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Panchagavya: An Unexplored Pathy in Healthcare

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ABSTRACT

Faecal transplant was first documented in 4th century China, known as "yellow soup". Faecal microbiota transplantation (FMT) refers to the infusion of a faecal suspension from a healthy person into the gastrointestinal (GI) tract of another person to cure a specific disease. But instead of administrating human feces why not try out traditional Ayurveda, since thousands of years, we worship cow as "KAMADEHNU", the God who fulfills our desire, give robust health and eliminates diseases, that is, Cow faecal transplantation in the form of PANCHAGAVYA, since it fits into our culture and also well accepted culturally and claimed to be prime rich resource base which has been clearly said in ancient text "*Gomaye Vasate Laxmi*". Panchagavya is a system of medicine just like homeopathy, allopathy, or naturopathy. We aim to decode the message and basis of this practice in modern scientific language.

INTRODUCTION

Panchagavya involves the use of five by-products of cow viz. Cow dung, urine, milk, curd, and ghee. The Ayurveda, the ancient Indian system of medicine, has detailed men7ons of the importance of cow's milk, curd, ghee, urine in the treatment of various human ailments. The ancient ayurvedic literature (Charak Samhita, Sushrut, Gadanigrah) suggests several pharmacological Applications of the substances obtained from Panchgavya. Religious ritual of Practice of Panchagavya prashan has been in existence for ages in our country. This practice was expected to deliver a person from all the sins. Sin in Sanskrit means papma. Papma is a synonym for disease. This ritual is practiced once every year during July and August at which time the *Vaccinia viraemia* is at its peak in cows. A systematic work needs to be carried out on chemical nature, biological activity, microbiology, and pharmaceutical aspects andmechanismofbioactivecompoundsinPanchgavya.Intherecentpastdueemphasishas not been given to cow therapy by the scientific community. We aim to decode the message and basis of this practice in modern scientific language.

Human gut microbiome: Human being is considered as Meta organism due to a symbiotic relationship with gut microflora. The human body has 100 trillions of microbes almost ten times more than body cells. It is like a forgotten organ. Aggregate genes in the microbiome are almost hundred times that of the human genome. Gut brain axis is now a fact. It consists of 3000-10000 species. Most of it makes up in colon is almost 60% dry mass of feces. Thus relation is not just simply a commensal, but a rather mutualistic symbiotic relationship.

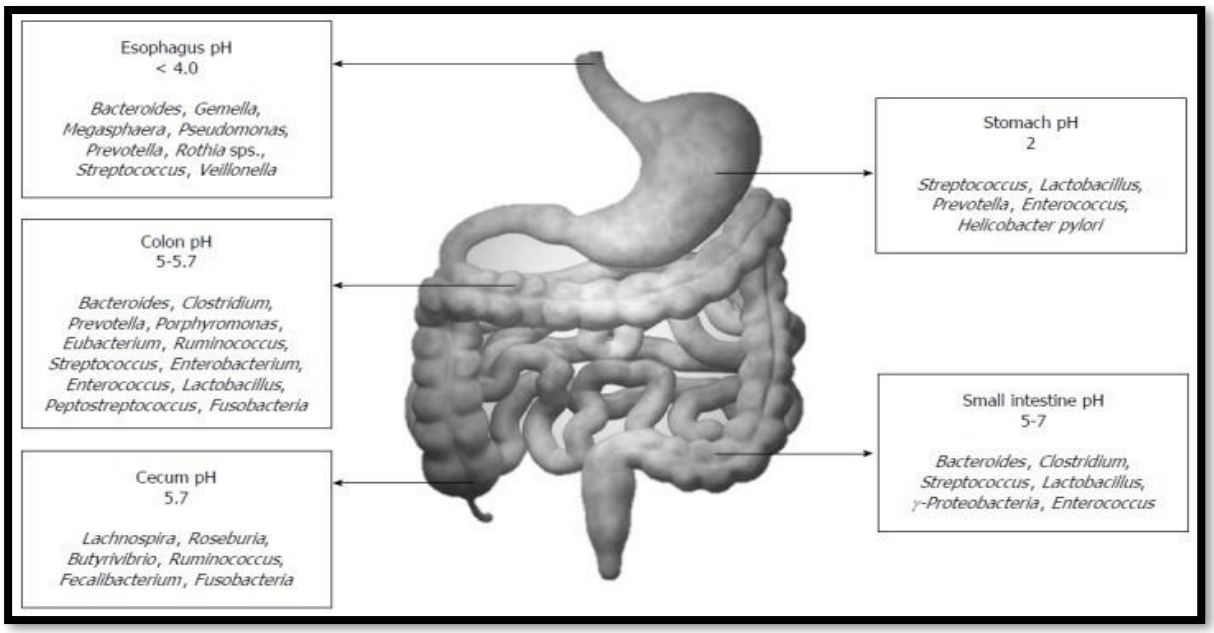

Figure No. 1: Distribution of the normal human gut flora.

(World J Gastroenterol. 2015 Aug 7; 21(29): 8787–8803)

The normal gut microbiota imparts specific function in host nutrient metabolism, xenobiotic and drug metabolism, maintenance of structural integrity of the gut mucosal barrier, immunomodulation, and protection against pathogens. Several factors play a role in shaping the normal gut microbiota. They include (1) the mode of delivery (vaginal or caesarean); (2) diet during infancy (breast milk or formula feeds) and adulthood (vegan-based or meat-based); and (3) use of antibiotics or antibiotic like molecules that are derived from the environment of the gut commensal community. A major concern of antibiotic use is the long-term alteration of the normal healthy gut microbiota and horizontal transfer of resistance genes that could result in a reservoir of organisms with a multidrug-resistant gene pool.

A preliminary study was carried out to confer the microbiological growth in every sample of panchagavya and a few combinations too.

Excellent microbial growth was observed in single samples of panchagavya. Good microbial growth was observed in the sample incubated with cow ghee compared to the sample incubated without ghee.

Table No. 1: Microbial count by the plating method

Sr. No.	Samples	CUF/ml
1	Cow dung	$4.8x10^7$
2	Cow urine	$3.2x10^7$
3	Cow milk	$5.6x10^8$
4	Cow curd	$6.1x10^8$
5	Cow ghee	$2.9x10^8$
6	Cow dung + Cow urine	$3.6x10^8$
7	Cow milk + Cow curd	$3.9x10^9$
8	Cow dung + Cow urine + Cow milk + Cow curd	$4.2x10^9$
9	Cow dung + Cow urine + Cow milk + Cow curd + Cow ghee	$3.8x10^{10}$

Properties of Panchagavya:

Panchagavya is by no means a new therapeutic modality, although it was only relatively recently that stool was shown to be a biologically active, complex mixture of living organisms with great therapeutic potential for recurrent *Clostridium difficile* infection and perhaps other GI and non-GI disorders.

Lyophilized Panchagavya helps in the optimized delivery of microbes as it provides enteric coating because of ghee. It enables to control of acid levels in the stomach.

Probiotic: The World Health Organization defines probiotics as live microorganisms that can provide benefits to human health when administered in adequate amounts. Several species such as *Lactobacillus casei*, *Lactobacillus plantarum*, *Lactobacillus bulgaricus*, *Lactobacillus acidophilus, Bifidobacterium longum, Bifidobacterium infantis, Streptococcus thermophilus*, *E. coli* strain, to name a few have been shown to impart immunomodulatory and gut barrier functions. These and several others have been used commercially in the management of human illnesses e.g., IBD and antibiotic-associated diarrhea. The fundamental concept of using these organisms in the treatment armamentarium is mimicking the physiological health-promoting functions of the "good" bacteria. The addition of a prebiotic could augment the effect of the probiotics. Prebiotics are defined as food ingredients that contain non-digestible oligosaccharides (e.g., galactooligosaccharides and inulin); and a probiotic and prebiotic are together called a synbiotic. The gut bacteria selectively ferment these fibers resulting in the synthesis of SCFAs, which in turn imparts the pro-health effects. Thus panchagavya acts as a health promoter.

Indications for Panchagavya:

1. Inflammatory bowel disease: Some suspect that IBD is due to a reduction in immune tolerance and subsequent overreaction of the host's immune system to harmful or non-harmful bacteria. IBD may be caused by the entire gut flora together or some specific types.

Some also suspect that inflammation in IBD is due to increased permeability of the inner lining of the colon, which may allow bacteria to invade the tissues and cause an immune reaction that leads to prolonged inflammation. Tissue damage in IBD results from the immunological misperception of danger within the naturally occurring flora or due to failure of normal tolerance to pathogenic bacteria. It is still unclear whether the inflammation that occurs is due to a specific subset of intestinal microbes or due to a problem with the tolerance of commensal gut flora.

2. Obesity: It is a physiological state that has emerged as a major health concern in populations. From literature, the animal models of obesity, the interplay between the dominant gut phyla, Bacteroidetes and Firmicutes, are shifted with a significant reduction of the former and a corresponding increase in the latter. The shift in the relative abundances of these phyla results in an increased capacity for harvesting energy from food and produces low-level inflammation. Several changes in host genetics and environmental factors have been used to induce obesity in animal models and thus provoke a change in microbiota composition. Remarkably, the energy harvest phenotype is transmissible simply by transplanting the obese microbiota.

3. Crohn's disease: It is a chronic gastrointestinal disorder with an unknown etiology characterized by an inflammatory response of the intestinal mucosa. An influential study by Cadwell et al. Sheds light on how the virome, genome, and microbiota might be interacting in the development of Crohn's disease. The gut microbiota, in addition to the virome and host genetics, were shown to play an important role in the etiology of a complex mammalian disease.

4. Autoimmune diseases: The auto-immune diseases (Diabetes, Multiple sclerosis, Psoriasis, etc) all result from inappropriate action of the adaptive immune system mediated by the gut microbiota. The introduction of bacterial polysaccharides from the commensal *Bacteroides fragilis* protects against the development of these autoimmune diseases.

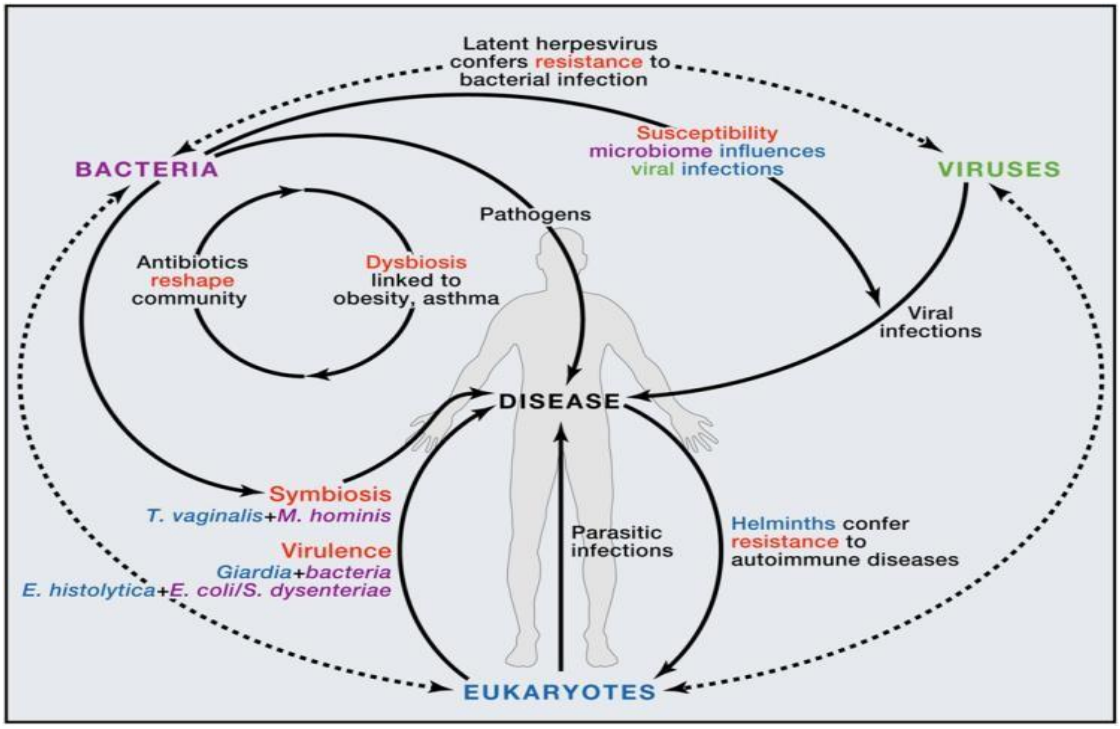

Figure No. 2: Effect of Interactions of Bacteria, Viruses, and Eukaryotes in Health and Disease

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Diseases have been traditionally studied under a paradigm of "one microbe, one disease." However, a new understanding is emerging on how disease phenotypes are a result of complex interactions between bacteria, viruses, and eukaryotes, as well as their interactions with the host or with certain drugs. Virulence of some eukaryotes is, for instance, linked to the presence of certain bacteria, such as in the case of E. histolytica and E. coli or S. dysenteriae. The susceptibility of the host to viral infections is conditioned by the particular configuration of the microbiota, whereas herpesvirus infection can confer resistance to certain bacterial infections. Antibiotics can significantly reshape the composition of the microbiota. As a clear correlation has been observed between many diseases and dysbiosis, the widespread use of antibiotics may be linked to the dramatic increase observed in autoimmune diseases over the last years. Conversely, helminths confer resistance to autoimmune diseases.

As we have seen, disease states are often correlated with imbalances in the gut microbiota. Restoring a healthy microbial community by the administration of panchagavya can be

proven to be a valuable tool in the treatment of certain diseases and also allow the impact of the microbiota in determining phenotype to be tested. For instance, obesity and several disease phenotypes induced by changes in host genetics cause dysbiosis in the gut. Remarkably, these phenotypes can be transferred to germ-free wild-type hosts simply by inoculating them with the microbiota from the deceased donors. Furthermore, the administration of panchagavya to a diseased individual can help in recovering microbial balance in the gut.

CONCLUSION

Taken together, the findings we have reviewed that to further advance our understanding of health and disease, we will require an improved characterization of the variability in the microbiota, a better understanding of how such variability can result in similar or different functional profiles, and more integrative studies that take into account the interaction between the microbiota, the host, and the environment to produce a phenotype. An increasing variety of disease states and disorders are being found to correlate with the host microbiota. Furthermore, detailed studies are to be done to elucidate microorganisms that show similarity to any identified culturable/non-culturable microbes.

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