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BRIEF REPORT

Iranian beet necrotic yellow vein virus (BNYVV): pronounced diversity of the p25 coding region in A-type BNYVV and identification of P-type BNYVV lacking a fifth RNA species

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Abstract Beet necrotic yellow vein virus (BNYVV) was detected in 288 of the 392 samples collected in Iran. A-type BNYVV was detected most frequently. The p25 coding region on BNYVV RNA-3 was amplified by RT-PCR and sequenced. Nine different variants of the highly variable amino acid tetrad at positions 67–70 of p25 were identified, i.e. ACHG, AHHG, AYHG, ALHG, AFHR, AFHG, AHYG, VLHG and VHHG. These are more different tetrad variants than have been reported from any other country. The first three variants were found most commonly. In 23 out of the 288 BNYVV-positive samples, we detected P-type BNYVV that had previously been identified only in France, Kazakhstan and recently in the UK. Surprisingly, none of these samples contained the fifth RNA species usually associated with P-type BNYVV in other countries. As in other BNYVV P-type sources, the p25 amino acid tetrad in positions 67–70 of the Iranian P-type consists of SYHG.

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Rhizomania is a major disease of sugar beet with worldwide distribution [2, 32]. In Iran, it was reported from the Fars province in 1996 and is now found in nearly all sugar-beet-growing areas of the country [11, 35]. Beet necrotic yellow vein virus (BNYVV) is responsible for the disease.

Molecular analysis of the four RNA species always present in natural BNYVV infections has revealed the existence of three major strain groups named A, B and P-types [15, 17, 20, 22, 23, 31, 42]. These three types were found to be highly conserved in Europe: recently determined sequences are practically identical to those determined more than two decades ago by Bouzoubaa et al. [3–5]. BNYVV sources from East Asian countries (Japan, China) are similar to the European A- and B-types, but not completely identical to them [17, 28, 30, 42].

The RNA-3-encoded p25 enables the systemic movement of the virus in sugar beet and is mainly responsible for symptom expression [12, 14, 36] and root proliferation [38]. Its ability to shuttle between the nucleus and the cytoplasm is necessary for symptom expression on leaves of *Chenopodium quinoa* [41]. The amino acid tetrad in positions 67–70 of p25 has been found to be highly variable in BNYVV sources collected at many different places in the world [18, 25, 29, 31, 34, 39, 42]. Chiba et al. [6, 7] found that the resistance response on leaves of selected lines of *Beta maritima* and the sugar beet variety Rizor depended on the composition of this tetrad. p25 was thus identified as an avirulence factor. Klein et al. [13] found that sequence variations of p25 influenced its oligomerization and pathogenicity in *Tetragonia expansa*. Acosta-Leal and Rush [1] identified $V_{67}E_{135}$ in p25 as the signature for resistance-breaking variants of BNYVV from the US as opposed to the WT motif $A_{67}D_{135}$. Koenig et al. [19] found that V_{67} P25 promoted a much higher virus accumulation in the rootlets of mechanically inoculated, partially resistant