

ABSTRACT

Viral diseases are one of the factors limiting potato productivity and accounts for 10-100% of the yield losses in Uganda. Infections by *Potato virus Y* (PVY) and or *Potato leafroll virus* (PLRV) are very important in inducing severe disease effects especially among varieties without *R* gene background. However, in Uganda there has been limited efforts to develop potato varieties with resistance to viruses largely due to lack of potential sources of *R* genes to guide the design of appropriate breeding schemes. The main aim of this study was to generate knowledge for enhancing resistance of potato varieties for improved management of viral diseases in Uganda using the reported *R* genes elsewhere. The specific objectives of this study were to: (i) establish the prevalence of potato viruses and their strains in the main potato growing regions of Uganda; (ii) identify potato varieties with *R* genes for resistance to potato viruses; and (iii) determine the level of resistance of *R* gene (*R_{yadg}*) to single and mixed infection by PVY and PLRV.

Virus diagnostic surveys were conducted in 15 potato growing districts across different altitudes in Uganda. Virus identification was done using Double Anti-body Sandwich Enzyme linked Immuno sorbet Assay (DAS-ELISA), Reverse Transcription Polymerase Chain Reaction (RT-PCR) techniques and virus sequencing. Varieties with *R* genes to PVY, *Potato virus S* (PVS), *Potato virus X* (PVX) and *Potato virus M* (PVM) were identified using molecular markers and their resistance status was evaluated based on variety reaction to the viruses. The level of resistance to viruses was assessed by measuring the severity of virus disease, type of symptoms induced by the viruses, virus titres in the plant, plant vigor and yield loss among varieties with *R* gene background relative to varieties without *R* gene background and was done in the screen house at Kachwekano.

The results of the survey showed that six viruses were widely distributed in Uganda. The most common viruses were: PVS strain^O (31-90.9%), PLRV (2.6-81.3%), PVY (7.1-54.5%) strain (PVY^O, PVY^N and PVY^{NTN}), and PVX strain X³ (8.3-53.3%), while the least frequently detected were PVM (18.2%) and PVA (9.0%). Single and mixed infection were detected in 42.8% and 26% of samples respectively. Double viral infections were 20.9%, triple infection were 4.2% and Quadruple infection were 0.9% of the samples analyzed. Of the double infections, PVY+PVS was the most common with prevalence of 2.1-18.2% followed by PVY+PLRV (1.8-21.3%),

PVM+PVS (7.9-16.7%), PLRV+PVX (2.4-14.3%), PVY+PVX (2.4-4.4%). Co-infection involving PVY+PLRV significantly ($P<0.05$) influenced disease severity. Low altitude areas (1,088-1,334 m.a.s.l) of Mbarara, Lwengo, Kibaale, Mubende and Pader had high viral disease incidence (48.29%-65.21%) and severity (3.69-4.20) relative to the areas in the highlands that displayed incidence of 14.64-40.53% and severity of 2.76-3.95. Molecular characterization of potato varieties in the Uganda germplasm revealed that 21 out of 71 varieties had at least one of the five *R* genes for virus disease resistance. The five *R* genes; *Ryadg*, *Rysto*, *Nbibr*, *Nsadg* and *Gmgt* that were detected condition resistance to PVY, PVX, PVS and PVM, respectively. Four varieties, *Markies*, *Sifra*, *Nakpot 5* and *Royal* had 3 *R* genes (*Ryadg*, *Nbibr* and *Nsadg*). The response of the varieties to viruses showed that varieties *Sifra* and *Royal* exhibited high levels of resistance to PVY and moderate reaction to PLRV and co-infection of PVY+PLRV. PVY titres from plants of *Royal* and *Sifra* which had *Ryadg* gene were approximately 10-15 fold less than that from plants without *Ryadg* gene. The *Ryadg* gene was effective in reducing the effects due to PVY on yield of *Sifra* and *Royal* varieties by 60-79% and for co-infection of PVY+PLRV by 22.1- 48.8%.

The study findings has provided the first large scale country wide evidence of PVY, PLRV, PVS, and PVX as viruses of agricultural importance in potato production occurring both as single and as mixed infections with a wide distribution affecting most of the potato varieties. The study identified 5 *R* genes for resistance to viruses PVS, PVX and PVY in 21 varieties. The extant *Ryadg* gene conferred high resistance to PVY and suppressed effects of mixed infection of PVY and PLRV to moderate levels. The virus disease management by pyramiding of *R* genes should be suitably applied to control single viruses and co-infections using the varieties identified with *R* genes and the resistant varieties should be deployed where the infection pressure was high especially in the low altitude areas.