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Structural basis for recognition of AvrPtoB by Pto

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Physical interaction of the host resistance (R) protein Pto kinase with two sequence-unrelated effector proteins AvrPto or AvrPtoB from *pseudomonas syringae(P.s.) pv. tomato* triggers Prf-dependent resistance to bacterial speck disease in tomato. It currently remains unknown about the mechanisms by which Pto recognizes AvrPtoB and thereby initiates disease resistance. In this report, we present the crystal structure of AvrPtoB in complex with Pto. Unlike the Gly-Ile-Asn-Pro loop utilized by AvrPto, a short loop formed by Ala-Val-Ala in AvrPtoB interacts with the P+1 loop of Pto, forming a distorted anti-parallel, rather than parallel as observed in AvrPto-Pto complex, β -sheet. Packing of a short α -helix from AvrPtoB against a large loop and an α -helix of Pto seems to dominate the AvrPtoB-Pto interaction. Current results uncover the mechanism of AvrPtoB recognition by Pto and, together with our previous data, provide the structural basis for how the same host protein can be targeted by two distinct effector proteins.