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Multi-locational evaluation of maize (*Zea mays* L.) genotypes for high grain yield and resistance to *Maize streak virus* infections under natural conditions

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Maize Streak Disease (MSD) is the most serious biotic constraint to maize production in sub-Saharan Africa, threatening food security and incomes of farmers in the region. Field trials were established at Ohawu, Kpeve and Nkwanta representing coastal savannah, forest and transition ecozones respectively of the Volta region, during 2015 minor season to evaluate 16 maize genotypes for high yielding and resistance to *Maize streak virus* (MSV) infection. The fields were laid out in a Randomized Complete Block Design (RCBD) with four replications. The study revealed significant varietal, locational and genotype x location interaction effect ($P < 0.05$) on mean MSD severity scores and grain yields. Mean MSD severity scores were highest at Nkwanta, followed by Kpeve and the lowest at Ohawu. The improved varieties namely Abontem, Aburohemaa, Akposoe, Dorke, Etubi, Honampa, Omankwa, Obatanpa, PAN 12 and the breeding lines CRI001, CRI002, CRI003, CRI004, CRI005 and CRI006 which exhibited mild MSD symptoms had higher yields than Dzinu-Eve (a local cultivar). However, the study revealed significant genotype x location interaction effect with Akposoe, Etubi, Honampa and Polyarteritis Nodosa 12 (PAN 12) showing higher MSD symptom severity scores at Kpeve than at Nkwanta and Ohawu, whereas the other 12 maize genotypes had higher mean MSD severity scores at Nkwanta than Kpeve and Ohawu. It is suggested that genotypes that showed mild symptoms of MSD and also gave high grain yields should be further evaluated and released as a variety for the locations where they performed better.

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