Rhizobium leguminosarum Genome Array-Ready Oligo Set™ (Version 1.0)

The Operon *Rhizobium leguminosarum* Genome Oligo Set Version 1.0 contains 7413 70-mer oligonucleotide probes representing 7413 genes from *Rhizobium leguminosarum* genome and seven plasmids including pRL7, pRL8, pRL9, pRL10, pRL11, pRL12 and UPM791. Each probe contains an amino linker at its 5' end.

Sequence source and gene selection

Gene sequences used for oligo design were obtained from Sanger Institute (http://www.sanger.ac.uk/Projects/R_leguminosarum/), England.

Probe design and selection rules

The 70-mer probes are selected with an optimal set of parameters as described below.

1. The melting temperatures (Tm) of the probes are restricted within the range of 79 ± 5 °C. Tm is calculated using the following formula: $Tm = 81.5 + 16.6 * \log[Na+] + 41 * (\#G + \#C)/length – 500/length$ where $[Na+] = 0.1$ M and $length = \#A + \#C + \#G + \#T$

2. The contiguous single nucleotide repeat or poly (N) tract within each probe is limited to 7 bases or shorter.

3. The hairpin stem length of each probe is controlled at 8 bases or shorter.

4. The cross hybridization score for the probe against other non-representing (non-self) genes in the genome is set 70% or less of BLAST percent identity score.

5. The contiguous base match to other non-self genes is constrained at 20 bases or less.

6. The selection distances of the candidate probes are 40 bases away from the 3' end of the genes. This design restriction is intended for the 3'-end priming of genes or random priming.

The probes with the highest specificity (or the least cross-hybridization scores) are selected from a pool of candidates satisfying all the rules as described above.

The exceptions (relaxation of one or more selection rules) are made for the probe candidates of 242 genes (3.3%), which don't meet the rules as mentioned above.

SUMMARY

Selection rules	Threshold	Probe number
Probe length (bases) Melting temperature (°C) Poly (N) tract length (bases) Hairpin stem length (bases) Distal distance from 3' end Cross-hybridization score (identity %) Contiguous base match to non-self genes (bases)	70 79 ± 5 < 8 < 9 >110 <= 70 <= 20	7171
Exceptions		242
Total		7413

The following illustrations show the distribution of all 7413 probes for melting temperature, GC content, distance from 3' end, hairpin stem length, and cross-hybridization identity.

Figure 1. Melting temperature

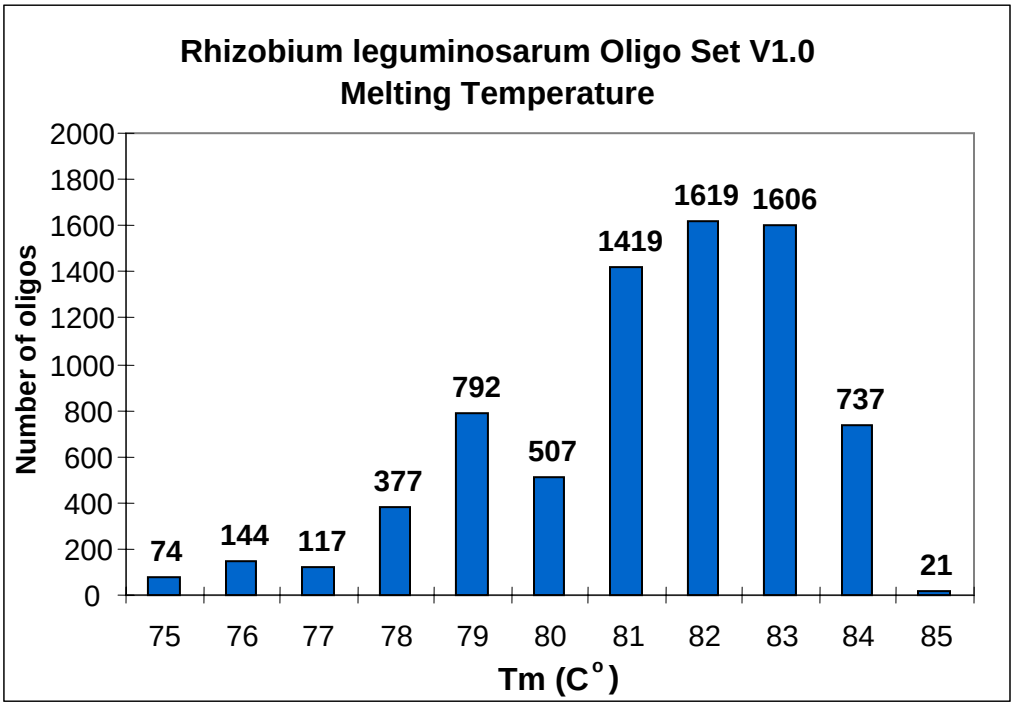

Figure 2. GC Content

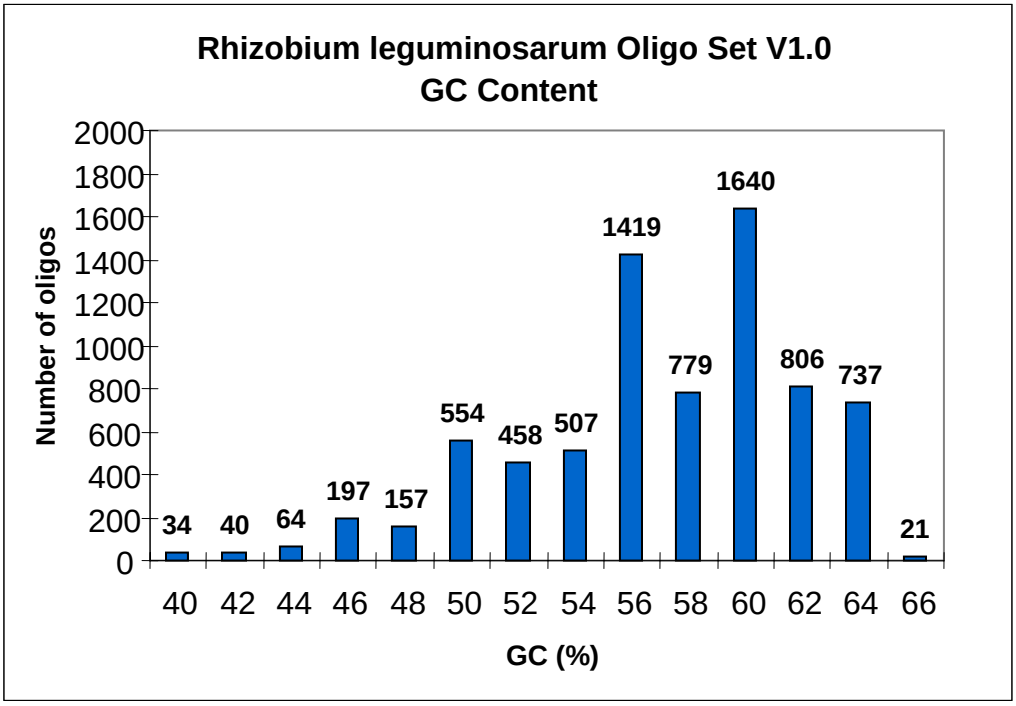

Figure 3. Distance from 3'-end

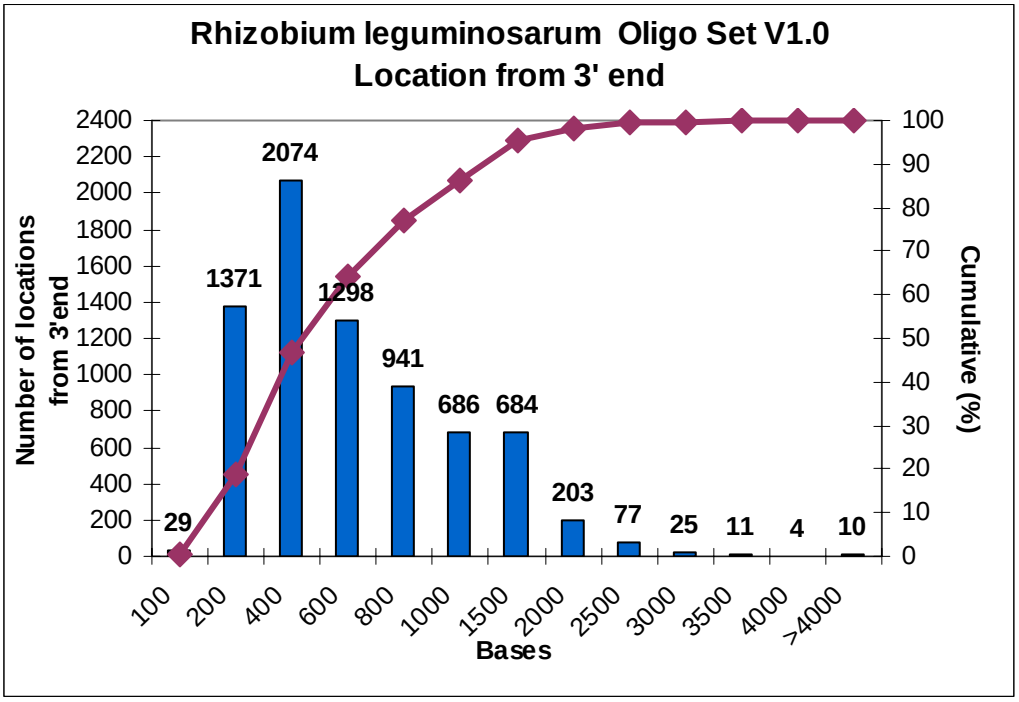

Figure 4. Hairpin stem length

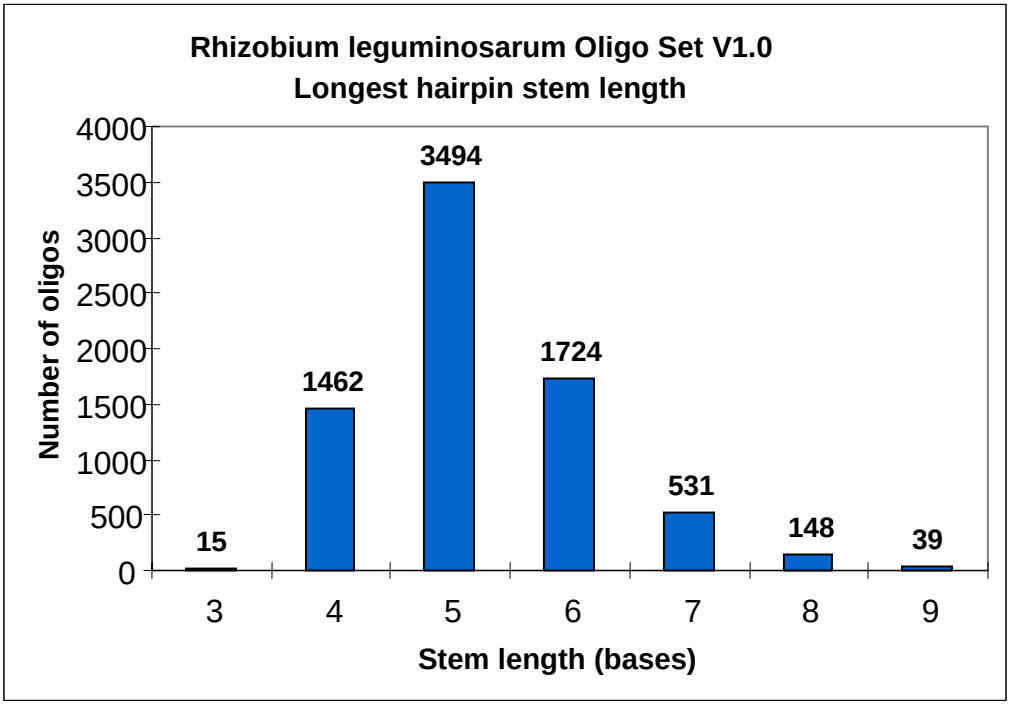

Figure 5. Cross-hybridization score