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Inferring the origin and trajectories of recent invasions of wheat yellow rust strains from worldwide population structure

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Several important cases of recent invasions have been reported at continental scales for *Puccinia striiformis* f.sp. *tritici* (PST), in line with its long distance migration capacity. These include the incursion of the disease into North America, South America, Australia, South Africa as well as the most recent worldwide invasion of two aggressive strains adapted to high temperature. Despite the economic importance of these invasions, little is known about their origin and invasion trajectories, crucial in anticipation of future invasions. Inference on their origin and trajectories could be made through genetic analyses of worldwide pathogen populations. We analyzed the multilocus microsatellite data and the pathotypes of a set of 409 isolates representative of the distribution of the fungus on six continents, including the recently invaded strains to infer on the worldwide PST population structure and the origin of recent invasions. The Bayesian and multivariate analyses of worldwide representative isolates, excluding these invaded strains and pathotypes, partitioned them into six distinct genetic groups associated with their likely geographical origin. The inclusion of the representative isolates of recent invasions into the analyses confirmed the origin of these invasions. Our results indicated Middle East-Red Sea Area as the most likely source of newly spreading, high-temperature-adapted strains; Europe as the source of South American, North American and Australian populations; and Mediterranean-Central Asian populations as the origin of South African populations. The worldwide population subdivision and the origin and trajectories of these invasions emphasize the importance of human activities on recent long-distance spread of the disease.