11 highly pathogenic isolates of *F. solani* and 7 of *Alternaria* spp. were amplified with transcribed spacer region (ITS), translation elongation factor 1-alpha (TEF1-α) and Endo-polygalacturonase gene regions (*Endo-PG*) and submitted in the GenBank. Evolutionary history was analyzed with available sequences of *F. solani* and *Alternaria* spp. Evolutionary trees were constructed by MEGA 7.0 using maximum likelihood method having isolates falling under different sub-trees due to genetic variation in nucleotides. Cultural, morphological, pathogenic and molecular characterization of pathogens associated with fruit rot of strawberry was first time recorded in Pakistan.

Colletotrichum spp. causing anthracnose of _Capsicum annuum_ and _Cap. frutescens_ in Peninsular Malaysia
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Colletotrichum species are pathogens of chili anthracnose worldwide. Most reports on chilli anthracnose in Peninsular Malaysia were based on the work done in the 1980s and relied on morphological characteristics as well as ITS sequences for species identification. Recent studies based on molecular identification and phylogenetic analysis of ITS regions, as well as β-tubulin, actin, and glyceraldehyde-3-phosphate dehydrogenase genes, identified five species - *C. siamense*, *C. fructicola*, *C. scovillei*, *C. fioriniae*, and *C. truncatum* - that were associated with anthracnose of green and red *Cap. annuum* and *Cap. frutescens* in Peninsular Malaysia. Phylogenetic analysis using combined sequences showed that the isolates of the same species were grouped with the epitype strains. Pathogenicity testing showed that the tested isolates from each species were pathogenic to green and red *Cap. annuum* and *Cap. frutescens* upon treatment of wounded fruit, using both mycelial plugs and conidial suspensions as inoculum. Only five isolates of *C. truncatum* and seven isolates of *C. scovillei* were found to be pathogenic upon treatment of non-wounded fruit. The occurrence of five *Colletotrichum* spp. associated with chili anthracnose indicates that correct species identification is important to formulate not only effective disease management, but also effective quarantine policy.

Characterization of disease causing agent of apical necrosis of mango
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Bacterial apical necrosis is observed as a major threat for healthy mango production in different mango orchards of Punjab, Pakistan during the field survey conducted in three selected districts of Punjab viz. Multan, Khanewal and Muzaffargarh in 2015. Symptoms of bacterial apical necrosis were noticed on newly buds, stems and leaves during the survey. To validate the status of mango apical necrosis thirty eight orchards were visited in these three selected districts with the objective to assess the prevalence, incidence and severity of disease and to characterize the pathogen causing the disease at molecular level. According to the results, disorder was found widely distributed with 100% prevalence in Multan and Khanewal and 70% in Muzaffargarh. The highest (0.9%) bacterial apical necrosis incidence was recorded in Multan and Khanewal followed by Muzaffargarh where the lowest (0.5%) incidence was recorded. The maximum (4-5%) severity of bacterial apical necrosis was observed in Multan and Khanewal while minimum (3-4%) disease severity was observed in Muzaffargarh. Overall disease index in Multan (31%), Khanewal (12%) and Muzaffargarh (8%) were recorded. Samples of diseased mango buds were collected from each location surveyed, isolated on Nutrient Agar and Kings' B media. Using "toothpick method" DNA with high molecular weight was extracted and molecular based analysis was done using the primers 27F and 1492R. The strains was identified based on 16S rRNA gene analysis as *Pseudomonas syringae* strain ICMP 3023, *Pseudomonas syringae* strain NCPPB 281, *Pseudomonas syringae* strain ATCC 19310, *Pseudomonas syringae* pv. *tomato* strain DC3000, *Pseudomonas putida* strain ATCC 12633, *Pseudomonas savastanoi* strain ATCC 13522, *Pseudomonas syringae pv. phaseolicola* 1448A strain.

Identification of species of Ganoderma and Assessment of Basal Stem Rot Disease in Oil palm Plantations of the Cameroon Development Cooperation
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Oil palm is an important estate crop in Cameroon because it produces crude and kennel oil which has diverse uses in cooking and industrial applications. However, basal stem rot disease caused by different *Ganoderma* species seriously reduced yield in plantations. The objective was to identify the species, carryout a disease assessment and elucidate the effect of soil physiochemical properties on disease incidence and severity. The Incidence and severity of basal stem rot disease was studied in five plantations. Seasonal monitoring on 2 ha plots of different ages at these locations was done. Soil physiochemical analysis was carried out. Molecular identification was inferred using the ITS and mtSSU rDNA. The results showed that during the first year of observation disease incidence ranged from 3.9% in Bota to 23% in Mungo of 16 year old palms. By the second year of observation, the incidence had more than doubled in all the estates surveyed, ranging from 6.8 in Bota to as high as 55% in Mungo. Severity was also highest at Mungo and least at Bota. Although the first four principal components were strongly associated with soil properties and accounted for 100% variation in incidence and severity, disease incidence and severity only had a strong positive correlation with fine sand content and a strong negative correlation with C/N ratio. Seven species; *G. ryvardense*, *G. lobenense*, *G. tornatum*, *G. chalceum*, *G. steyaertanum, G. zonatum* and *Ganoderma* sp. 3. were associated with basal stem rot disease of oil palm. This study has established the serious epiphytotic potential of the basal stem rot disease of oil palm in Cameroon which is important in establishing appropriate control measures.

New methods for testing rice seed: LAMP assays for the detection of _Fusarium fujikuroi_ and _Magnaporthe oryzae_
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Fusarium fujikuroi and *Magnaporthe oryzae* are the causal agents of bakanae and rice blast, respectively. The estimated worldwide losses caused by both pathogens can reach up to 30% of the total production. The identification of both fungi on rice seed is a prerequisite for the pathogen-free certification and essential for the control of the pathogens. ISTA currently recomends methods for the detection of rice pathogens, based on the plating of 400 seeds and morphological identification of cultures growing on the seeds 10-days post-plating. This method may result in misidentifications due to the high number of shared characteristics among closely related species and the co-growth of multiple organisms. The LAMP assays developed in this study can overcome the drawback caused by culturing-methods. The LAMP assays were designed from the elongation factor 1-alpha and calmodulin genes for *F. fujikuroi* and *M. oryzae*, respectively. Both assays were validated according to the international EPPO standard (PM7/98) in terms of specificity, sensitivity, reproducibility and repeatibility. The results showed a limit of detection of 100-999 fg DNA for *F. fujikuroi* and 10-99 pg for *M. oryzae*. Five infected rice seed lots were used to compare the traditional culturing method with the LAMP method using a commercial DNA extraction kit. The results demonstrated the reliability of the LAMP methods for the surveillance of *F. fujikuroi* and *M. oryzae* in seed testing laboratories.