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EP155 LAPVKTRRPIAADPLSQETVLSVKKWIQECSNNETRSHMLCSLSGPRYLPSRLVEVQPQDSGLHLKLVRGENLNPDAKYTALSYCWGNDS 90
EP146 LAPVKTRRPIAADPLSQETVLSVKKWIQECSNNETRSHMLCSLSGPRYLPSRLVEVHPQDSSLHLKLVRGENLNPDAKYTALSYCWGNDS 90

      EVLLAKALKTENLESYETEIPWETLPQTLQDAAVTTHRLGMHFVWVDSLCIIQDDDNDKVKEIAQMAQVYSHATLTIMVNRAARASDGFL 180
      EVLLAKALKTENLESYETEIPWETLPQTLQDAAVTTHRLGMHFVWIDSLCIIQDDDNDKVKEIAQMAQVYSHATLTIMVNRAARASDGFL 180

      HQRSPPLGTSNLLFRSPDGTEGWVSLYFKHEFWHEEKSKLDKRGWAMQEHLLSRRTLEIGTYMTEWSCRTERGLPSHSDGWSNDRLTRGF 270
      HQRSPPLGTSNLLFRSPDGTEGWVSLYFKHEFWYEEKSKLDKRGWAMQEHLLSRRTLEIGTYMTEWSCRKERGLSSHSDGWSTDRLTRGS 270

      GSPFQNARRRWSADDGGGRSMPEPSLAETNKTSWLEDSHILDVIMFSSANPDHQHPRPSVRGVLDTWEMVVKAYCDRSLSLPTDKILAIS 360
      GSPFQNVTWKWSTDDGRGRSTP--------ETSWLEDSHILDAIMFSSAHPDHQHPRPSVRGVLDTWKMVVKAYCDRSLSIPTDRILAIS 352

      GIAERFASSTPGIGRYAAGLWEEGLPTSLMWQTWDPSPSRPTEYQGPSWSWTAIRSRIWFEGAYGSLVSEILSVECVPLHPEAPFGALKS 450
      GIAERFASSNPGIGRYAAGLWEEGLLALLLWKTWHPSPSRPTEYQGPSWSWTAIRSDVWFMTVLKPLVSEILSVECVPLHPEAPFGALKS 442

      GTLRIKGPAIDIERRENEGLSSDARSSTLRIEPAVGIEGRENQGLSFDARRGYTRGWRCLGVDETYVDLDHYVRTLLDIADDVVDWAAPV 540
      GTLRIKGPAIDIERRENE-------------------------SLSFNAHPSHGHGWRCFGVDGAYVDFDDYVRIHLDLSDDVFDWTAPM 507

      TFLAIKRMVRLEVEQRYGLILRQEANGSWHRIGFLESHFDPEKPYPPIITADWPKREFTIV.                             602
      ALLAIEASERMEVEQRLGLILRQVSNDSWHRIGTVEFRIDPEKPYPSIFTADWPKREFTIV.                             569
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Figure S8 Amino acid alignment of candidate *vic7* alleles in strain EP155 (*vic7-2*) and in strain EP146 (*vic7-1*). The alignment was performed using MegAlign in Lasergene (DNASTAR Inc., Madison WI) with manually annotated amino acid sequences. Note that, in contrast to *vic2, vic4,* and *vic6*, the *vic7* alleles are quite similar to each other, except in the C-terminal region. The conserved HET domain found in this candidate *vic* gene is underlined.