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PROJECT 2 ABSTRACT

(1 Page Limit)

Efficient, high-throughput, and cost-effective transformation technology is key to functional analysis of genes underlying important agronomic traits. However, gene transformation has long been a bottleneck for gene cloning and gene-editing in barley. The spring variety Golden Promise has been one of few genotypes that can regenerate from immature embryo tissues mediated by *Agrobacterium tumefaciens*, but the genotype-dependence and technical challenges limit its broad-spectrum applicability for barley genomic studies. Therefore, an effective and genotype-independent transformation method is in need for barley functional genomics. Different from *A. tumefaciens*, *A. rhizogenes*, stimulates plants to generate adventitious, genetically transformed hairy roots at the site of inoculation. With a broad host-compatibility, *A. rhizogenes*-mediated hairy root transformation is usually achieved with ease, and genotype-independent *A. rhizogenes*-mediated hairy root transformation have been widely used in both dicots and monocots, such as tobacco, maize, soybean, chickpea, and *Alstroemeria*. Moreover, transgenic plants have been obtained from *A. tumefaciens*-transformed hairy roots in some species, which provides a new perspective that using *A. tumefaciens* to overcome the hurdle of genotype-dependence in barley transformation. In the present proposal, we will use the binary vector pANIC-12A expressing RFP reporter to develop a highly efficient and genotype-independent barley transformation system. In the meantime, we will compare the efficiency between our new method and transformation with immature embryos. We aimed to finish the whole project within two years. Very potentially, our project may lay a solid foundation for barley functional genomics and to serve the barley research community.