/bookshop/wp/wp203.pdf].

[22] Jagtap, S.D., Deokule, S.S., Pawar, P.K., A.A. Kuvalekar and A.M. Harsulkar. 2009. Antimicrobial activity of some crude herbal drugs used for skin diseases by pawra tribes of Nandurbar district. Ind J. Natural products and Resour. 1(2):216-220.

[23] Nascimento, G.C.F., Locatelli, P., P.G. Freitas and G.L. Silva. 2003. Antibacterial activity of plant extracts and phytochemicals on antibiotics resistant bacteria. Braz. J. Microbiol. 31: 247-256.

[24] Joshi, P. 1995. Ethnobotany of primitive tribes in Rajasthan. Printwell, Jaipur.

[25] Arora, A. 1997. Ethnobotanical studies on the wild plants from Aravalli hills of Rajasthan. Printwell, Jaipur.

[26] V. Singh and R.P. Pandey. 1998. Ethnobotany of Rajasthan India. Scientific publisher, Calcutta.

[27] B.V. Shetty and V. Singh. 1993. Flora of Rajasthan: Botanical Survey of India, Rajasthan. PhD thesis, Mohanlal Sukhadia University, Udaipur.

[28] S. Swarnkar and S.S. Katewa. 2009. Antimicrobial activities of some tuberous medicinal plants from aravalli hills of Rajasthan. J. Herb. Med. Toxicolog. 3(1): 53-58.

[29] Shokeen, P., M. Bala and V. Tondon. 2009. Evaluation of the activity of 16 medicinal plants against Neisseria gonorrhoeae. Int. J. Antimicrob. 33: 86-91.

[30] Janovska, D., K. Kubikova and L. Kokoska. 2003. Screening for antimicrobial activity of some medicinal plants species of traditional chinese medicine. Czech. J. Food Sci. 21(3):107-110.

[31] Iwu, M.W., A.R. Duncan and C.O. Okunji. 1999. New Antimicrobials of Plant Origin. In: Janick J (ed) Perspectives on New Crops and New Uses, ASHS Press, Alexandria pp 457–462.

[32] Cowan, M. 1999. Plant products as antimicrobial agents. Clin. Microbiol. Rev. 12: 564-582.

[33] Sharma, A., R. Verma and P. Ramteke. 2009. Antibacterial Activity of Some Medicinal Plants Used by Tribals against UTI Causing Pathogens. World Appl. Scie. J. 7 (3): 332-339.

[34] Ahmed and A.Z. Beg. 2001. Antimicrobial and studies on 45 Indian medicinal plants against multi-drug resistant human pathogens. J.Ethnopharmacol. 74: 113-123.

[35] Shihabudeen, M.S.H., D.H. Priscilla and K. Thirumurugan. 2010. Antimicrobial activity and phytochemical analysis of selected Indian folk medicinal plants. Int. J. Pharma. Sci. Res. 1(10): 430-434.

[36] K.P. Svoboda and J.B. Hampson. 1999. Bioactivity of essential oils of selected temperate aromatic plants: antibacterial, antioxidant, anti inflammatory and other related pharmacological activities. Aromatopia. 35: 50-54.

[37] Deans, S.G., Svoboda, K.P., M. Gundidza and E.Y. Brechany. 1992. Essential oil profiles of several temperate and tropical aromatic plants: their antimicrobial and antioxidant activities. Acta Hortic. 306: 229 – 232.

[38] Deans, S.G., Noble, R.C., L. Penzes and S.G. Imre. 1993. Promotional effects of plant volatile oils on the polyunsaturated fatty acid status during aging. Age. 16: 71 – 74.

[39] Bhaskarwar, B., P. Itankar and A. Fulke. 2008. Evaluation of antimicrobial activity of medicinal plant *Jatropha podagrica*. Roumanian Biotechnol. Letters. 13(5): 3873-3877.

[40] Kupchan, S.M., Sigel, C.W., Matz, M.J., Saenz Renauld, J.A., R.C. Haltiwangar and R.F. Brayn. 1970. J. Am. Chem. Soc. 92: 4476-4477.
[41] Sievers, A.F., Andrewarcher, W., R.H. Morre and E.R. Mcgovran. 1949. J. Econ. Ent. 42:549-551.
[42] Sidhu, S.S., G.D. Bader and C. Boone. 2003. Functional genomics of intracellular peptide domains with combinatorial biology methods. Curr. opinion in Chem. Biol.7: 97-102.
[43] D. Acharya and M.K. Rai. 2004. Traditional knowledge for curing various ailments among Gonds and Bharias of Patalkot valley, M.P., India [http://selfgrowth.com/articles/Acharya12.html].
[44] Delcher, A.L., Harmon, D., Kasif, S., O. White and S.L. Salzberg. 1999. Improved microbial gene identification with GLIMMER. Nucleic Acids Res. 27(23): 4636-41.
[45] R.K. Azad and M. Borodovsky. 2004. Probabilistic methods of identifying genes in prokaryotic genomes: connections to the HMM theory. Brief Bioinformatics. 5(2):118-30.
[46] Pestana-Calsa, M.C., I.L. Ribeiro and T. Calsa Jr. 2010. Bioinformatics-coupled molecular approaches for unravelling potential antimicrobial peptides coding genes in Brazilian native and crop plant species. Curr. Protein Pept. Sci. 11(3):199-209.
[47] Liu, J., M. Dehbi and G. Moeck. 2004. Antimicrobial drug discovery through bacteriophage genomics. Nature Biotechnol. 22(2):185-191.
[48] A.K. Bansal and C. Woolverton. 2003. Applying automatically derived gene-groups to automatically predicts and refines microbial pathways. IEEE Transactions of Knowl. and Data Engg. 15(4): 883-894.
[49] Bansal, A.K. 2001. Integrating co-regulated gene-groups and pairwise genome comparisons to automate reconstruction of microbial pathways. IEEE International Symposium on Bioinformatics and Biomedical Engineering, Washington. 209-216.
[50] Bono, H., Ogata, H., S. Goto and M. Kanehisa. 2008. Reconstruction of amino acid biosynthesis pathways from the complete genome sequence. Genome Research. 8(3):203-210.
[51] Menghani, E., Pareek, A., R.S. Negi and C.K. Ojha. 2011. Search for Antimicrobial Potentials from Certain Indian Medicinal Plants. Res. J. Medicinal Plant. 3(2):218-225.
[52] Kelley, B.P., Sharan, R., Karp, R.M., Sittler, T., Root, D.E., B.R. Stockwell and T. Ideker. 2003. Conserved pathways within bacteria and yeast as revealed by global protein network alignment. Proceedings of the National Academy of Science. 100(20): 11394-11399.
[53] Schilling, C.H., Covert, M.W., Famili, I., Church, G.M., J.S. Edwards and B.O. Palsson. 2002. Genome-scale metabolic model of *Helicobacter pylori 26695*. J. Bacteriol. 184(6): 4582-4593.
[54] Schuster, S., T. Dandekar and D.A. Fell. 1999. Detection of elementary flux modes in biochemical networks: a promising tool for pathway analysis and metabolic engineering. Trends Biotechnol. 17(2): 53-60.
[55] Tatusov, R.L., Mushegian, M., Bork, P., Brown, N., Hayes, W.S., Borodovsky, M., K.E. Rudd and E.V. 1996. Metabolism and evolution of Haemophilius Influenzae deduced from a whole-genome comparison with Escherichia Coli. Current Biol. 6: 279-291.
[56] Waterman, M.S. 1995. Introduction to Computational Biology: Maps, Sequence, and Genomes, London: Chapman & Hall.
[57] J.C. Whisstock and A.M. Lesk. 2003. Prediction of protein function from protein sequence and structure. Q Rev Biophys. 36(3):307-340.
[58] Bansal, A.K. 1999. An automated comparative analysis of seventeen complete microbial genomes. Bioinformatics. 15(11): 900-908.
[59] Bairoch, A. 2000. The ENZYME database in 2000. Nucleic Acids Res. 2000: 304-305.
[60] Goto, S., T. Nishioka and M. Kanehisa. 1998. LIGAND: chemical database for enzyme reactions. Bioinformatics. 14(7): 591-599.
[61] Henikoff, S., Henikoff, J.G., W.J. Alford and S. Pietrokovski. 1995. Automated construction and graphical presentation of protein blocks from unaligned sequences. Gene. 163(2):17-26.
[62] Menghani. E., Pareek, A., R.S. Negi and C.K. Ojha. 2011. Search for Antimicrobial Potentials from Certain Indian Medicinal Plants. Res. J. Medicinal Plant. 3(2):218-225.
[63] Halperin, I., Ma, B., H. Wolfson and R. Nussinov. 2002. Principles of docking: An overview of search algorithms and a guide to scoring functions. Proteins. 47(4): 409-43.
[64] D. Baker and A. Sali.2001. Protein structure prediction and structural genomics. Science. 294: 93-96.
[65] Sigrist, C.J., Cerutti, L., Hulo, N., Gattiker, A., Falquet, L., Pagni, M., A. Bairoch and P. Bucher. 2002. PROSITE:a documented database using patterns and profiles as motif descriptors. Briefings in Bioinformatics. 3(3):265-274.
[66] Altschul, S.F., Gish, W., Miller, W., E.W. Myers and D.J. Lipman. 1990. Basic alignment search tools. J. Mol. Biol. 215: 403-410.
[67] Altschul, S.F., Madden, T.L., Schaffer, A.A., Zhang, J., Zhang, Z., W. Miller and D.J. Lipman . 1997. Gapped BLAST and PSI-BLAST: A new generation of protein database search programs. Nucleic Acids Res. 15(17): 3389-3402.
[68] R. Hammami and I. Fliss. (2010) Current trends in antimicrobial agent research: chemo- and bioinformatics approaches. Drug Discovery Today 15(13-14):540-546.
[69] Suzek, B.E., Ermolaeva, M.D., S. Schreiber and S.L. Salzberg. 2001. A probabilistic method for identifying start codons in bacterial genomes. Bioinformatics. 17(12):1123-30.
[70] S. Swarnkar and S.S. Katewa. 2009. Antimicrobial activities of some tuberous medicinal plants from aravalli hills of Rajasthan. J. Herb. Med. Toxicolog. 3(1): 53-58.
[71] Alyar, S., Ozbek, N., K. Kuzukiran and N. Karacan. 2011. Quantitative structure –activity relationship studies for prediction of antimicrobial activity of synthesized disulfonamide derivatives. Mad. Chem. Res 2011, 20:175-183.
[72] C. Hansch and A. Leo. 1995 Exploring QSAR Fundamentals and applications in chemistry and biology. Washington, DC: Am Chem Soc.
[73] Juretic, D.,Vukicevic, D., Petrov, D., Novkovic, M., Bojovic, V., Lucic, B., N. Ilic and A. Tossi. 2011.

Knowledge based computational methods for identifying or designing novel , non homologous antimicrobial peptides. Eur. Biophy. J, in press.

[74] Yuan, X., Xu, J., Chai, H., Lin, H., Yang, Y., W. Xingde and S. Jiyan. 2010. Differences of rhizo-bacterial diversity and the content of peimine and peiminine of *Fritillaria thunbergii* among different habits. J. of Med. Plants Res. 4(6):465-470.