\subsection{Introduction}

Rice (\textit{Oryza sativa}) is a major crop in South and Southeast Asian. Generally, rice farmers cultivate 2 rice crops per year, with the typical seasonal crop cycles or rotations being rice-rice-fallow or rice-rice-secondary crops (corn, soybean, peanut). The Food and Agriculture Organization of the United Nations (FAO) estimates that approximately 70 percent of total lowland rice area produces 2 rice crops each year. The first crop is cultivated in the wet season, while another is in the dry season. The important role of seasonal cropping in the temporal dynamics of animal pests and diseases has been studied under farmers field survey in South and Southeast Asia by the use of multivariate techniques \citet{Savary\_2000\_Characterization, Willocquet\_2008\_Simulating}. The previous studies showed that Injuries profiles (the combination of injuries) differ from season to season in term of weather pattern. In the dry season, crop losses were lower than in the wet season. A previous study based on surveys done in farmers’ rice fields in the region of lowland rice were shown to be strongly associated with injury profiles.

In the previous chapter, the co-occurrence networks to yield co-occurrence networks, a methodological approach which has already proved fruitful in a variety of different applications. Basically, plant injuries caused by pests maybe affect on yield production. Therefore in this chapter, I attempted to characterize the yield-reducing factors by studying the changes in the co-occurrence patterns of rice injuries (e.g disease incidence, animal pest injury incidence) at different yield levels.

Differential network analysis aims to compare the connectivity of two nodes at 2 different conditions. As demonstrated by several studies, differential networks can identify important nodes implicated in my fields, and also provide critical novel insights not obtainable using other approaches. In this work, I explore the the properties of network of a complex association of rice injuries at different yield levels. Elucidating the rice injuries association represents a key challenge, not only for achieving a deeper understanding of injury association (injury profiles) but also for identifying the unique association. Given that the injury association is governed by a complex network of injuries association, it seems natural to explore network properties which may help elucidate some of different association presenting in the different seasons.

I explored the relation between local differential association and discuss the meaning of the results in the context of the crop health management, and discuss the potential implications of our findings for development of pest management with a view to future studies.

\subsection{Materials and Methods}

I used survey data were collected from farmers' fields ,analyzed co-occurrence relationships of rice injuries, and performed network analysis as described previously. Actual yield estimates were collected from each farmers' fields surveyed. Before analyzing. Survey data were grouped into 6 groups by different yield levels and seasons.

\textbf{Network Comparison Measures}

For the pair of $x\_{i}$ injury and $y\_{i}$ variable, I denoted the correlation coefficient based on Spearman's correlation coefficient by $c\_{xy}^1$ and $c\_{xy}^2$ in networks 1 and 2, respectively. To test whether the 2 correlation coefficients were significantly different of each network, I used Spearman's correlation coefficients, the p-values of the correlation test, the difference of the 2 correlations, the corresponding $p$-values, and the result of Fisher's z-test. First, I applied the Fisher $z$-transformation in order to stabilize variances due to sample size.

\begin{equation}

z\_{xy} = \frac{1}{2} \log\left[{\frac{1 + c\_{xy}}{1 - c\_{xy}}}\right]

\end{equation}

if we let $z\_{xy}^D $ and $z\_{xy}^W$ denote the $z$- transformation for dry and wet season variable pairs, respectively.

Next, differences between the two correlations can be test using following.

\begin{equation}

\triangle z\_{xy} = \frac{z\_{xy}^D - z\_{xy}^W}{\sqrt{\frac{1}{N\_{D}-3}+ \frac{1}{N\_{W}-3}}}

\end{equation}

$N\_{D}$ and $N\_{W}$ represent the sample size for each of season network for each country. The $Z$ has an approximately Gaussian distribution under null hypotheses that the population correlations are equal. The pair-wise correlation significants are considered at $p$vlaue < 0.05.

More and more researchers realized that gene module is high related with disease, but not individual gene. In gene expression network, gene is only related with other genes. Based on the characteristic of no self-loop, the graph of gene coexpression network is a simple undirected graph, and the diagonal elements of gene coex- pression matrix are all 0. The gene coexpression matrix is a square and symmetric matrix whose rows and col- umns correspond to the genes and whose element Aij denotes the coexpression relationship between genes. The graph of maximum clique network is a complete graph that every pair of nodes is joined by edge, and the adjacency matrix elements of the complete graph are all 1 except the diagonal elements. For a simple undirected graph G containing N nodes, its adjacency matrix A = (aij)N×N contains only 1 and 0. It is a square and symmetric matrix obviously. aij = 1 represents that gene i and j is coexpressed, aij = 0 means that gene i and j is not connected.

We set two thresholds T1 for adjacency matrix A1 in normal condition and T2 for adjacency matric A2 in dis- ease condition. A1(i,j) set to 1 if the value of A1 (i,j) greater than or equal to T1, otherwise, A1(i,j) set to 0. A2(i,j) set to 1 if value of A2(i,j) less than or equal to T2, otherwise, A2(i,j) set to 0.We integrated A1 and A2 into a matrix A after we had intersection the corresponding elements of A1 and A2. A (i,j) = 1 means coexpression value of gene i and gene j in A1 greater than or equal to T1, and coexpression value of gene i and j in A2 less than or equal to T2. Equation 6 summarized the pro- cess. We excavated cliques which have biological signifi- cance from A adjacency matrix to further investigate gene regulatory networks.

To differentiate the networks between yields

I set two thresholds T1 for adjacency matrix {A1} in high yield condition and T2 for adjacency matric A2 in low yield condition. A1(i,j) set to 1 if the value of A1 (i,j) greater than or equal to T1, otherwise, A1(i,j) set to 0. A2(i,j) set to 1 if value of A2(i,j) less than or equal to T2, otherwise, A2(i,j) set to 0. I integrated A1 and A2 into a matrix A after we had intersection the corresponding elements of A1 and A2. A(i,j) = 1 means coexpression value of gene i and gene j in A1 greater than or equal to T1, and coexpression value of gene i and j in A2 less than or equal to T2. Equation 6 summarized the process. We excavated cliques which have biological significance from A adjacency matrix to further investigate gene regulatory networks.

More and more researchers realized that gene module is high related with disease, but not individual gene. In gene expression network, gene is only related with other genes. Based on the characteristic of no self-loop, the graph of gene coexpression network is a simple undirected graph, and the diagonal elements of gene coexpression matrix are all 0. The gene coexpression matrix is a square and symmetric matrix whose rows and columns correspond to the genes and whose element $A\_{ij}$ denotes the relationship between injuries. The graph of maximum clique network is a complete graph that every pair of nodes is joined by edge, and the adjacency matrix elements of the complete graph are all 1 except the diagonal elements. For a simple undirected graph G containing N nodes, its adjacency matrix A = (aij)N×N contains only 1 and 0. It is a square and symmetric matrix obviously. aij = 1 represents that gene i and j is coexpressed, aij = 0 means that gene i and j is not connected.