Disease Notes should be prepared in abstract form of 250-300 words, with a maximum of three references. No figures are allowed.
Disease Notes are intended as a record of first reports of a pathogen in a new area, or in a new host in an area where the pathogen has previously been reported. In general reports based on identification of a pathogen based on a single infected plant will not be accepted; exceptions may be made for instances of very strong evidence for first reports of a pathogen in a region where the pathogen has not previously been reported, with potential significant consequence. It is expected that a clear description of when and where the pathogen was detected, the host(s) affected, and the symptoms and potential significance of the disease will all be included in the text. For all types of pathogen, two independent methods of identification are required (see information on different classes of pathogen below); where sequences are used as part of the species identification, the sequences obtained should be deposited in one of the sequence databases, and the sequence accession numbers provided in the text of the Disease Note, plus the level of identity (nucleotide and/or amino acid % identity) to the most closely related species/isolates, and the accession numbers of those related sequences. If the sequences obtained are too short to be accessioned in the databases, the minimum standard would be presentation of the nucleotide % identity to the sequence(s) of the most closely-related isolate(s), preferably with amino acid % identity also presented. Fungal pathogens: For molecular fungal identification DNA sequences should be compared to sequences from type or authentic specimens, whenever available. In many cases a BLAST search is not sufficient and a phylogenetic analysis must be performed with multiple gene regions. Current taxonomic literature should be consulted and cited. Authors are encouraged to deposit cultures in a curated culture collection registered with the World Federation for Culture Collections (http://www.wfcc.info/collections/) and voucher specimens in an herbarium registered on Index Herbariorum (http://sweetgum.nybg.org/ih/).

Bacterial pathogens: A pure culture must be deposited and preserved in a recognized collection. At least two molecular tests for identity must be based on different principles, preferably (partial) 16s rRNA analysis and MLST of several housekeeping genes and/or when available use of validated specific primer pairs. The use of 16S rRNA analysis alone is not sufficient for a reliable identification of an isolate; other phenotypic tests are also preferred. Importantly, a host test with re-isolation of the inoculated pathogenic strain is required when a bacterium is described to occur for the first time in a certain geographic area, in case the isolation and identification (and diagnosis of the disease) is involved in trade issues and when the bacterium is described to cause disease in a new host. A reference strain, preferably a type strain or pathovar type strain from an officially recognized culture collection should be included in tests leading to definite identification. Current taxonomic literature should be consulted and cited. Authors are encouraged to deposit cultures in a curated culture collection registered with the World Federation for Culture Collections (http://www.wfcc.info/collections/).

Phytoplasma pathogens: Reports based on less than three 16S rDNA sequences from different plants leading to the appropriate phylogeny will not be accepted; sequences must be released in the databases prior to review. PCR-RFLP identification of strains is needed, based on wet lab experiments (not in silico RFLP). Identifications based on sequence data alone must include the sequencing of at least one phylogenetically informative gene other than 16S rRNA. For epidemiological significance, strong association of the phytoplasma presence and the symptoms must be demonstrated if reproduction of symptoms in experimental plants is not possible. If vectors are tentatively identified, proof that the

phytoplasma strain in the diseased plant and the potential vector(s) are the same is required (usually by sequencing of 16S rRNA and at least one additional informative gene). Identification of new reservoir hosts will only be acceptable if potential epidemiological significance can be demonstrated.

Viral pathogens: Of the required two identification methods, one may be a generic test, but the second method must be species-specific. Generic tests might include electron microscopy revealing particles consistent with the particular viral group (i.e. size of isometric particles, length and flexuous/rigid appearance of rod-shaped virions); broad-spectrum antibody detection (e.g. cross-reactive monoclonal antibodies); DsRNA pattern analysis; or genus-specific or family-specific primers to amplify a generic PCR product. A second set of species-specific primers to amplify a product specific for the target virus must result in determination of the sequence, and determination of the level of identity to the most related isolates in the databases. Species identifications should follow current ICTV criteria for separation of species and strains.

JPP Disease Note Checklist

1- Locations of observations (Region/County and Country) are specified.
2- Time of discovery (month and year) is included.
3- Number of plants observed, and disease incidence by location is specified.
4- Disease severity is specified (optional) and disease symptoms are described.
5- Identification of pathogen requires minimal morphological details and DNA sequence data (one or two loci, depending on fungus) including GenBank accession numbers.
6- Statement on observation being either a first report for the location(s), or a first report for the host. Possibly, when appropriate, cite the USDA fungus: host database (https://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm)
7- If this is a first report for a host, Koch's postulate needs to be completed: describe synthetically how and how many plants were inoculated, type and extent of symptoms obtained, and percentage of re-isolation success, including re-isolation method.
8- Short statement on significance of finding.
9- No figures please
10- 300 words maximum, no exceptions
11- Maximum of three references