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Differential networks of rice pest injuries related to production situations and yield levels

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2 **ABSTRACT**

3   The changes of pest injuries relationships in provide the clues about the functions

4   **Keywords: Network analysis, Rice pests, Text Text Text Text Text**

1   INTRODUCTION

5 The aim of this study was to analyze how the structure of correlation network of pest injury co-occurrence
6 are different over 5 locations under investigation (?, Indonesia, ?, India, ?, Philippines, ?, Thailand, and
7 ?, Vietnam). By quantifying the important aspects of the position of the specific pest injury, information
8 based on network analysis could help to understand the formation and characteristics of co-occurrence
9 patterns. Furthermore, key factors for could be identified with this additional information.

2   MATERIAL & METHODS

10 The data are described in the previous article. We attempt to differentiate the patterns of co-occurrence of
11 rice pest injuries by constructing the networks from two type of production situations subgroups of dataset
12 from survey data. We identify

Co-occurence alaysis

14   We modified the scripts, which is designed to test for difference in co-occurrence patterns across
15 locations. We considered co-occurrence both of positive and negative correlations based on Spearman's
16 rank based correlation between paris of pest injuries within each dataset with the strength of relationship
17 represented by the correlation coefficient. The coefficients with p-values less than $p = 0.05$ were
18 considered. Negative correlations (indicative of) were also included in analysis. However, before
19 analyzing the data, identifying outlier sample using absolute hierarchical cluster analysis was performed.

2.1 Network analysis

Network models illustrated the co-occurring injuries within same locations where injuries represent nodes and the presence of a co-occurrence relationship based on correlation is represented by an edge. These correlation relation- ships were generated for each pair of microbial taxa within each ecosystem replicate as long as both taxa had abundance greater than 0. We made a consensus network of co-occurrence relationships within each ecosystem based on the strength of the correlation (from the Spearmans correlation), and co- occurrence relationships were only included if they occurred across all ecosystem replicates. Though this method has been illustrated to produce some spurious co-occurrence relationships, this rank-based correlation statistic does not require any transformation of variables to fit assumptions of normality and may outperform Pearsons correlations. To increase our level of stringency that may reduce the appearance of spurious co-occurrences within our networks, pairwise relationships had to be consistent across all datasets of a given location, greatly reducing the number of co-occurrence pairs.

Networks were produced using the igraph package where each network was the union of positive co-occurrences or negative co-occurrences (less than 0.25 or greater than 0.25) that were consistent within each ecosystem. Unconnected nodes were removed along with loops that indicate pest injuries were correlated with themselves using the delete.vertices and simplify functions, respectively.

We were also interested in generating statistics that describe the network that may be important for understanding co-occurrence relationships. We produced network statistics that describe the position and connectedness of microorganisms within each co-occurrence network. This included normalized node degree, which is the number of co-occurrence relationships that a microorganism is involved in a network normalized by the total number of nodes using the degree function (igraph package). We also calculated betweenness scores for each microbial taxonomic group using the between- ness function from igraph, which is defined by the number of paths through a focal microbial node. Additionally, we calculated clustering coefficients using the transitivity function for comparison to other networks.

2.2 Differential correlations

Fisher's z-test was used to identify significant differences between 2 correlations, based on its stringency test and its provision of conservative estimates of true differential correlations among molecules between 2 experimental conditions in the survey data. To test whether the 2 correlation coefficients were significantly different, we first transformed correlation coefficients for each of the 2 conditions, r_A and r_B, into $Z_A and Z_B, respectively. The Fisher's transformation of coefficient r_A is defined by : Z = \frac{1}{2} \log \frac{1+r_A}{1-r_A}. Similarly, Fisher's z-transformation of r is defined as$

$$Z = \frac{Z_A - Z_B}{\frac{1}{n_A} + \frac{1}{n_B}} \tag{1}$$

3 RESULTS

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$$\sum x + y = Z \tag{2}$$

4 DISCUSSION

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AUTHOR CONTRIBUTIONS

123 The statement about the authors and contributors can be up to several sentences long, describing the tasks
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125 the References section.

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