The population structure of *Ganoderma boninense* in first generation oil palm plantings



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Introduction

Ganoderma boninense Pat. is a basidiomycete which causes stem rots on oil palm (Elaeis guineensis Jacq.) in a number of countries. In PNG disease levels are relatively low. Efforts to control basal stem rot have been hampered by a lack of knowledge of the population dynamics of the pathogen and long term studies on disease epidemiology. The population structure of the G.boninense within one oil palm plantation in PNG was investigated using mating type markers. Evidence for disease spread by dispersal of basidiospores is presented.





oms of basal stem rot of oil palm. Top right: early sign





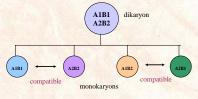
Palm collapse due to basal stem rot

In recent years the incidence of

Mating system of G. boninense

Heterothallic. bipolar incompatibility with a tetrapolar mechanism

Mycelia derived from fruiting bodies is dikaryotic and gives rise to spores of four different mating types (two parental and two recombinant) which can be determined by reciprocal mating tests amongst siblings e.g.



Homogenic mating incompatibility (rejection of identical alleles) restricts inbreeding and favours out-crossing within the population. Multiple alleles exist for both mating type loci. Recombination of these complex alleles or factors is known to occur in other basidiomycetes (Raper et al. 1958) but has not been detected in G. boninense (Pilotti, et al., 2002).



palms with disease in the upper portion of the stem has increased. Basidiospores are implicated in the spread of upper stem rot although no direct hereditary link has been found between isolates causing upper stem rot and those responsible for basal stem rot. However, a more distant hereditary link has been found (see map below)

Upper stem rot caused by G. boninense

Material and methods

Results

Spore prints were obtained from fruiting bodies on palms within the plantation in the Milne Bay Province, Papua New Guinea. Basidiospores from a single bracket (basidiocarp) were mated in all combinations with those from brackets collected from other infected palms in the field. Isolates obtained from other blocks within the plantation were also crossed with each other.

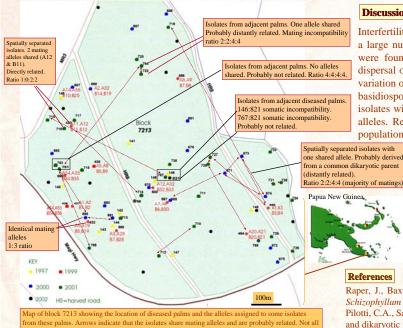
se on oil palm





Mating tests between dikaryotic isolates in the field showing mycelial

Mating tests amongst isolates from several blocks within the oil palm estate indicates that there are in excess of 100 mating alleles. Data for one block only is shown below. Different mating compatibility ratios have now been obtained amongst isolates within the population. The predominant ratio (2:2:4:4) strongly implicates basidiospores in disease spread. Within Block 7213 (shown below), isolate number 761 is from a palm with upper stem rot. This isolate is related to three other isolates within the same block. Two isolates have been found to have a direct hereditary link and two isolates have been found to share identical alleles.



Discussion

Interfertility tests between G. boninense isolates on many different palms has revealed a large number of mating alleles within the population. Several mating type alleles were found at distances of up to 15km in different estates, indicating successive dispersal of basidiospores after each breeding cycle by wind or vector(s). The genetic variation observed in the population on oil palm is derived from mating events between basidiospores. Mating events have previously been dominated by out-crossing between isolates within the population as indicated by the large number of unique mating type alleles. Recent results however, indicate that some alleles have persisted within the population for 2 to 3 years although new repeats are also being detected.

> In 2001, a higher proportion of isolates shared mating alleles with more than one other isolate. This may indicate that inbreeding is increasing and dominant isolates have successfully mated with more than one other isolate in the population. The majority of isolates however, still remain genetically distinct as indicated by their unique mating alleles. Further work using molecular markers is planned.

Acknowledgements

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References

Raper, J., Baxter, M.G. & Middleton, R.B. (1958). Genetic structure of incompatibility factors in Schizophyllum commune. Genetics 44, 889-900.

Pilotti, C.A., Sanderson, F.R. & Aitken, E.A.B. (2002). Sexuality and interactions of monokaryotic and dikaryotic mycelia of Ganoderma boninense. Mycological Research 106 (11): 1315-1322.