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Evolutionary dynamics of the restorer and a non-restorer allelic Rfo locus.

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The Rfo locus, first described in Asian radish cultivars and later introduced into Brassica, is involved in the restoration of fertility in the Ogura cytoplasmic male sterility system (CMS). CMS systems are constituted of two actors: a mitochondrial protein that causes male sterility and a nuclear gene that encodes a mitochondria-targeted protein able to impair the expression of the sterility gene.

The nuclear restorer gene in the Rfo-Ogura system, as all identified restorer genes (with the only exception of the Rf2 Texas maize restorer), encodes a protein belonging to the pentatricopeptide repeat (PPR) family. The PPR gene family is a very large family in plants, with about 450 members in *A. thaliana*, and their function is largely unknown, although some members have proven to play roles in posttranscriptional organelle gene regulation.

Recent studies analyzing chromosome regions with duplicated PPR genes (allelic variants of a restorer locus in rice and two chromosome regions in *A. thaliana*) suggest revealed high levels of recombination in these regions. In addition, restorer genes (because of their ability to adapt to specificity changing/fast evolving targets) are evolved in a similar way as “resistant genes”. Anyway, evolutionary dynamics of these loci is largely unknown so far.

In the Rfo region, the restorer gene seems to be duplicated too: three genes encoding highly related PPR proteins are present in the Rfo locus (even if just one of the proteins is able to restorer fertility). We recently sequenced a European non-restorer allelic locus. Analysis of this sequence shows the presence of only two PPR genes in an apparently very dynamic region.

In this study, we analyzed the European allelic variant sequence of the Rfo locus and the possible evolutionary events that occurred in both loci, in order to give insight into the dynamics and evolution of the Rfo locus.

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