

Prosopis alba cDNA library

Leaf tissue, 3 individuals

454 GS FLX Titanium Pyrosequencing

(1,103,231 raw reads, average length 421 bp)

Filtering for adaptors,
primer sequences and
low-quality sequences

Chloroplast Assembly

44,079 reads

(BLASTN e-50 TBLASTX e-10)

(AMOScmp)

Assembly

1,063,520 high quality reads

(Newbler 2.5)

15,814 isotigs
Average length 991 bp
(12,610 isogroups)

71,101 singletons

Average length 288 bp

Clustering
(CD-HIT-454
algorithm to
eliminate artificial
duplicates)

39,000 singletons

54,814 unigenes

>200bp

BLASTX
(e-value $\leq 10e-10$)
Blast2GO
Interproscan-Kass-
BlastP- TblastX

SSR webservice
GDR, SSAHASNP
Program

37,563
Unigenes with
putative
function

6,236 SNPs
6,147 in unigenes
with function

5,992 SSRs
3,440 in
unigenes with
function

11 Nuclear
polymorphic
SSR in stress
genes: wet lab
validated

123 Nuclear
polymorphic SSRs
In silico (135 GO
terms)