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AYURGENOMICS: A BRIEF NOTE ON AYURVEDA AND THEIR CROSS KINGDOM GENOMICS

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ABSTRACT

Genomics has led in an era of prognostic, defensive and personalized medicine wherein it is expected that not too far in the future there would be a prototype shift in the practice of medicine from a generalized symptomatic approach to an individualized approach based on his or her genetic makeup. Ayurveda, an ancient Indian system of medicine recognized and experienced in India since 1500 B.C has personalized methodology towards management of health and disease. We thought an addition of Ayurveda and genomics if endeavoured in an efficient way which we call as Ayurgenomics could assistance fill the gap. MicroRNAs (miRNAs) are a class of noncoding small RNAs, which play a vital character in post- transcriptional gene regulation. Currently, numerous study exposed that miRNAs could be transmitted between species to mediate cross-kingdom regulation by assimilating into a specific target gene-mediated governing pathway to apply applicable biological functions. Here, we discuss probable miRNA parallel transfer appliances from one species to another and analyze the relationship between miRNA-mediated cross-kingdom regulation.

Keywords: *Genomics, Ayurveda, Ayurgenomics, miRNAs, cross-kingdom*

Ayurveda

The origin of ayurveda has been around at 5000 BC. Ayurveda is medicinal system found in India and has survived at a remote place in present days. Atharvaveda talks about the origin ofayurveda and state the diseases along with their treatment information. The environmental factors and civilization decide our system of medicine. The earliest medicinal system divided into eight components. The components explained as follows:

- Kayacikitsa : General medicine
- Kaumara-bhartya :Treatment of children and pediatrics
- Salyatantra : Surgical technique
- Salakyatantra : Treatment of ailments affecting ears, eyes, nose, mouth etc
- Bhutavidya : Spirits
- Agadatantra : Toxicology
- Rasayantantra : rejuvenation and tonics for increasing lifespan and strength
- Vajkaranatantra : Semen and sexual pleasure

Ayurveda also have an eight way to diagnose diseases called Sparsha(touch), Mootra (Urine), Nadi (Pulse), Mala(stool), Aakriti (appearance), Shabda (speech), Jihva(tongue) and Druk (Vision). The three elemental substances vatta, pitta and kapha and five great element named as earth, water, fire, air and aether defined as prikriti and it is used in traditional medicinal system to check the balance of doshas in human health (Rotti et al. 2014). The imbalance of doshas resulted into diseases. Some important medicinal plant names from Vedas can be foundin Ayurvedic literature. The root, leaves, stem, and bark, seeds and fruits of medicinal plant used in this medicinal system. It would be interesting to study the ayurveda medicinal systemor ayurveda prikriti with advanced scientific technologies.

Ayur-Genomics:

Ayurveda is ancient times personalized medicinal system and genomics is predictive personalized what DNA tells about you based on your genetic makeup. The genetic network interaction and environmental factors are important for the phenotypic diversity in health and diseases. Every individual have their own genetic makeup or prikriti. Based on their prikriti, assessment of disease as well as selection of the preventive and curative regime is suggestingon their individual phenotypic characters (Esplin et al. 2014; Verma, 2012).Vata, Pitta and Kapha identified on the basis of ayurveda exhibit the striking difference at the biochemical and genome wide gene expression analysis(Prasher et al. 2008). Identification of the phenotypic and genotypic variant, designing the map for every individual for personalized medicine using modern technologies like Next Generation Sequencing and Microarray. If ayurveda and genomics together applied on appropriate manner which can be said asayurgenomics, would help fill the gap in translational medicinal system.

Cross Kingdom Genomics

The scientific advancement of modern generation to understand the balance between the healthy lifestyle and disease by altering or regulating the expression of genetic activity based on their human genetic makeup. The cause of global humanity is lifestyle related diseases, many of which can be addressed through ayurveda with its effect on healthy lifestyle and reducing the ill effect of chronic diseases. Ayurgenomics provide a genetic understanding and expression for how phytochemical affects the balance between human health and diseases. Plants have been thought to be used as medicinal agents since ages due to its lower toxicity and side effects than the synthetic drugs; moreover the complex cellular pathways are supported by phytochemical molecules (H. A. H. Said-al Ahl et al, 2017; S. Verma and S. P. Singh, 2008).

Plant miRNA are a class of recently discovered non-coding endogenous, 18-24 nucleotide (nt) small RNAs that negatively regulate specific messenger RNA (mRNA) (Frances T. Sheehan et al,2012). However, in a sequence-specific manner and silence, specific protein-coding genes at the post-transcriptional level by targeting the 3’ untranslated region (3’UTR) of mRNA operate by theMiRNA which leads to the mRNA cleavage and decreases protein translation. Quite a few laboratories and computational approaches have shown that this new class of small RNAs has a diverse and important role in development, stress response, growth, and other important physiological processes (Jiang, M et al, 2012). In 2012 Zhang et al found that in rice plants osa- miR-168a and other exogenous miRNAs are rich amounts that can be acquired by mice through food intake, as conformation by their presence in the mammalian in sera or tissues. In vivo and invitro functional studies indicated that in the mammalian miRNA are able to inhibit gene expressionin the liver which representing the first case of cross-kingdom regulation. This explanation showsthat the mammalian digestive tract absorbed plant miRNA and can target mammalian genes (Vaucheret, H et al, 2012). However, they also proposed the hypothesis that for cancer treatment edible plant producing mammalian tumor suppressor miRNA might be a new therapeutic approach. This treatment might be a useful, non-hazardous, and inexpensive chemo-preventive strategy for humans (Chen, X et al, 2008).

There is several evidence of Holy basil phytochemical on clinical and scientific research and confirming their beneficial effects. Tulsi having different medicinal properties like antimicrobial, antiviral, anticancer, antidiabetic, antioxidant, anti-inflammatory and antifertility. The establishment of high correlation of Prikriti and identify the genomics signature by isolating RNA and DNA studies through “Next Generation Sequencing”. Our review based on the advancement of ayurgenomics study directly correlates with the translational and preventive medicinal research.

In recent times, focused on aryuveda research has increased all over the world and especially in INDIA. An ayush has given the huge information of medicinal plants used in various regulatory functional systems in human. The different medicinal plants are source of medicines for number of diseases existing in human race. According to “Rigveda”, a medicinal use of plants in Hindu culture is an oldest knowledge information resource. Medicinal plants have animmense therapeutic potential and it is associated with human history for their use in traditional and aryuveda medicinal system. Plants like Tulsi, Aswagandha, Amla, Brahmi, Gudmar, Satavari, Senna, Neem, Moringa etc have eminence value as a cure for various human diseases. Their secondary metabolites and their bio synthesized active compounds are important for clinical drugs and many of chemicals (Das and Vasudevan 2006). Among these, Tulsi and Moringa have a great potential for human health. It is considered as a “holy herb” in India and important symbol of the Hindu religious tradition. Thus it is also known as Holy basil and botanical identification called *Ocimum Sanctum*, belonging to plant family Lamiaceae. Different known and important *Ocimum* Sp. is well characterized in literature (Simon et al. 1999). Tulsi has been mentioned in the Charaka Samhita, an ancient Ayurvedic text for its Ayurveda with its diverse medicinal properties. It is a rich source of essential oils and aroma compounds (Charles and Simon 1990; Bhateja and Arora 2012). *Ocimum Sanctum* has immense number of health benefits such as healing power, coughs, fever, common cold, throat infections, respiratory disorders, kidney stones, heart disorders, stress, skin disorder, traditional medicinal practitioners, as expectorants, analgesic, anticancer, antifertility, antiemetic, antiasthmatic, diaphoretic, antidiabetic, antifertility, hypertensive, hepatoprotactive, hypolipidmic and antistress agent (Gupta et al. 2002; Kashyap et al. 2011; Prakash and Gupta 2005). Thus number of Photochemical studies has been carried out to findout the bioactive compound from different medicinal plants including Tulsi which are used forcuring of various human diseases and also play an important role in healing but the genomic basis of their medicinal power still need to be explored in detail. With the advent of next- generation sequencing (NGS) technology, thousands of human genomes and expression data sets have been made available across many diseases and normal control individuals; however,their analysis is still incomplete (Chaudhary and Sharma 2016; Sala-Cirtog et al. 2015) On theother hand, some genomic and transcriptome study has also been carried on Tulsi plant to understand the mechanism of its medicinal value. Thus now there is a need to pay attention togene expression and its regulation to understand the human disease process and management (Dias et al. 2012) and simultaneously to know the effect of intake of medicinal herbs and its genetic basis. Thus cross kingdom genomics is a key to answer the regulation imparted by plant on human metabolic pathways.

Plants have provided as a vital foundation of nutraceuticals which are used by nearly two-thirds ofthe world's population for health advantages and avoidance of diseases. They also take part in an equivalent function in current pharmaceutical biology. In addition, a huge number of herbs have been developed for their anticancer properties (H. A. H. Said-al Ahl et al, 2017; S. Verma and S. P. Singh, 2008). Moringa oleifera belonging to the family of Moringaceae is an effective most useful nutritional and medicinal plant. However, Moringa is rich in nutritional value remaining tothe presence of a range of essential phytochemicals present in several organs like leaves, pods, and seeds which are edible and are used in numerous countries (including the various region of Africa)for their high relating to diet value (Anwar, F et al, 2007). Almost all tissue of the Moringa plant can be used as a traditional medicine for the treatment of a variety of illnesses such as respiratorydistress, skin diseases, ear and dental infections, diabetes, hypertension, anemia, and cancer (Oduro, I. et al, 2008; Charlette Tilokea et al, 2018). As well, the pharmacological and nutritionalvalues of the leaves extract containing bioactive compounds like antioxidants, vitamins A, B, andC, minerals, proteins and essential amino acids are well described by Leone et al (2015).Furthermore, the ilalian Ministry of health in compliance with the European Pharmaceutical Plantlegislation has to include Moringa seeds in the List of plant and Vegetal Integrators. In 2013, Charlotte Tiloke reported a Moringa extract to bring into play an antiproliferative effect in A549 lung cells by increasing oxidative stress, DNA fragmentation, and including apoptosis. In addition, In 2014 Jung published that M. oleifera leaf extract was able to prevent, inhibit, and halt the development of tumors in cancerous lung cells. In addition, In 2015, Tian and a co-worker found that a M. oleifera high-quality draft genome sequence and evaluate the genome to associated timbered plant genomes in order to elucidate the derivation of this species.

Conclusively, cross-kingdom regulation seems to be the key to answer the inevitable question of how do these medicinal plants regulate human transcriptome and hence identification of these novel mechanisms could greatly enhance our understanding of molecular signaling between species. Collectively, this concept not only prompts towards the role of these plant miRNAs in regulating the human target genes having a great significance in various diseases but also paves the path for future studies that might explore potential of miRNA mediated cross-kingdom regulation in, prevention and treatment of various human diseases including cancer.

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