

# ***CDF1* gene editing strategy in potato wild species within *de novo* domestication concept**

*Fomin I.N. \*<sup>1</sup>, Egorova A.A.<sup>1,2</sup>, Koloshina K.A.<sup>1</sup>, Gerasimova S.V.<sup>1</sup>*

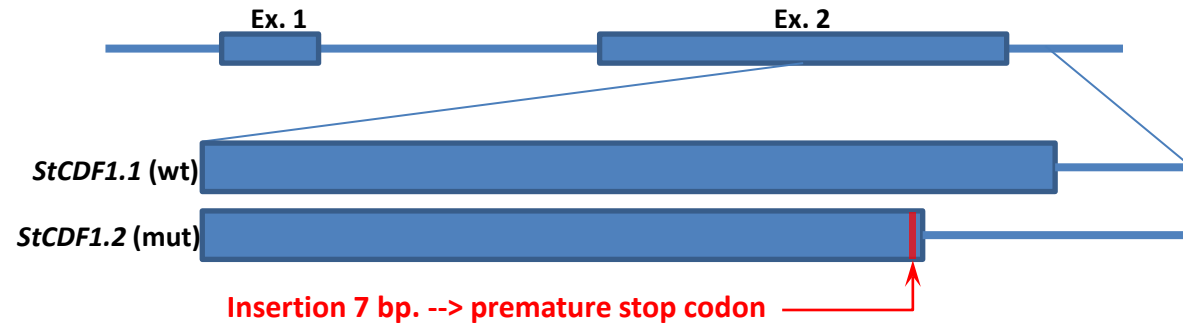
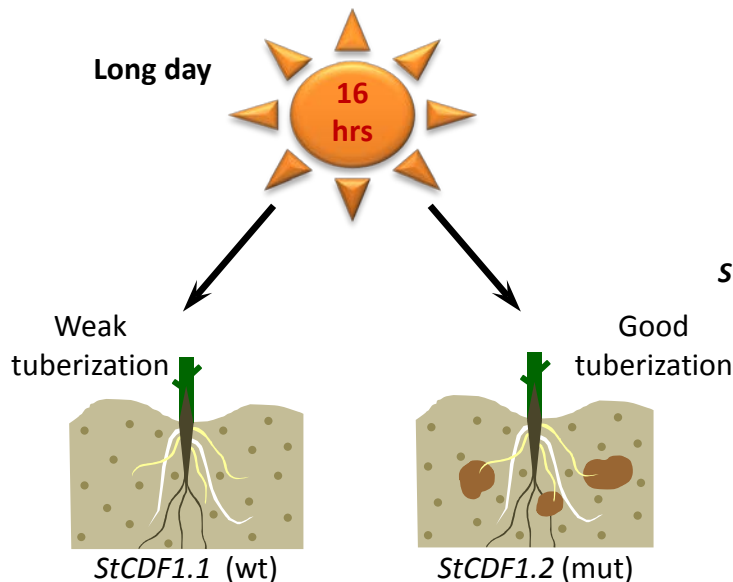
<sup>1</sup> Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia

<sup>2</sup> Novosibirsk State University, Novosibirsk, Russia

# Wild potato species as trait donors

- During long selection process modern potato cultivars have lost their ability to resist various negative environmental factors, while many wild species have retained these traits.
- As part of the *de novo* domestication concept, we are looking for genes with modification potential supposed to accelerate the production of new trait donors for their introduction into breeding.
- One of such genes is *StCDF1*, which is involved in the regulation of tuberization.

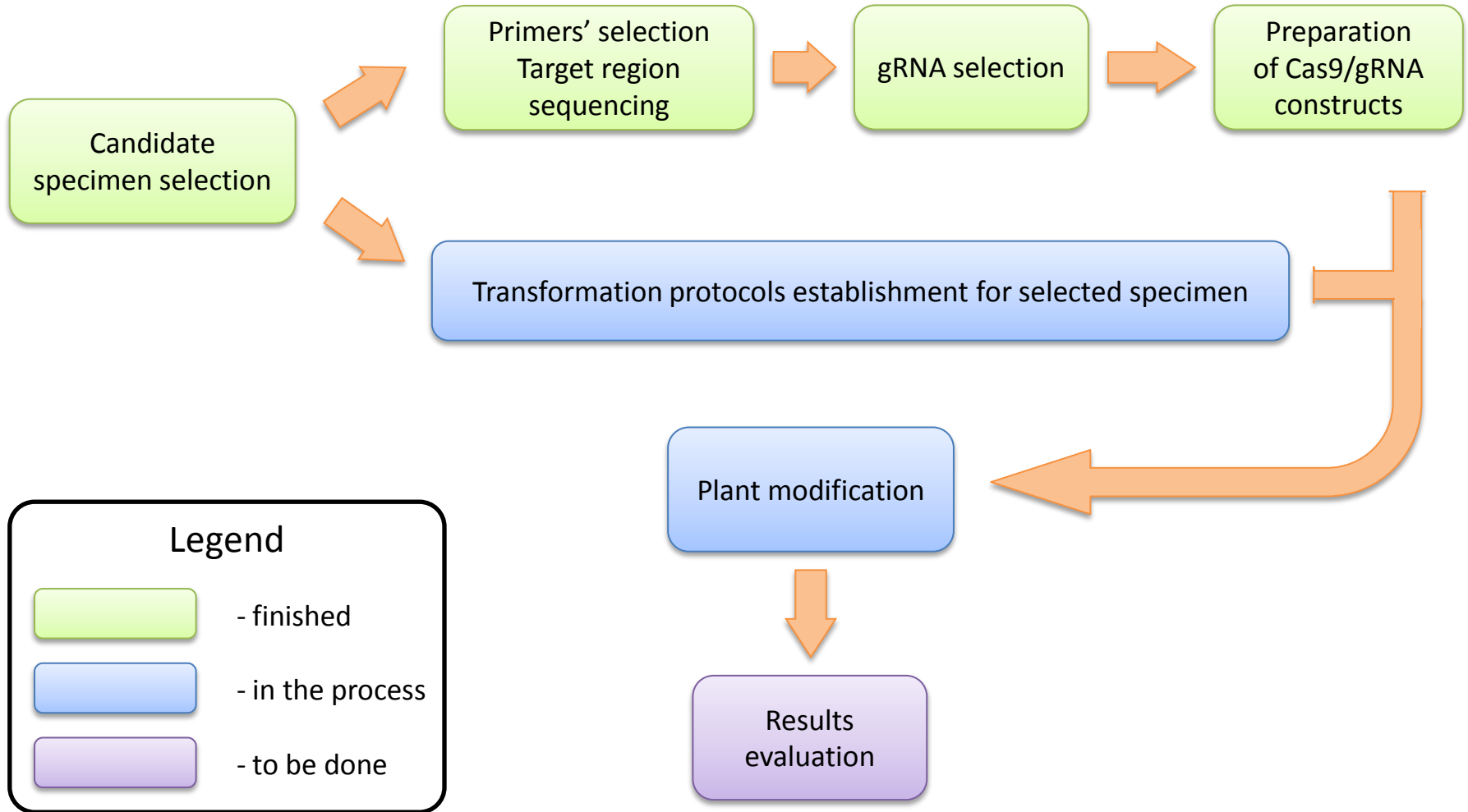
## StCDF1 exon-intron structure and allele difference



### The hypothesis:

- The modification of the *CDF1* gene in wild potato via Cas9/gRNA system will induce tuberization under long-day conditions

# Project pipeline



# *S. polyadenium* was chosen for modification

- During last 3 years 19 specimen of wild potato from VIR collection were cultivated and phenotyped in long-day conditions (<http://wildpetotadb.biores.cytogen.ru/ru>)
- *S. polyadenium* having some good traits doesn't tuberize under long-day conditions. Therefore it was selected for modification of the *CDF1* gene.

№ in collection	Specimen	Tuberization*	Steroidal glycoalkaloids**	Virus infection (virus type)	Resistance to Colorado potato beetle	<i>in vitro</i> regeneration	Ploidy, n
1	<i>S. verrucosum</i>	1		X		not established	2
2	<i>S. demissum</i>	0	-	Y	100%	established	6
3	<i>S. stoloniferum</i>	1	++	not found		not established	4
4	<i>S. polyadenium</i>	1	-	X	100%	established	2
5	<i>S. pinnatisectum</i>	2	-	X		not established	2
6	<i>S. ehrenbergii</i>	2	-	X		not established	2
12	<i>S. stoloniferum</i>	1	+	not found	65%	not established	4
16	<i>S. jamesii</i>	2	-	not found		not established	2
17	<i>S. tarijence</i>	2	-	Y		not established	2
19	<i>S. cardiophyllum</i>	2	-	X	100%	not established	2
24	<i>S. pinnatisectum</i>	2	-	X		established	2
27	<i>S. dolichostigma</i>	3	+++	not found	0%	established	2
28	<i>S. commersonii</i>	1	-	X, Y, S		not established	2
30	<i>S. fendleri</i>	2	-	X	15%	established	4
31	<i>S. kurtzianum</i>	2	++	not found			2
32	<i>S. vernei</i>	1	-	not found			2
33	<i>S. chacoense</i>	3	+++	not found	100%	established	2
34	<i>S. chacoense</i>	1	-	X, Y		established	2
36	<i>S. demissum</i>	0	-	X, Y		established	6

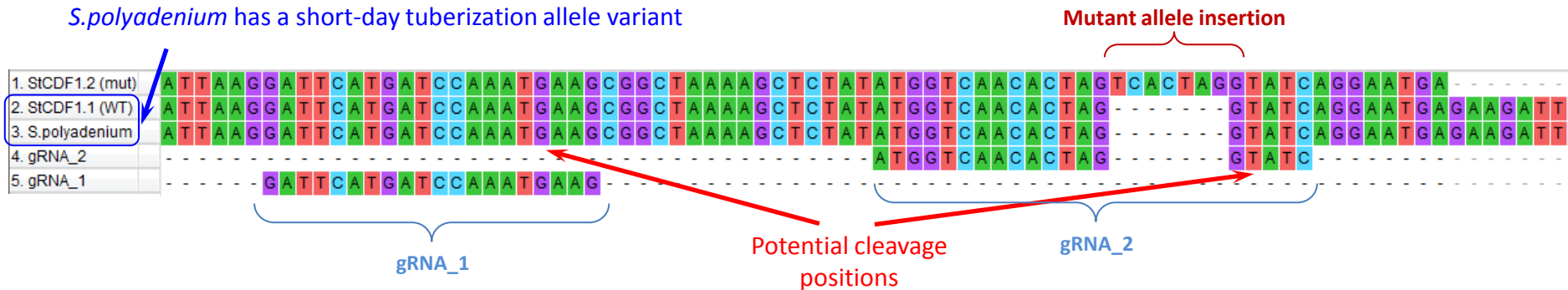
\* - Tuberization scale: 0 – no tubers; 1 - zero or few tubers during all three years; 2 – steady tuberization all three years; 3 – lots of tubers all three years

\*\* - Concentration of SGA: "-" – below 1mg/g of dry weight, "+" – between 1mg/g and 10mg/g, "++" – between 10mg/g and 20mg/g, "+++" – more than 20mg/g

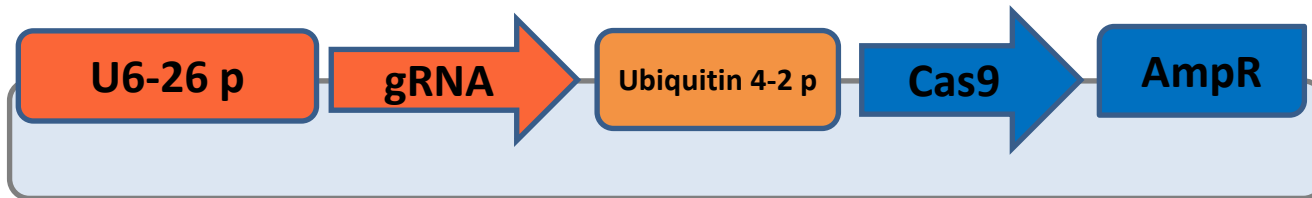
# Target site selection and gRNA design

Target sites were chosen in a region of natural mutation which leads to long-day tuberization allele

*S.polyadenium* has a short-day tuberization allele variant



## Vector structure



We expect a frameshift mutation leading to conversion from a short-day tuberization to a long-day tuberization allele

*Acknowledgements:* the study is funded by RFBR, project number 20-016-00217