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Molecular characterization of cytoplasmic male sterility (CMS) in perennial ryegrass (*Lolium perenne* L.)

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Perennial ryegrass (*Lolium perenne* L.) is a key grassland species in temperate climates. As an out breeding crop, ryegrass is currently being bred as population and synthetic families, thereby not fully exploiting the genetically available heterosis. Thus, hybrid breeding has the potential to increase biomass yield, improve nutritional value and tolerance towards abiotic and biotic stress.

Cytoplasmic male sterility (CMS) is an efficient tool to control pollination for hybrid seed production. In order to identify the causative polymorphism of the CMS phenotype, a cytoplasmic male sterile plant and the corresponding fertile maintainer genotype was established in the glasshouse. The mitochondrial DNA has been isolated from crude mitochondrial preparations of young leaf tissue of four months old ryegrass clones. Mitochondrial DNA was isolated, checked for contamination of genomic DNA, quantified and sequenced using 454 next-generation sequencing technology, resulting in approximately 800,000 high quality single reads.

Here we report on the sequencing and the assembly of the mitochondrial genome from perennial ryegrass. Moreover, the assembly and annotation of the male-sterile and fertile mitochondrial genomes will enable to identify the causative polymorphism of CMS phenotype in perennial ryegrass.