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Phylogenetic relationship of some Ethiopian *Phytophthora infestans* isolates and related species at mitochondrial DNA level

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Phytophthora infestans is a widespread and destructive pathogen on both potato and tomato. The objective of this study was to characterize and assess phylogenetic relationship of a group of isolates belonging to a previously unknown *Phytophthora* species recovered from potato leaves in Ethiopia. The characteristics of isolates were analyzed using mating type, SSR markers and mitochondrial DNA sequence. Phylogenetic analysis tools were employed to examine the position of Ethiopian isolates with other populations previously described in different regions worldwide through analysis of mitochondrial sequence data. The morphological characteristics of all isolates were typical of *P. infestans*. All isolates were of A1 mating type. The multi locus genotype system based on 9 SSR markers showed identical DNA fragment lengths characteristic of a single multi locus genotype. However, sequencing revealed that the isolates belong to two distinct lineages. One lineage corresponds to *P. infestans* haplotype Ia previously reported in Ethiopia and other lineage is new reported for the first time here. In later case the Ethiopian isolates, formed a distinct branch in the same clade with *P. infestans*, *P. mirabilis* and *P. phaseoli*. The isolates resemble a new species *P. andina* originally discovered in Ecuador (over 99% similar). Phylogenetic analysis using maximum likelihood supported the clustering of the same Ethiopian isolates with Ecuadorian isolates EC3421 and EC3425 from *S. muricatum* designated as *P. andina*. Unlike the *P. andina* lineages, the Ethiopian isolates appears to be primarily a pathogen of *S. tuberosum* indicating a deviation in host status previously reported for Ecuador lineages. Further, the Ethiopian isolates exhibited the A1 compatibility type with *P. infestans* tester isolates; while molecular data presented here clearly distinguished them from *P. infestans*, these Ethiopian isolates that share this feature form important component of the late blight pathogen causing disease on cultivated potato. Thus the isolates could represent putative novel species reported for the first time here.

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Usage of new method (molecular pathology) in tuberculosis diagnosis

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According to tuberculosis diagnosis, especially culture negative tuberculosis, pathology is the most important diagnostic method. Molecular pathology is a new method combining pathology and molecular biology method which improves sensitivity and specificity. In our hospital, *IS6110* gene fragment was chosen as the target gene of tuberculosis molecular pathology. *IS6110* has been found in *M. tuberculosis* and *M. bovis* but not in any of the other mycobacteria tested. Therefore, *IS6110* will be used as a specific probe for the identification of the *M. tuberculosis* complex. Moreover, *M. tuberculosis*, contain multiple copies of *IS6110*, therefore use of this target should result in enhanced sensitivity. Molecular pathology by *IS6110* was used in our hospital as a diagnostic method for 1 year. Dozens of patients were diagnosed successfully, which showed good sensitivity and specificity. However, sample of molecular biotechnology regularly confines to sputum or body fluid samples. In addition, diagnosis evidence of pathology only focuses on histomorphology and pathogen investigation. Both have low sensitivity and specificity. Molecular biotechnology leads pathology to a macromolecular level, which has better sensitivity and specificity than histomorphology. The usage of molecular pathology on tuberculosis diagnosis should be popularized.

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