

T.G. Terefe^{1*}, B Visser², W.H.P. Boshoff²

¹ARC-Small Grain, Private Bag X29, Bethlehem 9700, South Africa; ²Department of Plant Sciences, University of the Free State, P.O.Box 339, Bloemfontein 9300, South Africa

*Email: terefet@arc.agric.za

INTRODUCTION

Leaf rust caused by *Puccinia triticina* (*Pt*) is a major disease of bread wheat, particularly in the winter rainfall wheat growing regions of South Africa (SA). Studying the virulence profiles and genetic variation of the *Pt* population is crucial for effective management of leaf rust using genetic resistance. This poster presents results of *Pt* race surveys conducted in SA during four years (2017 to 2020), impacts of new races on commercial wheat cultivars, and the genetic relationships between new and existing *Pt* races.

MATERIALS AND METHODS

To determine the phenotypic diversity of *Pt*, infected wheat leaves were collected from commercial wheat fields and rust trap nurseries across the major wheat growing regions of SA. A suspension of urediniospores prepared in Soltrol-170 mineral oil was spray-inoculated onto one week old seedlings. Inoculated seedlings were placed in a dew chamber at ±100% relative humidity for 14-18 hours and then moved to a glasshouse at ±20°C. Infection types (ITs) were recorded two weeks after inoculation using a 0-4 scale. *Pt* races were identified based on their avirulence/virulence profiles on seedlings of 16 standard differential lines. To determine the impact of new *Pt* races on wheat seedling response, a collection of SA bread wheat cultivars and elite breeding lines, received from breeding companies during the 2020 evaluation cycle, was evaluated in the seedling stage. Procedures were similar as used during race analyses. Isolates of *Pt* races CBPS, MCDS, and CFPS were included as controls and all experiments were replicated. Infection types of 0; to 2+ were considered as avirulent. The genetic relationships between the new and existing South African races were determined using described microsatellite markers (Boshoff *et al.*, 2018).

RESULTS AND DISCUSSION

Nine races were identified from 366 isolates that were successfully pathotyped (Table 1, Fig. 1) Races CFPS, CDPS, MCDS and CBPS were most commonly found with average frequencies varying from 18% (MCDS and CBPS) to 27% (CFPS). The frequency of MFPS was about 10% whereas the remaining four races were observed at less than 3% frequency. Two new races (MFPS and MCPS) were identified during this study, increasing the number of new *Pt* races reported over the past 10 years to nine (Terefe *et al.*, 2014; Boshoff *et al.*, 2018). MFPS, which is virulent on the key resistance genes *Lr1*, *Lr24*, and *Lr26*, was first detected in 2020. Its virulence profile is similar to that of existing races CFPS, CDPS and MCDS. Race MFPS differs in virulence from CFPS on *Lr1*, from CDPS on *Lr1* and *Lr26* and from MCDS on *Lr3ka*, *Lr24* and *Lr30* (Fig. 2). Race MCPS was first detected in 2017. Except for its virulence on *Lr3ka* and *Lr30*, MCPS is similar in its virulence profile to the existing race MCDS.

Seedling infection type data for 103 South African wheat varieties revealed that 35 of the entries are susceptible to races CBPS and MCPS, followed by race MCDS (38 susceptible), MFPS (51) and CFPS (77). With virulence to *Lr24* and *Lr26*, races CFPS and MFPS are considered to remain prevalent and threatening compared to the other races.

Microsatellite analysis revealed a close genetic relationship between race 3SA146 (MCDS) and the two new races 3SA127 (MCPS) and 3SA170 (MFPS) (Fig. 3). This grouping was supported with STRUCTURE analysis (Fig. 4), where an F_{ST} value of 0.58057 indicated significant differentiation between the four sub-populations. Thus, while the phenotypic data suggested that race MFPS developed locally through a single step mutation from race CFPS by gaining virulence for *Lr1*, the genetic data rather supports the development of both MFPS and MCPS from 3SA146 (MCDS).

CONCLUSION

Two new races, namely MCPS and MFPS, were identified in this study. MFPS appears relatively more virulent on current cultivars than most of the existing *Pt* races. With the detection of MCPS and MFPS, the number of new *Pt* races reported over the past 10 years increased to nine, which means that on the average, about one new race has been identified every year. The results indicate continued variability of the *Pt* population in SA and underscore the need for regular surveillance to timely detect and use new races to screen and identify effective sources of resistance.

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Table 1. Avirulence/virulence profiles of *Puccinia triticina* isolates collected from different localities in South Africa from 2017 to 2020.

Pt race		Avirulence/virulence formula
SA notation	NA notation [#]	
3SA10	CFPS	1, 2a, 2c, 9, 11, 16, 18/3, 3ka, 10, 14a, 17a, 24, 26, 30, B
3SA38	CDPS	1, 2a, 2c, 9, 11, 16, 18, 26/3, 3ka, 10, 14a, 17a, 24, 30, B
3SA146	MCDS	2a, 2c, 3ka, 9, 11, 16, 18, 24, 30/1, 3, 10, 14a, 17a, 26, B
3SA115	CBPS	1, 2a, 2c, 9, 11, 16, 18, 24, 26/3, 3ka, 10, 14a, 17a, 30, B
3SA145	CCPS	1, 2a, 2c, 9, 11, 16, 18, 24/3, 3ka, 10, 14a, 17a, 26, 30, B
3SA248	CFPS	1, 2a, 2c, 9, 11, 16, 18/3, 3ka, 10, 14a, 17a, 24, 26, 30, B
3SA144	SDDN	3, 3ka, 9, 10, 11, 16, 18, 26, 30/1, 2a, 2c 14a, 17a, 24, B
3SA127	MCPS	2a, 2c, 9, 11, 16, 18, 24/1, 3, 3ka, 10, 14a, 17a, 26, 30, B
3SA170	MFPS	2a, 2c, 9, 11, 16, 18/1, 3, 3ka, 10, 14a, 17a, 24, 26, 30, B

[#]Races are named using a letter code based on their virulence pattern on differential lines (Long and Kolmer, 1989).

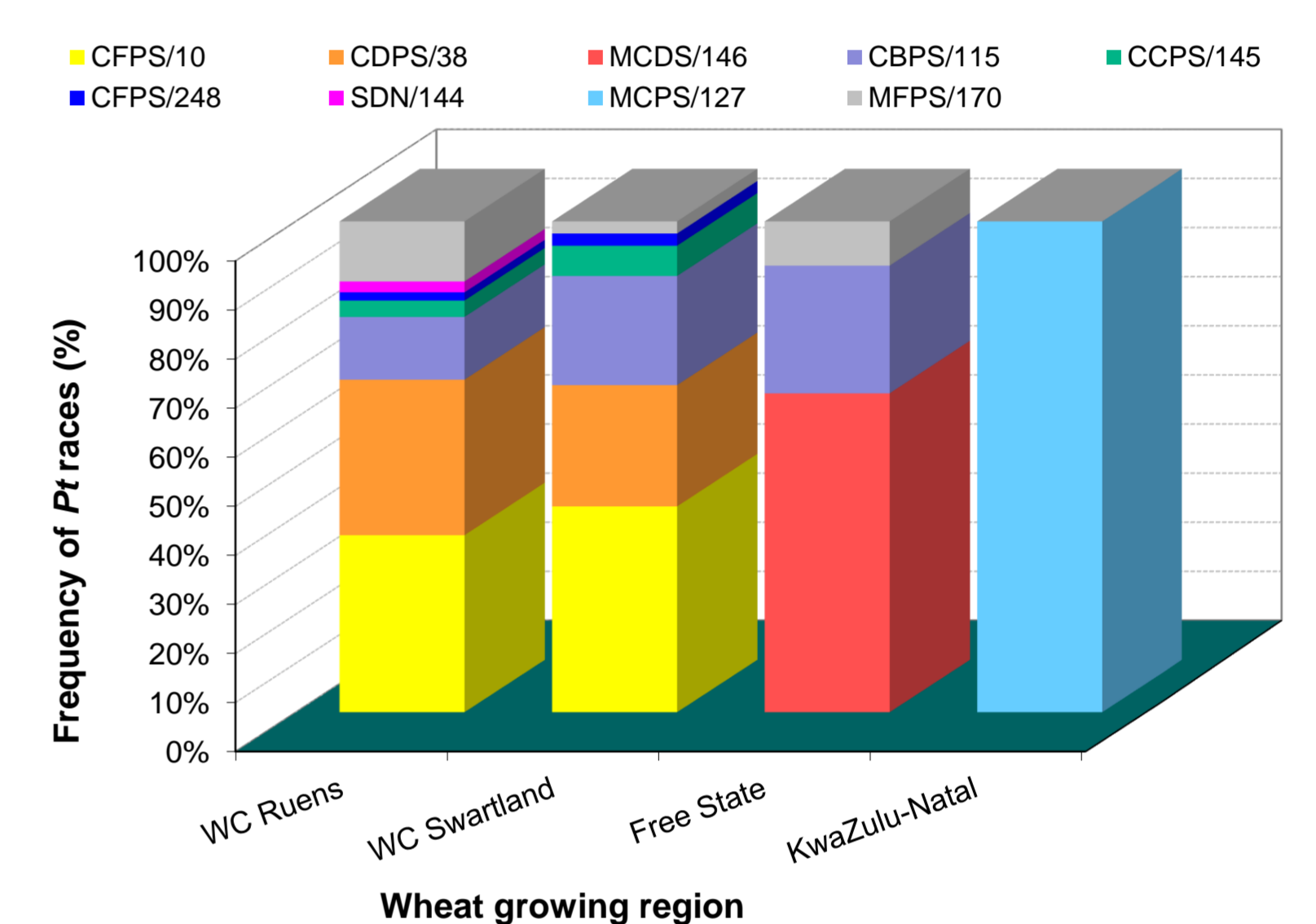


Figure 1. Distribution of *P. triticina* races in the Western Cape (WC), Free State and KwaZulu-Natal wheat growing regions of South Africa during 2017-2020.



Figure 2. Comparative seedling response for RL6007 (*Lr3ka*) to an isolate of *P. triticina* race MCDS (low, 2 leaves left) and race MFPS (high, two leaves right).

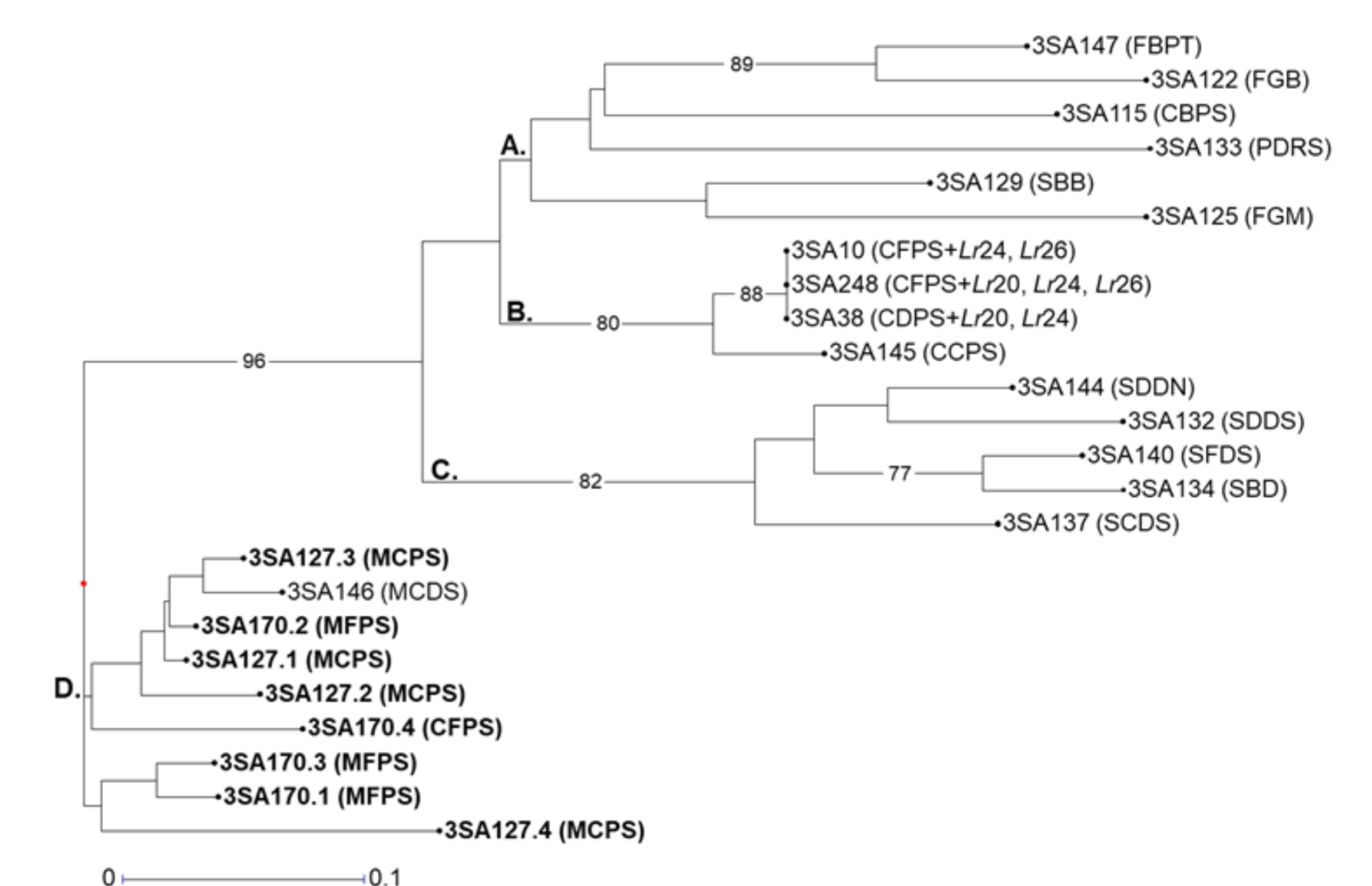


Figure 3. Detecting genetic relationships between new (bold script) and existing South African *Puccinia triticina* races using an unrooted neighbour-joining tree prepared with DARwin 5.0.158 (Perrier *et al.*, 2003). Bootstrap values above 75% are indicated on the connecting branches.

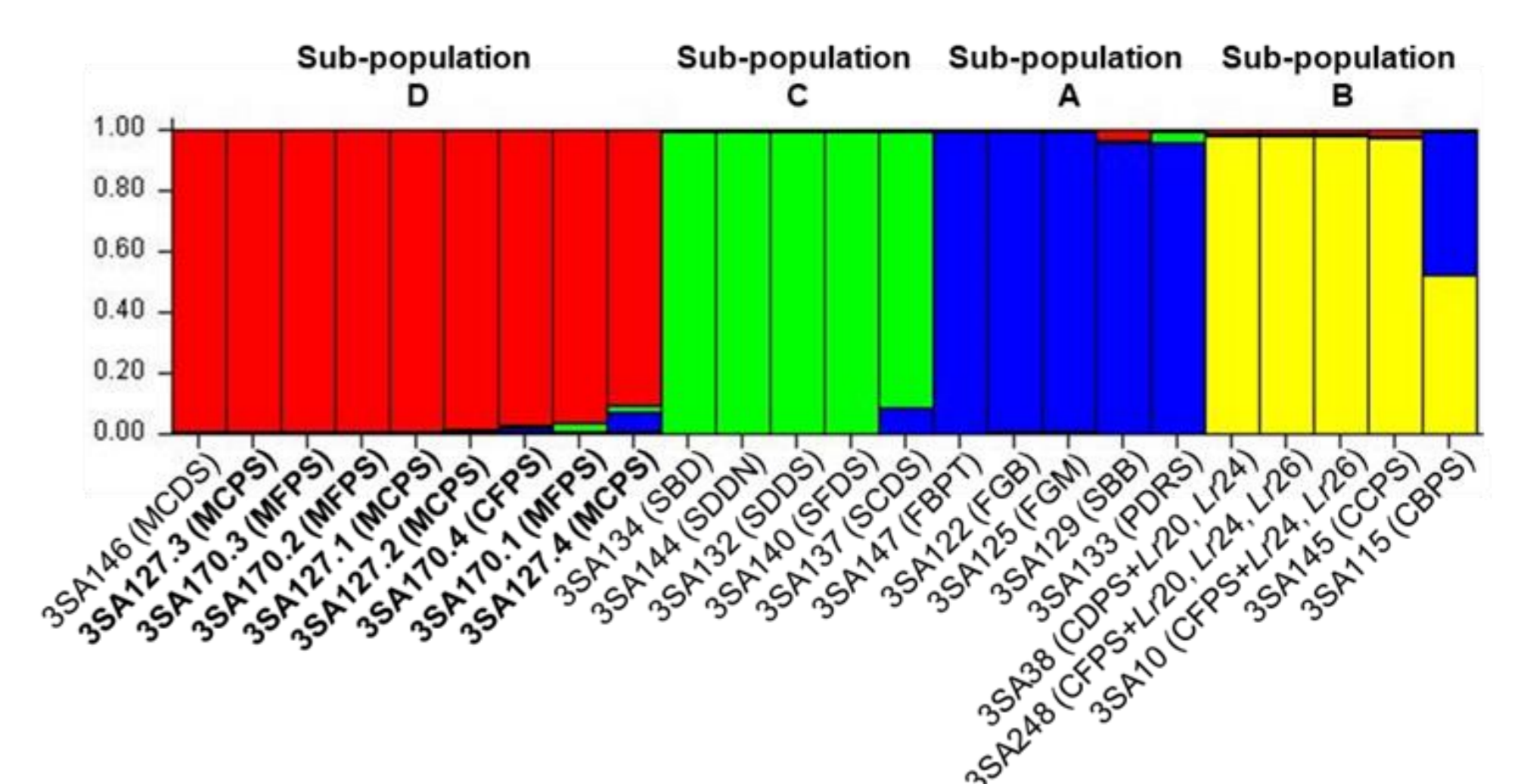


Figure 4. Grouping of new (bold script) and existing South African *Puccinia triticina* races into four sub-populations based on the ad hoc ΔK statistic (Evanno *et al.*, 2005) within STRUCTURE 2.2.3. Labelling of the sub-populations mirror the neighbour-joining tree.