

Table S1. Selection of HA producing *E.coli* Colonies.

Strain	Plate one	Plate two	Plate three
pMM <i>hasA</i> Rosetta2	LB+glucose1%+chl oramphenicol34ug/ ml	LB+glucose1% +0.5%Xylose	LB+glucose1%+0.5%Xylose + Ampicillin100ug/ml
pP _{T7} <i>has ABC</i> <i>LysY/Iq</i>	LB+glucose1%	LB+glucose1%+0.5 mM IPTG	LB+glucose1%+1mM IPTG+ Ampicillin100ug/ml
pP _{T7} <i>hasABC</i> Rosetta2 DE3pLysS	LB+glucose1%+ chloramphenicol 34ug/ml	LB+glucose1%+0.5 mM IPTG + chloramphenicol3 4ug/ml	LB+glucose1%+ Chlorampheincol 34ug/ml +1mM IPTG+ Ampicillin100ug/ml
pP _{T7} <i>hasABC</i> Rosetta B- gammiDE3pLysS	LB+glucose1%+ chloramphenicol34 ug/ml	LB+glucose1%+0.5 mMIPTG + chloramphenicol3 4ug/ml	LB+glucose1% + Chlorampheincol 34ug/ml +1mM IPTG+ Ampicillin100ug/ml
pP _{T7} <i>hasABCDE</i> Rosetta B- gammiDE3pLysS	LB+glucose1%+ chloramphenicol34 ug/ml	LB+glucose1%+0.5 mMIPTG + chloramphenicol3 4ug/ml	LB+glucose1% + Chlorampheincol 34ug/ml +1mM IPTG+ Ampicillin100ug/ml

Table S2. List of oligonucleotides.

Primers Name	Sequence (<u>Restriction sites</u>)	Purpose
Forward <i>hasA</i> pJet	ATCGGAT <u>CCT</u> GAGGAGACACAACATGAGAACATTA AAAAACCT (<i>Bam</i> HII).	Cloning in pJet and pMM1522
Reverse <i>hasA</i> pJet	AGAATT <u>GAGG</u> CTTATAATTTTTACGTGT (<i>Sph</i> I).	Cloning in pJet and pMM1522
Reverse <i>hasAB</i> pJet	TTCT <u>GAGG</u> CTAGTCTCTTCAAAGAC (<i>Sph</i> I).	Cloning in pJet and pP _{T7}
Reverse <i>hasABC</i> pJet	TATCG <u>GCAT</u> GCTTACTGGGGCTGATC (<i>Sph</i> I).	Cloning in pJet and pP _{T7}
Forward <i>hasABCDE</i> pP _{T7}	ATAAT <u>CAGA</u> TCTGAGGAGACACAACATGAGAACAT TAAAAAACCT (<i>Bg</i> II).	Cloning in pP _{T7}
Reverse <i>hasABC</i> pP _{T7}	ATAAT <u>CAGA</u> TCTTACTGGGGCTGATC (<i>Bg</i> II).	Cloning in pP _{T7}
Reverse <i>hasABCDE</i> pP _{T7}	ACTGAT <u>CCCGGG</u> TTACAAGCGTGC (<i>Xma</i> I).	Cloning in pP _{T7}

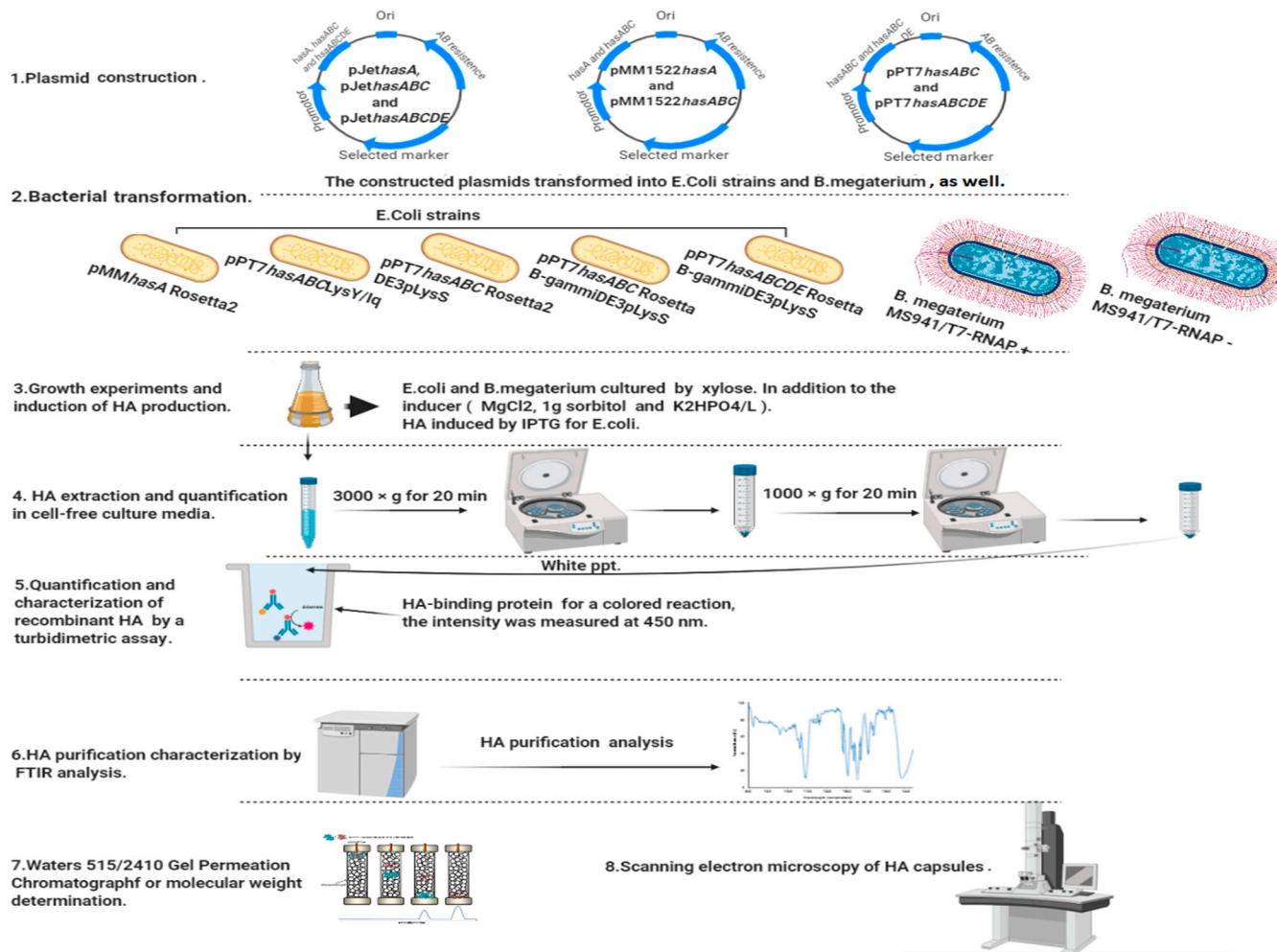


Figure S1. The graphical abstract of Materials and Methods.

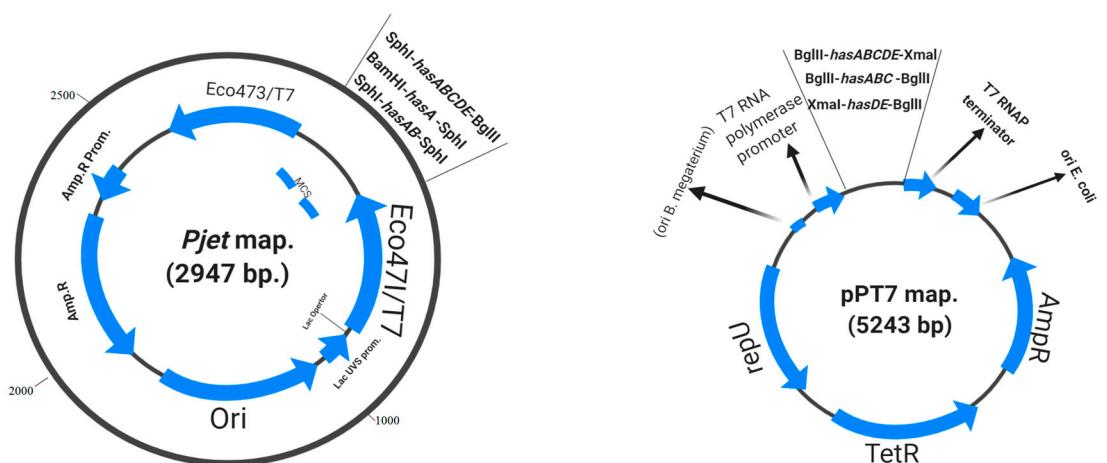


Figure S2. Plasmid construction of *hasaABC/DE* cloned into Pjet and pPT7

Table S3. Selection of HA producing *Bacillus megaterium* MS941 Colonies

Strain	Plate One	Plate Two	Plate Three
pMM1522 <i>hasA</i> in <i>B.megaterium</i> MS941	LB + glucose 1 %	LB + glucose 1 % + 0.5 % Xylose	LB + glucose 1 % + 0.5 % Xylose + tetracycline 4 ug/ml
pP _{T7} <i>has ABC</i> in <i>B. megaterium</i> MS941 pretransformed with T7RNAP.	LB + glucose 1 % + chloramphenicol 3.4 ug/ml	LB + glucose 1 % + chloramphenicol 3.4 ug/ml + 0.5 % Xylose	LB + glucose 1 % + chloramphenicol 3.4 ug/ml + 0.5 % Xylose + tetracycline 4 ug/ml
pP _{T7} <i>has ABCDE</i> in <i>B. megaterium</i> MS941 pretransformed with T7RNAP	LB + glucose 1 % + chloramphenicol 3.4 ug/ml	LB + glucose 1 % + chloramphenicol 3.4 ug/ml + 0.5 % Xylose	LB + glucose 1 % + chloramphenicol 3.4 ug/ml + 0.5 % Xylose + tetracycline 4 ug/ml

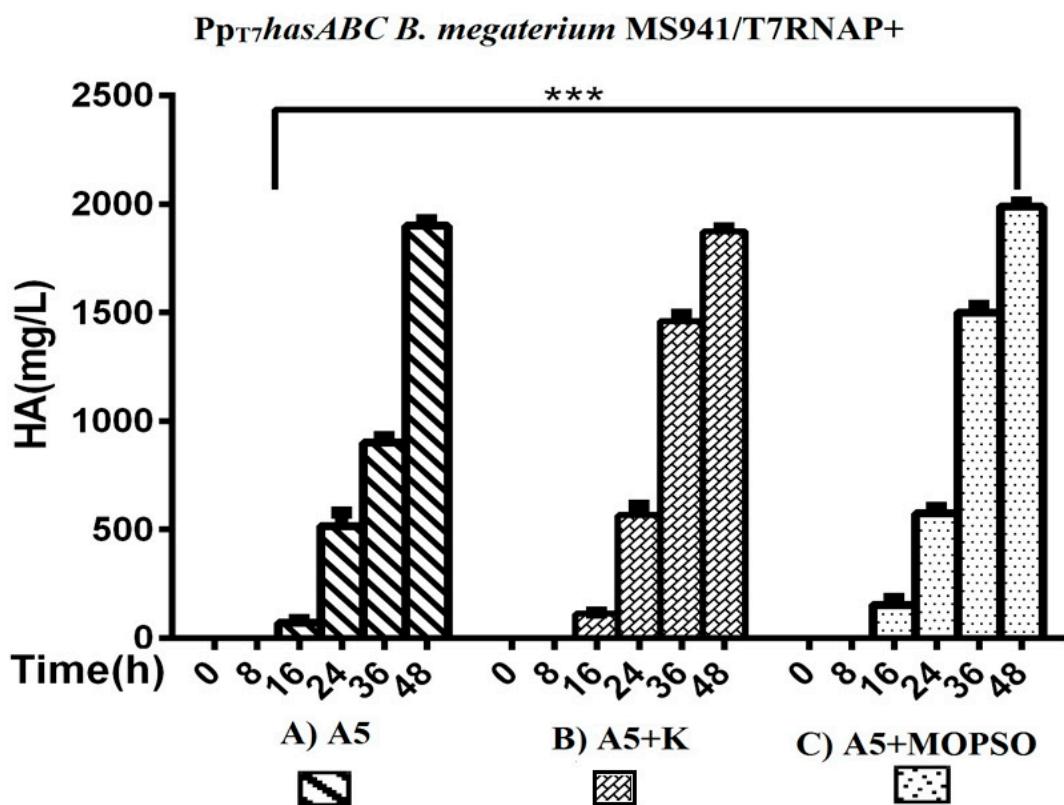


Figure S3. HA production by pP_{T7}*hasABCDE* *B. megaterium* MS941 pre-transformed with T7RNAP in (A) A5, (B) A5 + K and (C) A5 + MOPSO, (***) $P < 0.0001$.

Table S4. FTIR peaks; reference HA-standard FTIR, and HA produced by pPT7hasABCDE *E. coli* Rosetta-gami B pLysS and pPT7hasABCDE B.

Wave length (cm ⁻¹)	Functional group
3600-3604	confirms the presence of OH stretching
2897.89-2936.59	C-H stretching
1612.79-1653.02	Presence of amide II group
1410.64-1414.68	presence of C-O group with C=O combination,
1042.30-1058.73	C-O-C stretching
612.32-555.39	C-O-C stretching
3600-3605	confirms the presence of OH stretching
2897.89-2937.73	C-H stretching
1612.79-1650.02	Presence of amide II group
1410.64-1425.93	presence of C-O group with C=O combination,
1042.30-1058.49	C-O-C stretching
612.32-520.39	C-O-C stretching