Importance of Using DNA Microarray in Studying Medicinal Plant

Corresponding Author:
Prof. Rajendra Sharma,
Professor, School of Life sciences, Dr. B. R. Ambedkar University Agra, 282004 - India

Submitting Author:
Dr. Avnish Kumar,
Lecturer, Department of Biotechnology, School of Life sciences, Khandari Campus, Dr. Bhim Rao Ambedkar University, 282004 - India

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Medicinal Plants:

Medicinal plants have promised a positive concept of health based upon certain basic principles of physical, chemical and biological sciences in present busy life. Drugs from these are said to be potentially safe casting no side effects over synthetic drugs like antibiotics, analgesics, antihelminitics etc., Pyrostegia venusta (Ker Gawl.) Miers, (Bignoniaceae), is native to the Brazilian Cerrado and popularly known as “cipó-de-são-joão” (Sandwith and Hunt, 1974; Scalon et al., 2008). Pyrostezia venusta have reported folklore used as medicinal plant for common diseases of disease of eye, nose, etc. The flowers of P. venusta are used as a general tonic and a treatment for diarrhea, vitiligo, cough, and common infections and inflammatory diseases of the respiratory system (Ferreira et al., 2000). The flower consist of gallo-tannic acid and glycoside bellericanin, which is bitter, pungent acid, digestible, laxative, anti-helminthic, anti-bronchitis, sore throat, anti-inflammatory, anti-asthamic. The fruit in combination with other drugs is prescribed for snake bites (Ferreira et al., 2000, Scalon et al., 2008; Velosa et al 2010, Roy et al 2012).

Economical importance:

Although herbs had been prized for their medicinal, flavouring and aromatic qualities for centuries, the synthetic products of the modern age surpassed their importance, for a while. However, after a boom of allopath now these days herbs are staging a comeback and herbal ‘renaissance’ is happening all over the globe (Huff & Toby, 2003; ). The herbal products today symbolise safety in contrast to the synthetics that are regarded as unsafe to human and environment (Wealth of India Dictionary CSIR, 2007). Over 80% of the world population depends mainly on plants and plant extracts for health care (Joy et al 1989, WHO 2002, Jawla et al 2009). Thus business world estimated that plant derived drugs may account for about Rs. 2,00,000 crores. Presently, India contribution is less than Rs. 2000 crores which is growing steadily. The annual production of medicinal and aromatic plant’s raw material is worth about Rs. 200 crores and it supposed to be raised to US $5 trillion by 2050 (Joshi et al, 2004). Even developed countries such as United States constitute 25% of the total drugs as plant drugs, while in most populated as well as fast developing countries such as China and India utilizing about 80% plant based drugs (Jawla et al 2009). The World Health Organization (WHO) has estimated the present demand for medicinal plants is approximately US $14 billion per year (Sharma, 2004).

Epidemiology:

These developing countries provide two third of the plants used in modern system of medicine and the health care system of rural population depend on indigenous systems of medicine. At present it is reported that there are more than 80,000 are medicinal higher plant species on earth. Among plant based drug producer, India is one important biodiversity centres with the recognition of over 45000 different plant species. India’s biodiversity have 16 different agro-climatic zones, 10 vegetation zones, 25 biotic provinces and 426 biomes (habitats of specific species). This constitute, about 15000-20000 plants with good medicinal value. Of these 7000-7500 species are used for their folk medicinal values since ancient time (Kirtikar & Basu 1995). In India, drugs of herbal origin have been used in traditional systems of medicines such as Unani and Ayurveda since ancient times. The Ayurveda system of medicine uses about 700 species, Unani 700, Siddha 600, Amchi 600 and modern medicine around 30 species. About 8,000 herbal remedies have been codified in Ayurveda. The Rigveda (5000 BC) has recorded 67 medicinal plants, Yajurveda 81 species, Athravaveda (4500-2500 BC) 290 species, Charak Samhita (700 BC) and Sushrut Samhita (200 BC) had described properties and uses of 1100 and 1270 species respectively, in compounding of drugs and these are still used in the classical formulations, in the Ayurvedic system of medicine (Astin, 1998; Barnes et al 2002; Christie, 1991; Engebretson & Wardell, 1993; Francis, 1994; Indian Herbal Pharmacopoeia 1999; Jugalbandhi of Ayurveda with Allopathy, 2006; Mohar, 1999; Maclennan et al.,1996; Mukherjee, 2002; Rangari, 2002; WHO 1993 Research Guidelines; WHO 2002 Policy Perspectives of Medicines; Traskie, 1997; Govt of India 2001 The Ayurvedic Pharmacopoeia of India; Evans, 2006).

Source of plant drugs:

Plant drugs can be derived either from the whole plant or from different organs, like leaves, stem, bark, root,
flower, seed, etc. and even from excretory plant product such as gum, resins and latex. Presently, Allopathic medicine (e.g. Codeine – Anticough; Morphin- painkiller; Artemisinin- antimalarial, etc.) has also been derived from a number of plants (Papaver somniferum, Papaver somniferum, Artemesia annua, respectively etc.) which form an important segment of the modern pharmacopeia (Kumar et al 1997, Yue-Zhong Shu, 1998). Some more examples of important drugs obtained from plants are digoxin from Digitalis spp., quinine and quinidine from Cinchona spp., vincristine and vinblastine from Catharanthus roseus, atropine from Atropa belladonna and morphine and codeine from Papaver somniferum. It is estimated that 60% of anti-tumour and anti-infectious drugs already on the market or under clinical trial are of natural origin (Yue-Zhong Shu, 1998). Few important chemical intermediates needed for manufacturing the allopathic drugs are also from plants origin (e.g. diosgenin, solasodine, b-ionone) (Tal et al 1983). In addition, a large number of natural products, especially plant-derived drugs, continues to be discovered on the basis of traditional or empirical local medical practices (Farnsworth et al 1985). A single medicinal plant may contain hundreds of natural constituents, and a mixed herbal medicinal product may contain several times that number. About 25% of the drugs prescribed worldwide come from plants, 121 such active compounds being in current use. Of the 252 drugs considered as basic and essential by the World Health Organisation (Farnsworth et al 1985). These and more similar molecule can be searched by using modern scientific tools. For example, GC-MS study of Pyrostelgia venusta flower indicated that the phytochemicals myoinositol, hexadecanoic acid, linoleic acid, oleic acid, stigmasteryl tosylate, diazoprogesterone, arabipyranose, propanoic acid, linoleic acid, oleic acid, stigmasteryl tosylate, diazoprogesterone, arabipyranose, propanoic acid, pentamethyldisilanyl ester, acetophenone, trans-3-Hexenedioic acid, and 9-Octadecenoic acid (Z)-methyl ester were present in the flower (Roy et al 2012). These compounds exhibit diverse activities, including: antiseptic; bactericidal; fungicidal; antiviral; analgesic; anesthetic; antihistaminic; anti-inflammatory; expectorant; antitussive; spasmylic, spasmogenic; sedative; antiedemic; antidiabetic; anticancer and cancer preventative; antiatherogenic; liver protection; and fever reduction (Johnson & Gitksan, 2006).

**Importance of Medicinal Plants in Modern Age:**

Traditional systems of medicine practice have several benefits on many accounts like population rise (Samal et al 2004), prohibitive cost of treatments, side effects of several allopathic drugs (Kala, 1998, Kala 2005, Kala 2006) and development of resistance to currently used drugs for infectious diseases. In the Year 2006, US Uppasala based research Centre received over 3,600,000 Adverse Drug Reaction (ADR) reports. Of these there were just over 17,000 (0.5%) where a herbal drug is listed as being the suspected or interacting cause (Mills, 2006). About 80% of world population cannot afford the products of the Western Pharmaceutical Industry and have dependence only on the use of traditional medicines and folk medicine which are mainly derived from plant material. In many of the developing countries the use of plant drugs is increasing because modern life saving drugs are beyond the reach of major portion of world population although many under developed countries spend 40-50% of their total wealth on drugs and health care. Studies have suggested that nature-derived approaches to therapeutic are not only remedial effective, but also 53-63% cost-effective (WHO 2002-2005) and ecological awareness also suggests that “natural” products are harmless. As a part of the strategy to reduce the financial burden on developing countries, it is obvious that an increased use of plant drugs will be followed in the future.

**Need of Scientific Analysis:**

Plants can synthesize variety of biochemical products because of their metabolism, many of which are extractable and used as chemical feed stocks or as raw material for various scientific investigations. Many secondary metabolites of plant are commercially used in a number of pharmaceutical compounds (Hussain et al 2012). However, a sustained supply of the source material often becomes difficult due to the factors like environmental changes (Li et al 2009), cultural practices (DiCosmo et al 1995), diverse geographical distribution, labour cost, and selection of the superior plant stock and over exploitation by pharmaceutical industry. Investigators have reported fractions of flowering plants that have yielded about 120 therapeutic agents of known structure from about 90 species of plants. Presently, in market we can see many plant drugs include vinblastine, vincristine, taxol, podophyllotoxin, camptothecin, digitoxigenin, gitoxigenin, digoxigenin, tubocurarine, morphine, codeine, aspirin, atropine, pilocarpine, capscicine, allicin, curcumin, artemesinin and ephedrine. In some cases, the crude extract of medicinal plants may be used as medicaments. On the other hand, the isolation
and identification of the active principles and elucidation of the mechanism of action of a drug is of paramount importance. Hence, the scientific studies of traditional medicines, derivation of drugs through bioprospecting and systematic conservation of the concerned medicinal plants have its own importance. A major lacuna in ancient medicine preparation (like Ayurveda) is the lack of drug standardisation, information and quality control and can fail to give desired activity. This is now known that activity of the plants extract is the synergistic effect of its various components. In the absence of pharmacopoeia data on the various plant extracts, it is not possible to isolate or standardise the active contents having the desired effects.

**DNA -Micro Array:**

There are estimated 250,000–500,000 plant species, only a small percentage has been investigated phytochemically and even a smaller percentage has been properly studied in terms of their pharmacological properties; in most cases, only pharmacological screening or preliminary studies have been carried out. The World Health Organisation (WHO) has also suggested around 21,000 plant species with potential medicinal values. Among these 2500 species are in India, out of which 150 species are used commercially on a fairly large scale. The potential use of higher plants as a source of new drugs is still poorly explored. It is estimated that 5000 species have been studied for medical use (Payne et al., 1991). Between the years 1957 and 1981, the NCI screened around 20,000 plant species from Latin America and Asia for anti-tumour activity, but even these were not screened for other pharmacological activities (Hamburger and Hostettman, 1991). The WHO considers phytotherapy in its health programs and suggests basic procedures for the validation of drugs from plant origin in developing countries (Vulto and Smet, 1998; OMS, 1991). Asian countries like China and India, have a well-established herbal medicines industry and Latin American countries have been investing in research programs in medicinal plants and optimization and regulation of phytomedicinal products, following the example of European countries, such as France and Germany. In Germany, 50% of phytomedicinal products are sold on medical prescription, the cost being refunded by health insurance (Gruenwald, 1997). In North America, where phytomedicinal products are sold as “health foods” (Brevoort, 1997; Calixto, 2000), consumers and professionals have struggled to change this by gathering information about the efficacy and safety of these products. To develop phytomedicines it would be essential to adopt a holistic interdisciplinary approach, based on scientific understanding of the plant systems, as well as new innovations and their conservation for utilisation in future on a sustainable basis. In our opinion these task can be achieved by using DNA chip technology. Since 1995, DNA micro-arrays have become an accepted and functional tool with which to meticulous study gene expression in cells and tissues in response to various agents and treatments (Lobenhofer et al., 2001). Theoretically, one can evaluate, all together, changes in gene expression (transcriptome, metabolome, kinome etc.) of the entire genome under single study. Therefore, micro-array tools have been applied by many investigators involved in cancer research (Jiang et al., 2012; Gschwind et al 2004; Mischel et al 2004), differentiation and development (Kelly & Rizzino, 2000; Takebe et al., 2006), toxicity (Vrana et al., 2002; Clarke et al., 2001; Nuwaysir et al., 1999; Baker et al., 2001; Gerhold et al., 2001; Bartosiewicz et al., 2001), and the effects of pharmaceuticals on cells and animals (Chavan et al 2006). Additionally, few latest studies have shown the application of technique for revealing the novel response of important genes which were unstudied previously. Nevertheless, comparatively a small number of attempts have been made so far to evaluate herbal medicines, even though a number of relevant questions can be solve on applying this.

Already at a relatively early stage of its application in plant science, DNA microarrays are being utilized to examine a number of metabolic activities including the circadian clock (Schaffer et al., 2001; Duffield, 2003), plant defence (Glazebrook, 2007), environmental stress responses (Liu et al., 2008, Rabbani et al., 2003), fruit ripening (Aharoni et al., 2000; Aharoni and Vorst, 2001), phytochrome A signaling (Aharoni and Vorst, 2001; Spiegelman et al., 2000), seed development (Gregersen et al., 2005; Venglat et al., 2011) and nitrate assimilation (Vlieghe et al 2003; Wang et al 2003). Novel insights are obtained into the molecular mechanisms co-ordinating metabolic pathways, regulatory and signalling networks. Exciting new information will be gained in the years to come not only from genome-wide expression analyses on a few model plant species, but also from extensive studies of less thoroughly studied species on a more limited scale. The value of microarray technology to our understanding of living processes will depend both on the amount of data to be generated and on its intelligent analysis and application with other biological knowledge arising from functional genomics tools for
 dela signation of genome, proteome, metabolome and pheneim.

**Construction of DNA chip:**

Southern hybridisation technique was introduced by E M Southern in 1975. In this method, the gel with separated intact DNA fragments would get denatured in a basic solution and placed in a tray. A porous nylon or nitrocellulose membrane is subsequently laid over the gel, and the whole weighted down. All the DNA restriction fragments in the gel transfer as single strands by capillary action to the membrane. All fragments retain the same pattern on the membrane as on the gel (Southern, 1975). A DNA microarray is a microscopic collection of DNA probes (or features) arrayed onto a solid surface (Allen et al. 2010). Microarrays take advantage of the highly selective nature of nucleic acid interactions (either DNA–DNA or DNA–RNA) and are most commonly used for expression profiling and comparative genomic hybridization (Allen et al. 2010). Southern (DNA) and northern (RNA) blots (Southern, 1975, Alwine et al. 1977) hybridisation is the foundation behind the technique of DNA microarrays. Hybridisation is the reaction that concerns with the fluorescent probes and the DNA on the microarray. The hybridisation conditions also depend on the application of the array like detection of mutations which requires high hybridisation stringencies occurs at lower salt concentration and higher temperature, for short time periods (hours). Using microarray for “expression monitoring” requires lower stringencies, to ensure overnight low-copy number sequences annealing at lower temperatures and higher salt concentrations. After this overnight hybridisation, the reaction can be scanned using a laser confocal scanning microscope, which read each spot of DNA and separately measures the fluorescence for each dye. This produces data to determine the ratio, and in turn the relative abundance of the sequences of each specific gene in the messenger RNA or DNA samples. The comparative study of hybridisation pattern can then be used to identify the genes that are expressed differently in the tissues or cells. The principle of the hybridisation reaction is to expose two single-stranded DNA sequences to each other, and measure the amount of double-strands that form. Microarray technology is a modern automation of southern hybridization technology combining miniaturization and the application of fluorescent dyes for labelling. The fluorescent dyes provide combination of two differently labeled samples in a single hybridization experiment with reduced experimental error. Miniaturization helps in developing relative expression levels of large numbers of genes in lesser time then traditional hybridization system with a high degree of sensitivity. There are two fundamentally different microarray-based technologies are available for large-scale expression analyses.

First, photolithographic method in which high-density spatial synthesis of oligonucleotides, that contain up to a few hundred thousand distinct elements (Fodor et al., 1991). Construction of such arrays requires prior sequence knowledge as well as complicated design and production methodologies (Lipshutz et al., 1999). The second method utilized PCR-amplified cDNA clones and the resulting arrays are referred to as cDNA microarrays or printing cDNA microarrays. The cDNA microarrays contain pre-synthesized nucleic acids which are mechanically deposited, similar to ‘ink-jet’ printing onto a solid surface. That provides more flexible design for the fabrication of microarrays (Duggan et al., 1999).

**Photolithographic microarray production:**

Synthesis of oligonucleotides on a surface using photolithography is used to formulate high-density oligonucleotide microarrays. The most widely used method is the Affymetrix GeneChip technology. Photolithographic microarray fabrication involves DNA synthesis directly on the solid carrier surface by using combinatorial chemistry methodology. This ‘in situ’ fabrication technique was developed by Affymetrix, and is used to produce their GeneChips. They make use of semiconductor technologies. In it mercury lamp is used, and the light activates modified photospecific versions of the four DNA bases to solid surface, derivatized with chemical linkers containing photolabile protective groups with presence of photolithographic masks which ensure the DNA synthesis is stimulated in defined positions - the masks predetermine which of the nucleotides are activated. Subsequently, the surface is flooded with a modified nucleotide to be coupled to the activated region of the chip. A repeated series of steps involving selective activation of specific regions and nucleotide coupling allows parallel oligonucleotide synthesis at many locations (Lemieux et al., 1998).

Microarrays presently produced by Affymetrix normally contain 25-mer oligonucleotides within 20–24 mm feature size. Typically, for expression monitoring, 16 oligonucleotide probe pairs (16 perfect match (PM) and 16 additional mismatch oligonucleotides (MM) for increased sensitivity and specificity of detection) are designed on non-conserved regions of a gene (http://www.affymetrix.com). The MM oligonucleotide is identical to the PM except for a single-base difference at the central position. A single microarray
Preparation of Probes:

several months prior to hybridization. The DNA on the slide is denatured (by heat or alkali treatment). Processed slides may be stored dry for anhydride or sodium borate) and, as a final step, the baking), the unused surface is blocked (by succinic anhydride or amino silanes. There is at present two processes i.e. either contact printing or non contact printing. In contact printing method, either solid or split pins are dipped into the DNA solution then a micro-droplet subsequently deposited upon direct contact with the solid surface of the array. The system uses a motion control structure that spots or prints an accurate amount of sample probe onto multiple surfaces (often 50 to 100 microscope slides) in a sequential operation. According to objective, one can use contact printing typically to produces sub-nanolitre droplets at a pitch of 100–250 mm. Presently, mechanical spotting mentioned above is most common way for the fabrication of cDNA microarrays. Non-contact printing consist a controlled ejection of small (nano- to picolitres) volumes of DNA solution from a dispenser onto the surface from a defined distance which allows flexibility in printing volume. Universally, non-contact dispensing uses various types of ink-jet technology (e.g. thermal, solenoid, piezoelectric) for droplet generation and delivery (Okamoto et al., 2000).

cDNA microarrays produced by ink jet printing may contain thousands of array elements. After spotting, the DNA is immobilized (either by UV cross-linking or baking), the unused surface is blocked (by succinic anhydride or sodium borate) and, as a final step, the DNA on the slide is denatured (by heat or alkali treatment). Processed slides may be stored dry for several months prior to hybridization.

Printing CDNA microarrays production:

cDNA microarrays are habitually made-up on solid surfaces generally microscope slides of glass. In order to boost the adhesion of probes as well as to lesser background and to restrict spreading of the droplets, the slides are pre-coated with substances like poly-lysine or amino silanes. There is at present two processes i.e. either contact printing or non contact printing. In contact printing method, either solid or split pins are dipped into the DNA solution then a micro-droplet subsequently deposited upon direct contact with the solid surface of the array. The system uses a motion control structure that spots or prints an accurate amount of sample probe onto multiple surfaces (often 50 to 100 microscope slides) in a sequential operation. According to objective, one can use contact printing typically to produces sub-nanolitre droplets at a pitch of 100–250 mm. Presently, mechanical spotting mentioned above is most common way for the fabrication of cDNA microarrays.

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Preparation of Probes:

Initiation of cDNA microarray fabrication necessitates the assortment of suitable probes to be applied. Generally, fluorescent probes are prepared to hybridise to the microarray. These are prepared from messenger RNA from the cells or tissues of interest. Depends on key property, required mRNA can be isolated and extracted from the cells or tissues of interest. These mRNAs employed to synthesize complimentary DNA using reverse transcriptase enzyme. Then synthesized cDNA is labelled by the incorporation of fluorescent or radioactive nucleotides into the DNA. The two samples with contrast to property are labelled using two different fluorescent dyes - say, Cy3 (red) or Cy5 (green). These labelled cDNA then hybridised to the microarray slide or DNA chip. Two differentially labelled cDNA mixtures permit the measurement of ratio of fluorescence; this circumvents most of the problems of hybridisation kinetics.

Gene Typing:

The spectrum of genetic variation may be ranges from the single base pair to large chromosomal events. In order to understand its importance regarding human disease, complex traits and evolution, there is a great challenge to discover the full extent of structural variation and to be able to genotype. In routine analysis microarray is a promising tool because the sequence that hybridizes in oligonucleotide-based microarrays is very short (i.e. 20–25 nucleotides); the hybridization reactions are very sensitive to single nucleotide mismatches, unlike DNA fragment-based microarrays. Therefore, oligonucleotide-based microarrays are well-suited to genotyping or resequencing applications (Wang et al 1998).

Genotyping technology has been instrumental to producing a high-resolution genetic map of the human genome (and others); yielding DNA blocks (haplotypes) that could help in the localization of disease genes by identifying those blocks that are associated with phenotypic traits (The International HapMap Consortium, 2005). The use of microarrays for genotyping is technically further advanced than for transcript profiling. One reason for this is that a qualitative analysis is usually adequate for genotyping: simple discrimination is sufficient to detect individual base differences (SNPs). Genotyping experiments also generally contain direct internal controls, which enable better data interpretation. For example, if detection is done by hybridization of a sample DNA to an oligonucleotide array, three of the four oligonucleotides that represent a SNP function as
mismatch controls (Alkan et al 2011).

**Medicinal Gene Expression Profiling:**

Gene expression profiling holds tremendous promise for dissecting the regulatory mechanisms and transcriptional networks that underlie biological processes. Microarrays take advantage of existing EST collections and genome sequence data (and are thus limited by the availability of the same), robotic instrumentation for miniaturization, and fluorescent dyes for simultaneously detecting nucleic acid abundance in RNA populations derived from multiple samples. Populations of fluorescent cDNA targets (following the definition of target and probe adopted in the The Chipping Forecast, 1999) representing the mRNA populations of interest are queried via hybridization with a large number of probes that have been immobilized on a suitable substrate (Chen et al., 1998; DeRisi et al., 1996; Shalon et al., 1996; Schena et al., 1995). The arrays themselves are composed of collections of DNA sequences (typically PCR products, cDNAs, or oligonucleotides) that have been printed as a microscopic grid of catalogued features by a high-throughput robotic system. This technique for gene expression profiling has important advantages when compared with RNA-blot analysis, cDNA sequencing, differential display, AFLP analysis, and SAGE. Microarrays make it possible to monitor the expression of an entire genome in a single experiment (Gill et al., 2002; Jiang et al., 2001; Wang et al., 2003).

**Genome-wide Studies:**

Understanding complex functional mechanisms requires the global and parallel analysis of different cellular processes. DNA microarrays have become synonymous with this kind of study and, in many cases, are the obvious platform to achieve this aim. They have already made important contributions, most notably to gene-expression studies, although the true potential of this technology is far greater. Whereas some assays, such as transcript profiling and genotyping, are becoming routine, others are still in the early phases of development, and new areas of application, such as genome-wide epigenetic analysis and on-chip synthesis, continue to emerge.

Microarray is better tool of gene expression monitoring, and in a single hybridization experiment we could get quantitative results for more than 18,000 genes (Alizadeh et al., 2000) simultaneously. Automation in high density and miniaturization has given genome-wide expression studies feasible, by using either cDNA or oligonucleotide arrays. Genome-wide expression profiling at the transcript level is one of the most exciting tools to study the cell and its integrative processes. Firstly, it is possible to measure transcript levels of every gene. This is something that is not yet feasible for proteins or metabolites. Secondly, expression patterns of genes can provide strong clues to elucidate their function. This assumption is based on numerous examples in which gene function was tightly connected to precise expression patterns under certain conditions. Consequently, global observation of gene expression patterns allows evaluation of the association between conditions of gene expression and function as well as the generality and strength of this link (Aharoni & Vorst, 2002).

**Conclusion:**

As a natural source of medicinal molecule herbs and plants are the primary choice of health care research, which is gaining popularity and hope of world’s population living in developing countries. The economical aspects have increased demand for botanical products by an expanding industry and accompanied by calls for assurance of quality, efficacy and safety. Poor quality control of medicinal herbs has led to instances of toxicity, poisoning and even deaths. Recently, DNA-based methods have been developed for the identification of medicinal plants. Genomic fingerprinting can differentiate between individuals, species and populations and is useful for the detection of the homogeneity of the samples and presence of adulterants. Phytochemical and genetic data are correlated but only the latter normally allow for differentiation at the species level. Combinatorial biosynthesis is another approach in the generation of novel natural products and for the production of rare and expensive natural products.

The fundamental step in quality control of herbal medicine is accurate identification of herbs. Array-based techniques have recently been adapted to authenticate or identify herbal plants. We further suggested microarray tools to investigate important gene expression, gene typing and fingerprinting. The applicability of the array-based methods for fingerprinting depends on the availability of genomics and genetics of the species to be fingerprinted. For the species with few genome sequence information but high polymorphism rates, variants of microarray techniques are recommended because they require less labour and lower material cost.
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