Letters

Multiple rounds of ancient and recent hybridizations have occurred within the Aegilops–Triticum complex

In response to the Letter by Sandve et al. (2015) in New Phytologist (this issue, pp. 9–10), we reiterate our earlier conclusion that multiple rounds of both ancient and recent hybridizations have likely occurred within the Aegilops–Triticum complex.

The nomenclature of Aegilops–Triticum complex

We agree with Sandve et al. (2015) that the nomenclature of Aegilops/Triticum lineages is complex. Indeed, there is a contradiction in how they themselves have defined ‘the D genome lineage’ in their Letter (Sandve et al., 2015), compared to their earlier paper (Marcussen et al., 2014). Fig. 1 of Sandve et al. (2015) defines it as a clade comprising D + S* + M genome species; this definition is consistent with the clade we identified in our cpDNA phylogeny (Fig. 1 of Li et al., 2015). By contrast, the nuclear gene phylogeny of Marcussen et al. (2014) places M-genome species (e.g. Ae. comosa) within the B-genome lineage, not the D-genome lineage (see Fig. S6 of Marcussen et al., 2014). This contradiction between the chloroplast and nuclear phylogenies is consistent with our previous inference of a complex hybridization history for the D-genome lineage. It is not consistent with a single homoploid hybrid origin of the D + S* + M clade, as inferred by Sandve et al. (2015).

Moreover, contrary to the assertion by Sandve et al. (2015) that we confounded the modern D genome and the D-genome lineage (as defined in Fig. 1 of Sandve et al., 2015), we explicitly drew this distinction in our analyses (e.g. Table 2 of Li et al., 2015; showing results both for extant D-genome species and for ‘the ancient D-genome lineage’). We also explicitly considered the single homoploid hybrid origin model favored by Sandve et al. (2015) for the D-genome lineage (see Fig. 2a of Li et al., 2015); however, the conflicting chloroplast and nuclear phylogenies described earlier led to our inference of a more complex hybridization history.

Ancient and recent hybridizations within the Aegilops–Triticum complex

Regarding the timescale of the hybridization event(s), we agree with Sandve et al. (2015) that ancient homoploid hybridization between ancestral genomes of A- and B-genome lineages likely played a role in the formation of the ancestor of the D-genome lineage. However, we reassert that the inference of a single, ancient homoploid hybrid origin specific to the D-genome lineage (D + S* + M species) – is not conclusively supported by the nuclear gene trees of Marcussen et al. (2014). Under their hypothesis, Aegilops tauschii and Ae. sharonensis should share the same pre-speciation ancestry because they are included in the (D, (S*, M)) clade. As such, the two species should be phylogenetically sister, relative to species in the lineages of the two putative ancestral genome donors, S and A. However, as we noted in our previous Letter, in 40% of the nuclear gene trees, one of these D-genome lineage species is grouped as sister to an S- or A-genome lineage species (Li et al., 2015). Two of these topologies are shown in Fig. 1. These data imply a more complex evolutionary history than can be explained by any single hybridization event.

Finally, we agree with Sandve et al. (2015) that sequencing and analysis of additional diploid and polyploid Aegilops–Triticum species will likely provide new evidence for additional hybridization events.

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