

Fig. 17.1 Natural mechanisms of CRISPR / Cas systems in microbial adaptive immunity.

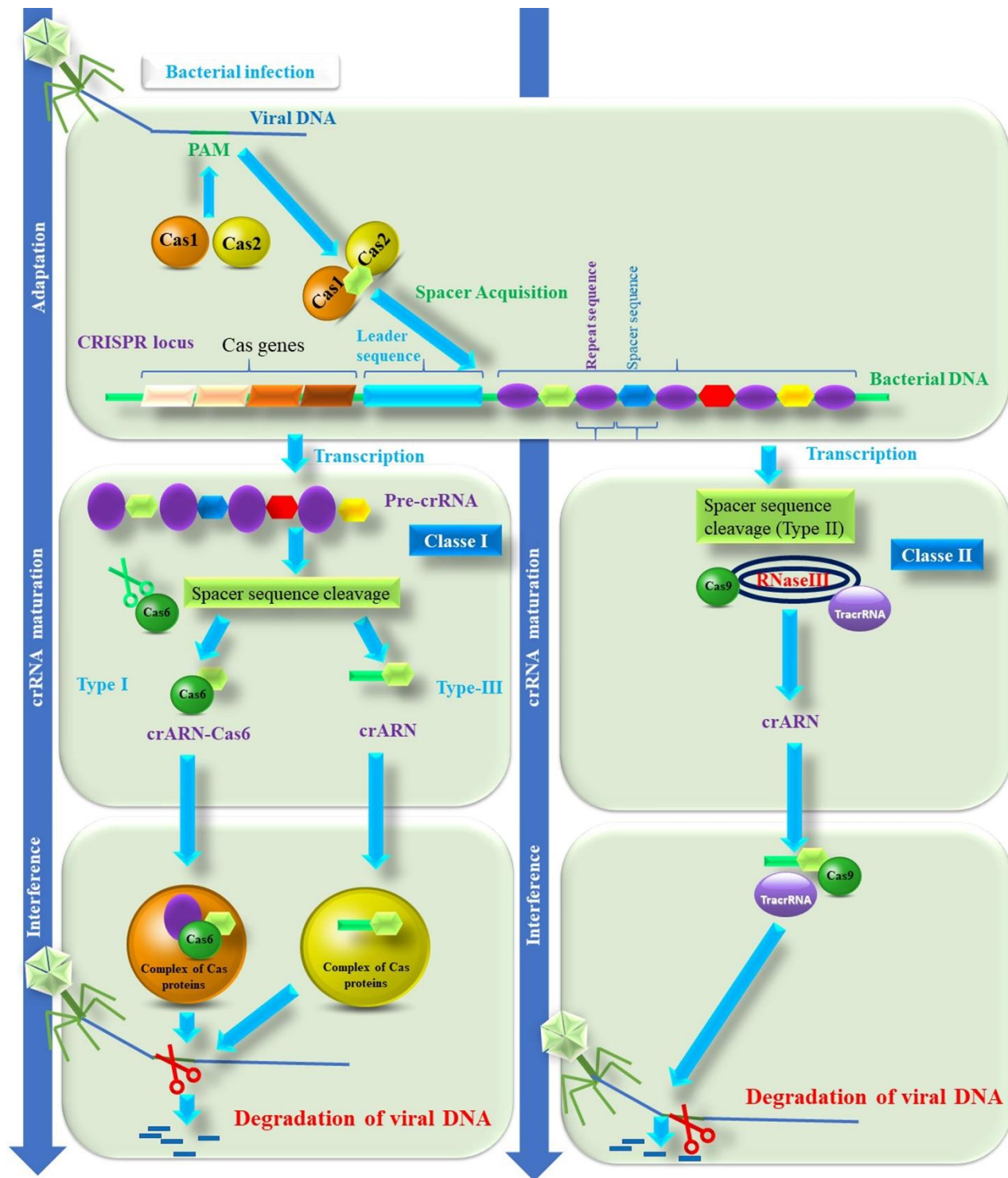


Fig. 17.2 Development of plants resistant to viruses by targeting viral factors in the virus by CRISPR / Cas genome editing.

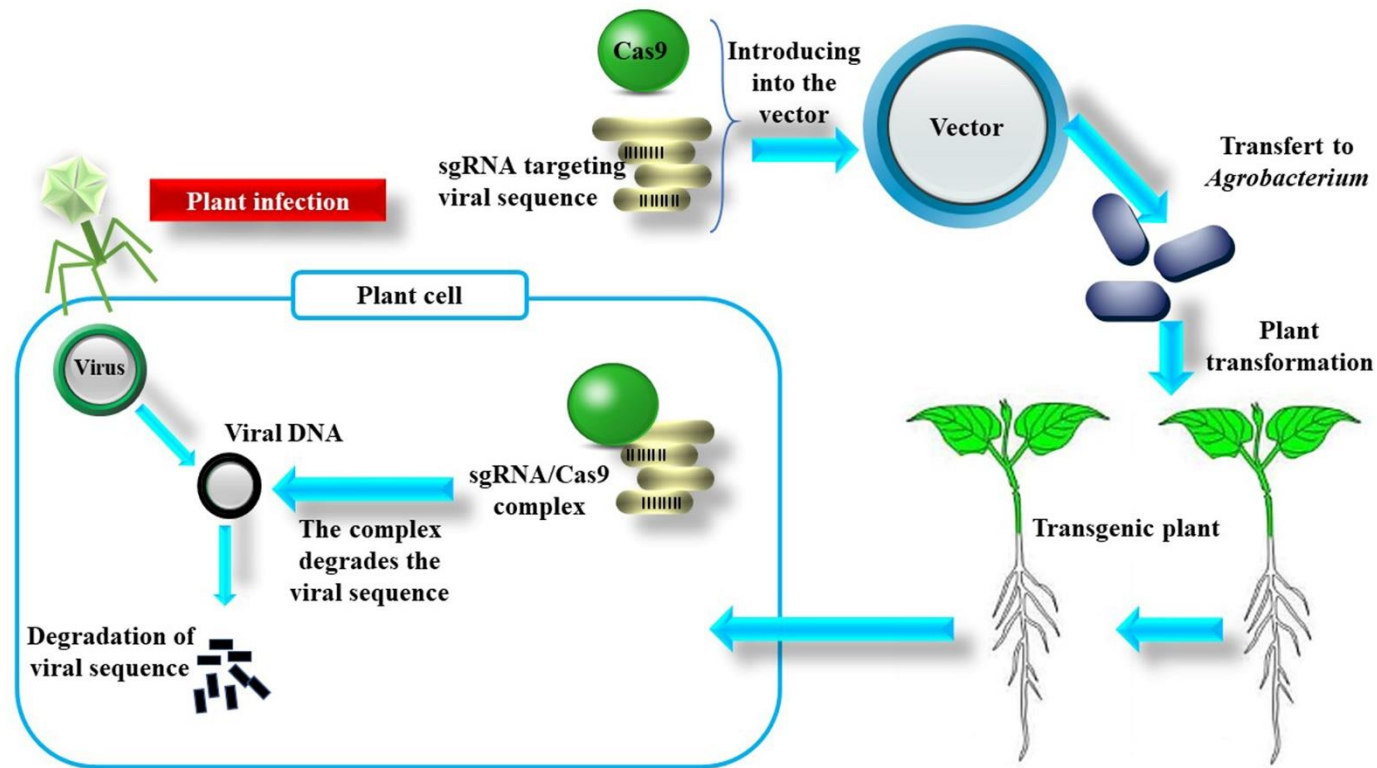


Fig. 17.3 development of plants resistant to viruses altering factors favoring development of virus in the host plant by plant genome editing.

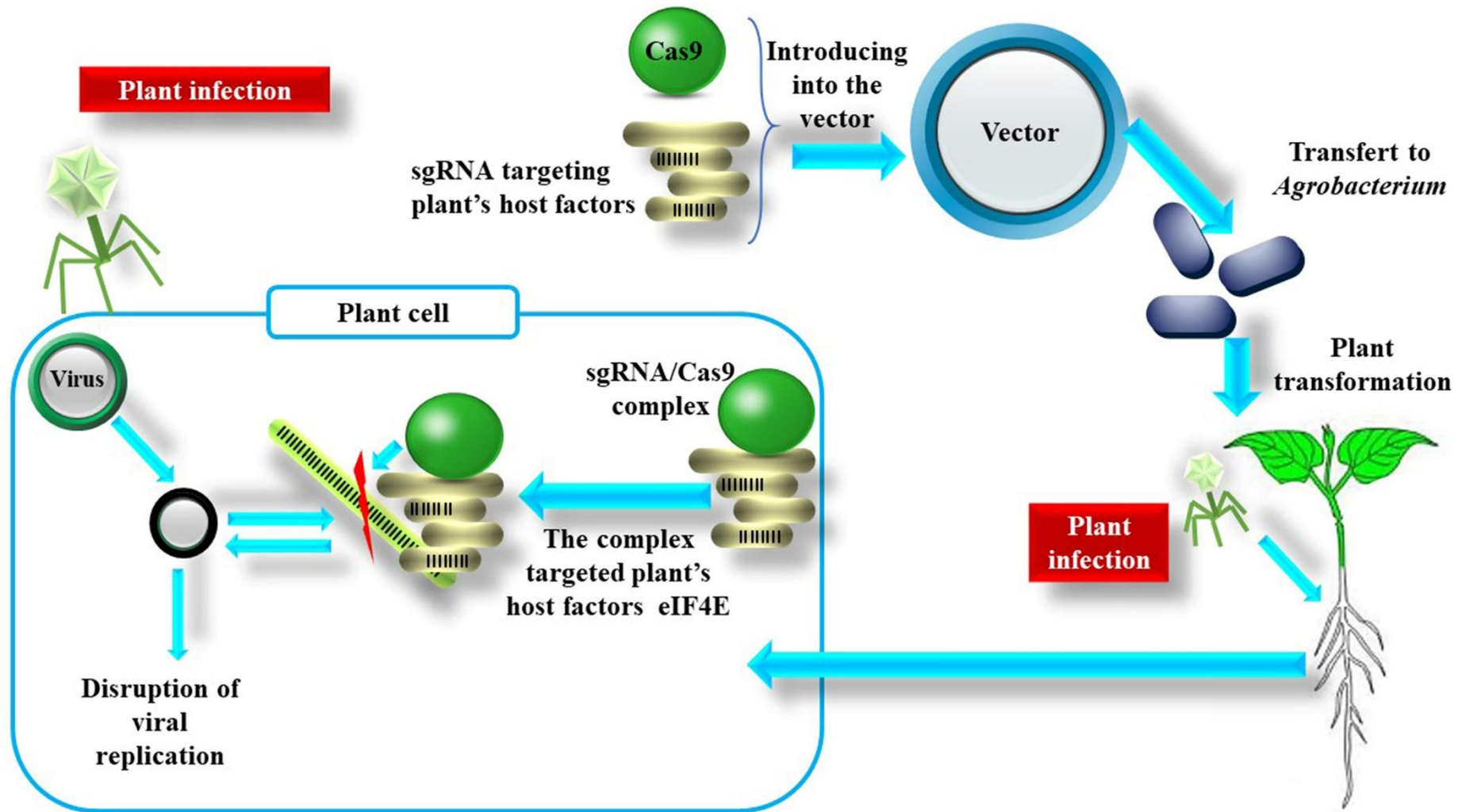


Fig. 17.4 Progress of fungal resistance in transgenic and non-transgenic plant obtained by CRISPR / Cas-9.

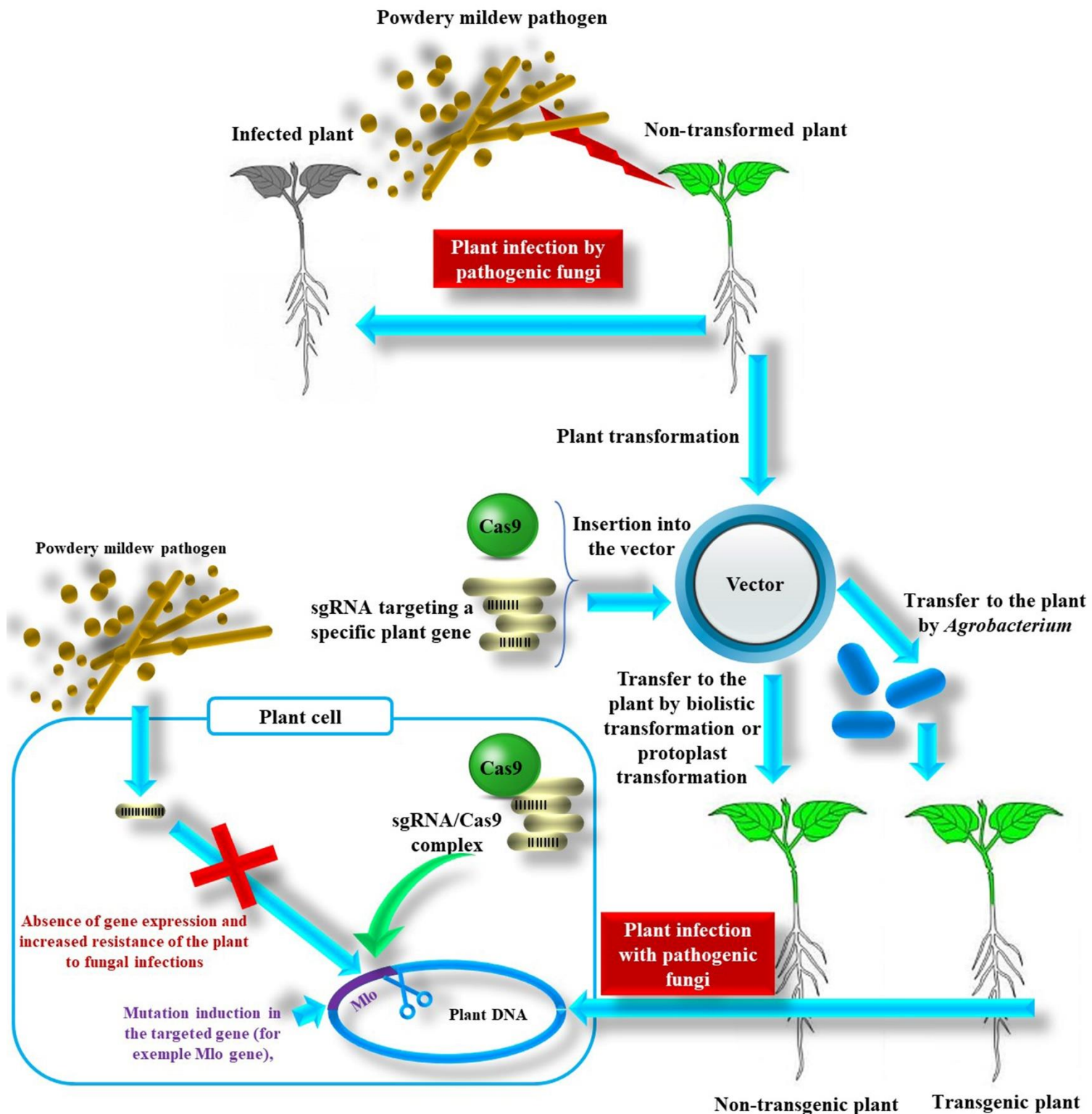


Fig. 17.5 Progress of the fight against bacterial resistance in transgenic and non-transgenic plant obtained by CRISPR / Cas-9

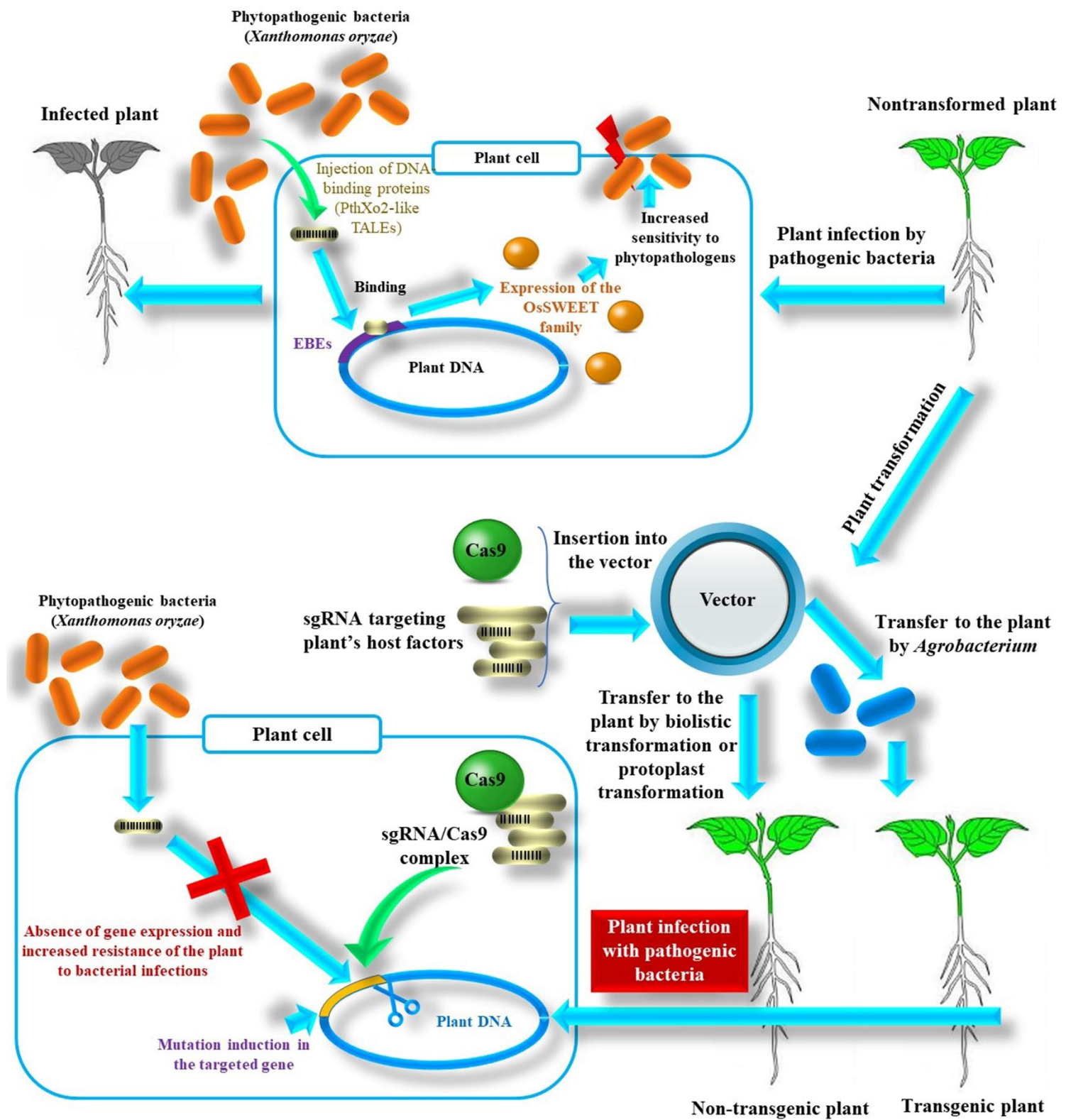


Table 17.1. Classification of CRISPR (clustered regularly interspersed short palindromic repeat) -Cas (CRISPR-associated) systems.

CRISPR-Cas systems

Class I (This system has effector modules composed of multiple Cas proteins that form a crRNA-binding complex)			Class II (This system has a single, multidomain crRNA-binding protein)		
Type I	Type III	Type IV	Type II	Type V	Type VI
I-A <i>Archaeoglobus fulgidus</i>	III-A <i>Staphylococcus epidermidis</i>	IV-C <i>Thioalkalivibrio sp. K90mix</i>	II-B <i>Legionella pneumophila</i> str. Paris	V-A <i>Francisella cf. novicida</i> Fx1	VI-A <i>Leptotrichia shahii</i>
I-B <i>Clostridium kluyveri</i>	III-D <i>Synechocystis SP. 6803</i>	III-A <i>Synechocystis sp. 6803</i>	II-A <i>Streptococcus thermophilus</i>	V-E <i>Deltaproteobacteria bacterium</i>	VI-D <i>Ruminococcus bicirculans</i>
I-C <i>Bacillus halodurans</i>	III-E <i>Candidatus Scalindua brodae</i>	III-B <i>Rhodococcus jostii</i> RHA1	II-C1 <i>Neisseria lactamica</i>	V-I Freshwater metagenome	VI-C <i>Fusobacterium perfoetens</i>
I-G <i>Geobacter sulfurreducens</i>	III-F <i>Thermotoga lettingae</i> TMO		II-C2 <i>Micrarchaeum acidiphilum</i> ARMAN-1	V-B1 <i>Alicyclobacillus acidoterrestris</i>	VI-B1 <i>Prevotella buccae</i>
I-D <i>Cyanothece sp. 8802</i>	III-C <i>Methanothermobacter thermautotrophicus</i>			V-B2 <i>Planctomycetes bacterium</i>	VI-B2 <i>Bergeyella zoohelcum</i>
I-E <i>Escherichia coli</i> K12	III-B <i>Pyrococcus furiosus</i>			V-H Hypersaline lake sediment metagenome	
I-F2 <i>Shewanella putrefaciens</i> CN-32				V-C <i>Oleiphilus sp.</i>	
I-F1 <i>Yersinia pseudotuberculosis</i>				V-D <i>Bacterium CG09-39-24</i>	
I-F3 <i>Vibrio crassostreae</i> J5-20				V-F1 Uncultured archaeon	
				V-F1(V-U3) <i>Bacillus thuringiensis</i>	
				V-F2 Uncultured archaeon	
				V-U2 <i>Cyanothece sp. 8801</i>	
				V-U4 <i>Rothia dentocariosa</i> M567	
				V-F3 <i>Candidatus Micrarchaeota archaeon</i>	
				V-U1 <i>Gordonia otitidis</i>	
				V-G Hot springs metagenome	
				V-K (V-US) <i>Cyanothece sp. 8801</i>	