PREDICTION OF MICROBIAL COMMUNITY STABILITY THROUGH LORENZ CURVE: A POTENTIAL TOOL FOR MICROBIAL COMMUNITY STUDIES

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Abstract: Microbial communities are organised, functionally active ecological units that are found widely spread in every ecosystem of the planet. They hold a significant place in most of the ecosystems they reside. This biological assemblage of microbial cells not only help in easy signalling between the microbial network for different metabolic activities but also in a way helps in rapid degradation of complex organic compounds into simpler inorganic ones. Stabilisation of the microbial communities is important to maintain a healthy and metabolically and functionally active ecosystem. These microbial assemblages are under constant environmental stress that results in alterations of its structure and composition which ultimately hampers the stabilisation of the microbial community. Functional diversity of the microbial community with significant functional evenness contributes extensively towards stabilisation of a particular microbial community. The higher the functional evenness of a microbial community, the higher will be its stabilization potential. The functional evenness of a particular microbial community is graphically represented by using Pareto-Lorenz curve. The extent of divergence or convergence of the curve from the line of evenness, decides the structure and microbial composition of the particular microbial community. This review focuses on the parameters that alter the structure and composition of a microbial community, the significance of stabilization and its measurement by the well known Lorenz curve.

Keywords: microbial community, stabilisation, functional evenness, Lorenz curve

1. Introduction:

Community refers to potentially interacting species existing in a particular niche or habitat at a particular period of time [1]. A community established with the involvement of multi-species microbial assemblages residing in a proximate habitat is termed as microbial community. Microbial assemblages contributing towards a microbial community interacts with each other for its proper functioning and metabolic activity. This interaction or the spatial arrangement among the microbial species enables the microbial population in enhancing certain activities like DNA exchange, signalling between the species and also for easy degradation of the complex substrates [2]. In other hand some of the ecologists define community in a far different way. According to them, community refers to a wide, diverse group of microorganisms co-existing in a particular niche with similar physical and chemical conditions but without any interaction between them [3]. Communities are highly complex but significantly organizational and operational ecological units that exists at a level that neither corresponds to a sample that is significantly small enough to be relevant for microorganisms and large enough to be relevant for ecosystem processes [1]. In reference to soil microbial ecology, the complexity of the soil microbial community can be observed by taking into account the example of a single gram of soil that harbours around 4000 diverse genomic microbial cells [4]. Apart from the complex nature of the microbial communities some of the other significant characteristics of microbial community like the structure, composition and the significance of a microbial community also vary from niches to niches. In this context, the microbial community residing in landfill leachate and that in the normal agricultural soil can be taken into account. In relation to their functional significance, the microbial assemblage contributing towards the microbial community in landfill leachate are responsible for the conversion of organic and complex matter into simpler and less toxic ones [5]. Similarly, microbial communities residing in the agricultural soil are responsible for regulating the nutrient cycles going on in it [6]. These communities in the soil are extensively important not only in maintaining soil quality but also on the crop productivity of the particular area [7]. In relation to the composition of a microbial community, the microbial species contributing towards an organised community also varies, as for example, the landfill leachate

harbours a diverse and a complex group of microorganisms but among them the predominant ones observed were Firmicutes, Proteobacteria and Bacteroides. In addition to these, archael and metagenomic species were also recorded. Thus it can be considered that microbial communities are the house of the rarer of the microbial species and also an inexhaustible resource [8] and a stabilization buffer of microbial cells [9].

Soil harbours the most diverse and the most complex microbial communities. Rich microbial colonization is the stepping stone for a series of phenomenon and processes going on in the soil for increasing its quality and structure [10]. They perform highly significant functions in the soil that either directly or indirectly affects soil quality, its fertility, nutrient cycling and also crop productivity [11]. The structure of a microbial community undergoes alterations in response to soil disturbances [12-16] and due to different farming activities like soil amendments, irrigation and soil tillage [17-23]. These agricultural management practices have a direct effect on soil microbiota [24, 25]. The variation in a microbial community also occurs with the distribution of individual plants in a particular niche space. The microbial communities are the indicators of environmental changes or perturbations as these communities responds to environmental changes more rapidly than the other microbial communities like the plant communities [26, 27]. In addition to this, dense microbial communities have the potential to colonize to the complex freshly exposed substrates available in the environment more rapidly and efficiently in comparison with the lichens, vascular and non vascular plants [28-33]. As they are the important ecological factors that drives Earth's biogeochemical cycles [34] any alterations or changes in the microbial community will ultimately affect the ecosystem process and results in decrease in ecosystem productivity. Thus soil microbial community can be used as a potential tool for the evaluation of soil quality [35, 36]. There are certain studies that demonstrate that plant species inhabiting a particular habitat controls or influences the microbial community [37-39] and the ecosystem processes [40, 41] of the particular niche space. The studies of Loreau et al [42] reveal that there is certain underlying mechanism that regulates the alterations of microbial community with definite loss of plant species which ultimately hampers the ecosystem functions. Experimental works of Hector et al [43] and Tilman et al [44] indicates that a greater functional richness of plants of a particular niche will encourage higher rates of primary productivity as it was already been revealed by the studies of Loreau et al [42] that there is certain underlying mechanisms or relationship between plant richness and microbial community, so with increase in plant richness there will increase in functional richness of microbial cells inhabiting that particular niche. Each microbial community has a well defined boundary. The boundary of a particular microbial community refers less significantly to the physical dimensions of a community rather than the extent over which stronger interactions are prevailing between populations [45]. Moreover, microbial communities can be divided into local community and phenomenological community. The local microbial community indicates microbial population interacting among each other within a smaller environment whereas the phenomenological community takes into account a range of macro scale habitats that is it takes into account the patches of local communities [46]. The phenomenological community can be constrained down to another subclass referred to as indexical community which indicates a set of population interacting directly with the defined population alongwith the local communities which ultimately affects the directly interacting populations [46]. Whether local or phenomenological communities, there is constant interaction among the microbial species. The constant and simultaneous interaction between them regulates or influences the conditions of the microenvironments which ultimately affect or catalyses the biogeochemical transformations [47]. These microorganisms enhance the conversion rates of organic compounds into inorganic ones thus enabling the primary producers to enhance the rate of biomass synthesis. At the same time the others involved in the community are responsible for inter-conversion of elements that uphold the interacting species and also have great impacts on the geological processes [48].

The microbial species involved in the community development are either in maximum abundances or are very negligible. But majority of the taxa involved in microbial community development are many of times tending to appear in relatively low abundances and only a few tends to occur in high abundances [49, 50]. In this context, it is clear indicative of the fact that microbial communities harbours majority of the taxa in low abundances which indicates that some of the taxa present in the microbial community as its members are either dormant or have least interacting ability and so less impact on the environment [1]. State of dormancy obtained by the microbial cells involved in the development of the microbial community mostly because of the different environmental stresses that causes the microbial cells to enter the state of dormancy [51, 52]. The microbial communities as a cluster are sometimes responsible for shifting of the environmental gradients on time scale that cannot be attained by microbes [53]. This is because of the heterotrophic nature of the microbial community they are capable of performing diverse function in addition to functioning as electron donors and acceptors [54, 55]. It is observed there are high similarities between the bio geographical patterns of microbial and microbial communities [56, 57]. But at the same time there are certain parameters that showed differences

in their patterns on comparison between the macrobial and microbial communities like the relationships between latitude and diversity as well as elevation and diversity [58-60].

2. Stabilizing microbial community:

Microbial communities are highly complex, significantly organisational and operational ecological units which predominate every corner of the planet. Microbial community network becomes complex depending on the surrounding environmental conditions. The higher the availability of the nutrient content the more complex the microbial community [61] whereas in low availability of nutrient content the complexity of the microbial community decreases [62]. The pre existing members of a microbial community are at times replaced by the newer ones due to implication of different environmental stresses. The stability, complexity and the heterogeneity of a particular microbial community depends mainly on the resilience and resistance of the microbial cells against the environmental uncertainty. In reference to soil microbial community, the array of environmental stress or disturbances confronted by the soil microbial community does allow the microbial community to stabilize themselves and thereby there are frequent structural changes in the pre-existed soil microbial community. In simpler words, disturbance can be referred to as a biotic or abiotic cause that results in the effect of a physiological or functional response of an ecosystem or as causal events that either alter the immediate environment or have possible repercussions for a community. Disturbances might also result in complete change or alteration of the structure of a microbial community [63, 64] thus implicating a complete shift of a microbial community from one stable state to alternative stable state [65, 66]. In certain cases, disturbances can also occur without any change in stable state. Stability in simpler words refers to the ability of maintaining a balance of the ecological stress conditions. Stability generally refers upon stable state and alternative stable state. Stable state refers to a condition where a community returns to its original composition or function following a disturbance. Alternative stable state refers to a condition where a community moves to a different but stable composition or function following a disturbance [67]. Stability of a particular ecosystem comprises of two significant matrices that are highly functional for comparing of disturbance responses of microbial communities residing in the particular ecosystem [68]. The property of resistance and resilience plays a significant role in rendering stability to a microbial community. Resistance and resilience are generally assessed based on the microbial community composition and function [68, 69] where resistance merely mean the capability of withstanding high degree of environmental stress and shows high degree of flexibility and physiological tolerance to different environmental stress by the microbial cells [70] whereas resilience refers to the capability of a microbial community to revert back to its predisturbance state after the period of perturbation [68]. In relation to this, there is another parameter that is closely associated with microbial community stability residing in a particular ecosystem, is adaptation. Most of the microbial communities inhabiting a particular niche posses the capability of resisting the compositional change at the time of disturbances only if the microbial community is complex and contains versatile physiologies [71]. There are studies that reveal that microbial communities' uses alternate options for withstanding the incoming environmental stress, either they start expressing a range of metabolic capabilities [70, 72] through gene expression. Existing literature indicates that a mixotrophic microbial community shows greater survival rates in fluctuating environment because of their ability to use alternate and diverse sources of carbon for generation of energy [73]. Studies and experiments carried out by Fenchel and Finlay [58] and Meyer [70] is indicative of the fact that there are certain specific traits of microbial communities and the member involved in the formation of it are responsible for rendering resistance or resilience to the particular microbial community. These traits include potential growth rates of the community members, high abundances and their widespread dispersal. The studies carried out by Allison and Martiny [68] explains the impact of disturbances on different existing microbial communities. In case the microbial community is resistant and does not change by the stress imposed upon by the environment, the pre-disturbance state of the microbial community is negligible. On other hand, if the particular microbial community is sensitive but resilient than the metabolic activity and other parameters occurring in the environment pre-distubance will regains its original state. Unlike to the previous situation, if a community is sensitive and not resilient, due to high redundancy of microbial species, the respective microbial community will produce the same process rates as that of the original. There are existing literatures that shows that even diversity of a microbial community plays an important role in confronting environmental stresses. The studies demonstrated by Allison [74], Downing and Leibold [75], Van Ruijven and Berendse [76] showed that the higher the richness and evenness of a particular microbial community, the higher is the resilience of the microbial community. The existing literature reports the recovery rates of the pre-existing microbiota of the amended as well unamended soil after severe drought condition [77]. The water stress experienced by the microbiota of the particular ecosystem was evaluated by taking into account physiochemical, chemical, biological and the biochemical parameters such as microbial biomass carbon [78], basal respiration and ATP or

eco physiological quotients [79], as well as specific biochemical properties such as hydrolytic soil enzymes related to C, N and P cycles [80,81]. Fernandez et al [82] tried defining microbial community stability by using a broad spectrum of definitions and the definitions encompasses two components- functional properties of the ecosystem and the change over time of the community composition. Finally Fernandez et al [82] and Juliastuti [83] concluded after long term experiments the ecosystem functional stability of a microbial community depends mainly on the complexity of microbial communities. Wittebolle et al [84] based on his microcosm based experiment explained the role of initial evenness of a microbial community on its functional stability. After long term experiments it was found that high initial evenness was important for attaining stability of the desired microbial community. One significant study carried out by van Elsas et al [85] indicated the impact of diversity on stability by constructing synthetic combinations of soil isolates rather than considering the normal pre-existed microflora and he concluded with a significant correlation between species richness of the microbial community with its resistance to invasion by an *E.coli* strain. Initially Griffith et al [86] tried to tease apart the relations set between microbial diversity and functional stability but finally Griffith et al, after long term experimenting works using high intensities of soil fumigation following a disturbance concluded that though there was no affect on the microbial production with the decrease in microbial diversity but there was significant decrease in some of the important ecosystem processes. So it was concluded that lower the microbial diversity, lower the resistance of the microbial community. Velasco et al [87], in his experimental studies indicated another parameter for the stability of the microbial community with high resistance and resilience is the extent of adaptation the community members to the incoming stress.

3. Lorenz curve:

Lorenz curve is a parameter that relates to the functional organisation of a particular microbial community residing at a particular niche space. The organisation of a particular microbial community in a definite ecosystem or niche depends on its response against the ongoing ecological-microbial interactions of the desired niche space. Previous studies on long term existence of a microbial functional organisation in a particular ecosystem was found mainly due to the dominance of the particular microbial community towards the ecological niche space and ongoing ecological process [88]. Lorenz curve can be in simpler words referred to as the graphical representation of the growth and distribution pattern of a particular microbial community in a definite niche space, which is also referred to as Pareto-Lorenz evenness curve [89]. It was first developed by an American economist Max Lorenz in 1905. In other words, it can be said that Pareto-Lorenz curve graphically represents the evenness of a microbial community inhabiting a particular niche space. These curves were based on the number of bands and band intensities of the DGGE profiles as described by Mertens et al [90]. Functional evenness of a microbial community is significant in gathering information regarding the distribution pattern of a microbial organisation. Functional evenness is a parameter used to measure the degree of species trait distributed regularly or evenly within the occupied the trait space which allows effective utilization of the entire range of resources available in the niche space [91].

These distribution curves are normally plotted to check the cumulative relative abundance of a particular species contributing towards development of microbial community [92]. The straight diagonal line on the graph represents perfect equality of the microbial distribution residing in a particular niche space and it is referred to as perfect evenness line that is 45˚ diagonal. The difference between the straight line and the curve line represents the extent of inequality of evenness of the microbial community. The cumulative proportions of the microbial species were plotted on the X-axis and the cumulative proportions of their intensities were plotted on the Y-axis of the graph. The graph that is obtained generally in this context is a convex curve. The more the Lorenz curve deviates from the line of evenness, the lesser is the evenness of the microbial community concerned. Lower evenness of a microbial community indicates that members of the microbial community are less evenly organised and a very small fraction of the microbial species is present in dominant numbers [93].

4. Conclusion:

Microbial community is a microbial network involving wide array of microorganisms controlling some of the significant environmental processes like nutrient cycling, degradation of complex organic substances into simpler inorganic substances, promoting plant growth by enhancing soil fertility and many more. This complex association of microorganisms are under continuous environmental stress that hampers the stability of these communities. Stabilization of any microbial community is of high significance to be metabolically and functionally active and so it is of great importance to check for the stability of a desired microbial community. Microbial stability of a heterogeneous microbial association can be achieved only if there is high functional
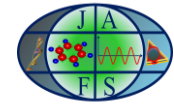
evenness in the community. The functional evenness of a microbial community can be determined by graphically representing with the help of Lorenz evenness curve. More the curve deviates from the line of evenness, more uneven is the microbial community and vice versa. So, it can be said that by using the Pareto Lorenz curve the functional evenness of microbial community residing within the human body can be estimated which will help in knowing the approximate dosage of drug required in destroying the pathogenic microflora without affecting the normal microflora of the body during a particular disease condition. In the same way it will help in knowing about the microbial community residing in the soil that will not only benefit the crop yield but the soil quality.

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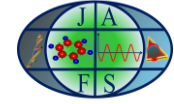
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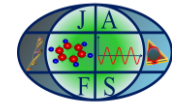
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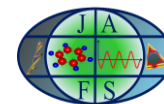
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