



Corrigendum: Whole Genome Sequencing of Australian *Candida glabrata* Isolates Reveals Genetic Diversity and Novel Sequence Types

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A Corrigendum on

Whole Genome Sequencing of Australian *Candida glabrata* Isolates Reveals Genetic Diversity and Novel Sequence Types

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In the original article, there were a small number of transcription errors in **Figure 1** as published.

There are:

The label “Norway 6” (at position 6 o'clock) was incorrectly “positioned” with isolate WM_18.31 (ST45) and should have been positioned with “Norway 5.” This is now corrected.

Isolates Taiwan 1 and Taiwan 2 should be positioned together. In addition, the isolate WM_18.57 was inadvertently omitted from the ST16 “bubble.”

Isolate WM_18.51 should have been placed in the group under ST46 instead of ST59. The corrected **Figure 1** appears below.

The authors apologize for these errors and state that they do not change the scientific findings of the article in any way. The original article has been updated.

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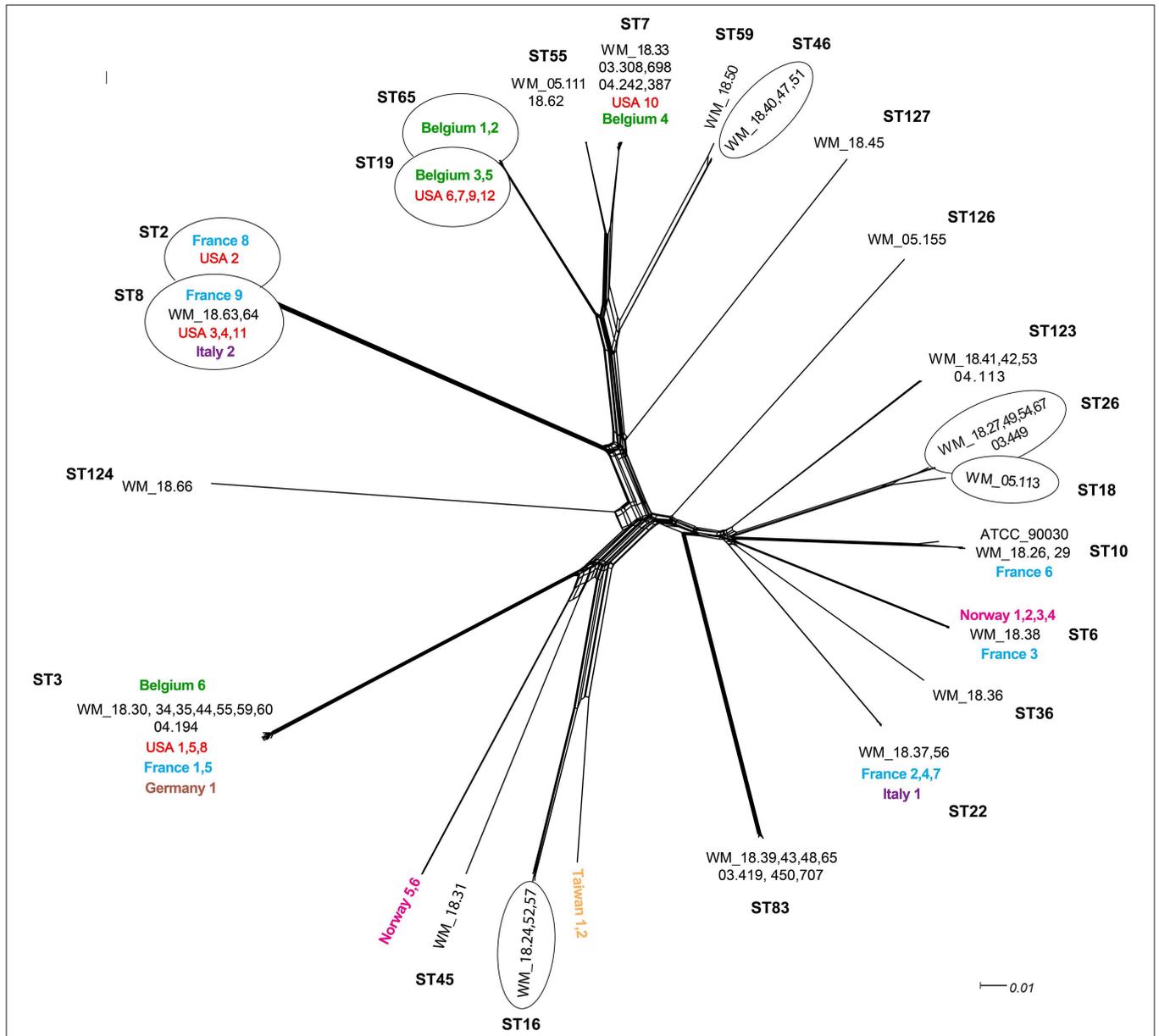


FIGURE 1 | Unrooted network tree depicting the association between Australian *Candida glabrata* isolates and international isolates from seven countries based on their whole genome sequences. All clusters in the tree have been represented by different sequence types (STs) except Norway 5, Norway 6, Taiwan 1 and Taiwan 2 which have previously unassigned (new) STs. New sequence types (STs) from Australia are ST123, ST124, ST126 and ST127. Isolates representing a particular ST in branches, which contain multiple STs, are put in circles. The colors depict isolates from different countries: Black, Australia; Green, Belgium; Blue, France; Brown, Germany; Purple, Italy; Pink, Norway; Yellow, Taiwan; Red, United States. The Australian isolates have names starting with WM_ and the international isolates where named according to the country of origin, all followed by a numerical scheme. For isolates from same country in a cluster, the country name was followed by numerical identities of the isolates separated by commas. For example, in ST7 cluster, WM_18.33, 03.308,698, 04.242,387 (where 18, 03 and 04 are years of isolation followed by isolate number).