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Sommario/riassunto	The broad host range pathogenic bacterium Agrobacterium tumefaciens has been widely studied as a model system to understand horizontal gene flow, secretion of effector proteins into host cells, and plant-pathogen interactions. Agrobacterium-mediated plant transformation also is the major method for generating transgenic plants for research and biotechnology purposes. Agrobacterium species have the natural ability to conduct interkingdom genetic transfer from bacteria to eukaryotes, including most plant species, yeast, fungi, and even animal cells. In nature, A. tumefaciens causes crown gall disease resulting from expression in plants of auxin and cytokinin biosynthesis genes encoded by the transferred (T-) DNA. Gene transfer from A. tumefaciens to host cells requires virulence (vir) genes that reside on the resident tumor-inducing (Ti) plasmid. In addition to T-DNA, several Virulence (Vir) effector proteins are also translocated to host cells through a bacterial type IV secretion system. These proteins aid in T-DNA trafficking through the host cell cytoplasm, nuclear targeting, and

T-DNA integration. A recently discovered bacterial type VI secretion system may also export bacterial proteins and impact transformation. Genes within native T-DNAs can be replaced by any gene of interest, making Agrobacterium species important tools for plant research and genetic engineering. Agrobacterium-mediated genetic transformation is easy to use, relatively inexpensive, and generally results in a low copy number of transgene insertions when compared to other means of plant transformation, such as particle bombardment. In this research topic, we shall provide updated information on several important areas of Agrobacterium biology and its use for biotechnology purposes.