

ChemComm

Accepted Manuscript



This is an *Accepted Manuscript*, which has been through the Royal Society of Chemistry peer review process and has been accepted for publication.

Accepted Manuscripts are published online shortly after acceptance, before technical editing, formatting and proof reading. Using this free service, authors can make their results available to the community, in citable form, before we publish the edited article. We will replace this *Accepted Manuscript* with the edited and formatted *Advance Article* as soon as it is available.

You can find more information about *Accepted Manuscripts* in the [Information for Authors](#).

Please note that technical editing may introduce minor changes to the text and/or graphics, which may alter content. The journal's standard [Terms & Conditions](#) and the [Ethical guidelines](#) still apply. In no event shall the Royal Society of Chemistry be held responsible for any errors or omissions in this *Accepted Manuscript* or any consequences arising from the use of any information it contains.

COMMUNICATION

Re-purposing bridging flocculation for on-site, rapid, qualitative DNA detection in resource-poor settings

Cite this: DOI: 10.1039/x0xx00000x

E. J. H. Wee,^{a,†} H. Y. Lau,^{a,b,†} J. Botella^b and M. Trau^{a,c}Received 00th January 2012,
Accepted 00th January 2012

DOI: 10.1039/x0xx00000x

www.rsc.org/

1 **Developing molecular diagnostics in resource-poor settings** 31
 2 **challenging. As such, we purpose-built a novel bridging** 32
 3 **flocculation assay for qualitative evaluation of isothermally** 33
 4 **amplified DNA by naked eye. The flocculation assay was** 34
 5 **dependent on pH, DNA polymer amounts and lengths. The** 35
 6 **method was first applied to the rapid and sensitive detection** 36
 7 **of important plant pathogens and subsequently extended** 37
 8 **other pathogens across the animal kingdom to demonstrate** 38
 9 **the wide applications of our approach.** 39

10 Nucleic acid point-of-care bioassays that can be performed on-site 40
 11 are in high demand.¹ However the challenge is further confounded 41
 12 resource-poor settings due to the lack of infrastructure and skilled 42
 13 labor. To address this, new methods tailored for low resource 43
 14 settings requires considerations from sampling 44
 15 detection/amplification and to evaluation of results. The agricultural 45
 16 industry is one area in urgent need of bioassays requiring minimal 46
 17 infrastructure especially in agriculturally reliant developing regions. 47
 18 Traditionally, an experienced plant pathologist identifies the disease 48
 19 by a subjective visual examination of disease symptoms.³ To address 49
 20 this, more analytical diagnostic methods have since been 50
 21 developed.⁴⁻¹⁰ However, these methods require expensive and 51
 22 sophisticated equipment and can only be performed in specialized 52
 23 laboratories by well-trained technicians. This results in delayed 53
 24 intervention which may eventually lead to the loss of the entire crop 54
 25 harvest. 55

26 As the distinction between diseased and healthy samples is binary 56
 27 readout method mirroring a digital yes/no result may be useful 57
 28 Herein we describe a novel method to cheaply visualize amplified 58
 29 disease-specific DNA/RNA with minimal equipment via bridging 59
 30 flocculation. A key characteristic of flocculation is the abrupt 60

transition from solution phase to flocculate which makes this phenomena ideal for binary yes/no applications. To the best of our knowledge, the detection of DNA/RNA has not yet been demonstrated via a DNA-mediated bridging flocculation mechanism which can be readily observed by the naked eye (Fig 1a). Indeed, it is the unique feature of the bridging flocculation process to discriminate between long and short DNA polymer segments which lies at the heart of enabling a very attractive, versatile, field-ready system for the detection of any pathogen DNA or RNA sequence.

Bridging flocculation is a well-known phenomenon in colloid chemistry and is used for a wide variety of colloidal separation processes (e.g., to clarify contaminated water). The phenomenon was first described in the 1950's by Ruehrwein, R.A.¹¹ and explained in the 1960's by La Mer and Healy¹²⁻¹⁴ to be the result of the surface adsorption of polymers which are long enough to cross-link multiple particles together and thus (reversibly) flocculate out of solution. A key aspect of this phenomenon is that the polymers (in our case DNA amplicons) must be of sufficient length to induce this flocculation. DNA primer pairs, by contrast, are typically too short to enable this type of particle cross-linking, hence flocculation can only occur if the primer pairs are successfully amplified to create long polymer strands, which in turn, represents the presence of an offending DNA sequence. Another key aspect of bridging flocculation is that the solution conditions (e.g., salt concentration and pH) must be adjusted so that polymer/surface interactions are stronger than the polymer/solution interaction (as defined by the relevant Flory-Huggins Parameters¹⁵⁻¹⁷). Under, such conditions longer polymer chains (DNA amplicons) will displace surface adsorbed shorter polymers (primers) to induce a spontaneous flocculation. As a consequence, the bridging flocculation process is also reversible and may have the added versatility to "tune" the assay possibly for quantitative applications.

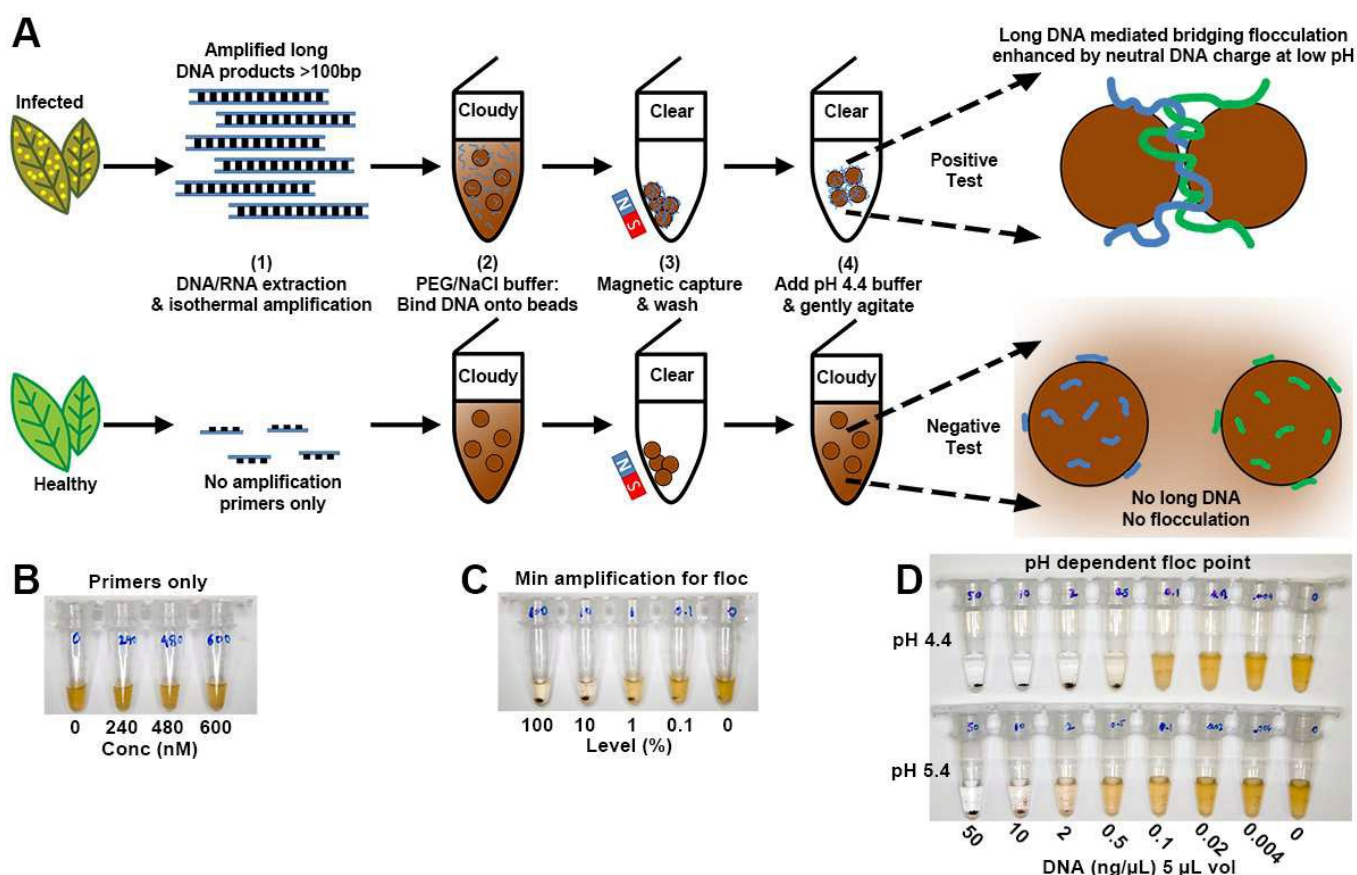


Fig 1. The bridging flocculation assay. (A) Conceptual representation of the DNA-mediated bridging flocculation assay which only occurs in the presence of pathogen DNA which is subsequently amplified to produce high molecular weight DNA amplicons/polymers. (B) Excess primers (low molecular DNA polymers which have not been amplified) do not induce flocculation. (C) Only 10% or higher amplification results in flocculation. (D) Cut-off concentration of amplified DNA for DNA-mediated bridging flocculation is pH-dependent. Each figure is a representative of at least 3 experimental replicates.

1 As a proof-of-concept we used the Solid Phase Reversal
 2 Immobilization (SPRI)¹⁸ method of DNA purification to first select
 3 for DNA lengths above 100 bp. Briefly (see ESI for detail
 4 method), high molecular weight DNA were first precipitated onto
 5 the bead surface in a high polyethylene glycol (PEG)/NaCl buffer.
 6 DNA loaded beads were next enriched with a magnet and the
 7 PEG/NaCl was removed with an ethanol wash. Then instead of
 8 eluting the captured DNA, we used a low pH acetate buffer to trigger
 9 DNA loaded magnetic beads to flocculate while long amplicon-
 10 beads are readily dispersed back into solution. To confirm that only
 11 amplified amplicons of lengths longer than primers could trigger
 12 flocculation, we tested the assay using only primers (Fig 1b). As
 13 expected, even up to 600 nM of primers were inert to the
 14 flocculation assay. Next, to determine how much amplification was
 15 required to trigger the flocculation, various ratios of product to
 16 primers mixes representing various levels of amplification were
 17 evaluated. As little as 10% amplification efficiency for a 250 bp
 18 amplicon was enough to trigger a visually distinct positive response
 19 (Fig 1C). This was estimated by assuming that the maximum amount
 20 of amplified products was equivalent to the initial primer amount
 21 (480 nM) in the reaction. We also observed that long single strand
 22 DNA such that produced by rolling circle amplification, could also
 23 mediated a flocculation response (ESI Fig S2). Therefore, the
 24 flocculation assay could potentially be a universal readout of high
 25 molecular weight DNA produced by a plethora of amplification
 26 systems.

Another interesting feature of the assay was its sensitivity to pH
 changes (Fig 1D). At pH 4.4, 0.5 ng/μL (5 μL volume) of amplified
 product could be detected. However, at pH 5.4, the cut-off
 concentration for clear and distinct flocculation increased 20-fold to
 10 ng/μL (5 μL volume). In addition, titrating pH with NaOH
 reversed flocculation (results not shown). Thus, this feature could
 offer some level of “tuning” and may be beneficial for certain
 applications. This pH versatility is however, absent in current
 nanoparticle approaches. Considering these observations: (1) the
 requirement for long DNA polymers, (2) pH dependence, (3)
 reversible agglutination and (4) sharp transition between solution
 phase and flocculate, we concluded that the mechanism was a DNA-
 mediated bridging flocculation of the particles.^{19,20} We hypothesized
 that the accumulation of beads to the magnet facilitates the
 DNA/bead entanglement by bringing neighbouring DNA/beads into
 close proximity such that DNA strands from one bead may also
 facilitate interaction with adjacent beads. On introduction of an
 acidic buffer eg. acetate buffer pH4.4, two mechanisms may occur to
 enhance flocculation: (1) DNA charge is neutralized at pH4.4, thus
 making the bead/DNA surface hydrophobic and will spontaneously
 flocculate in an aqueous environment. (2) Precipitated high
 molecular weight DNA “intertwine” on the beads surface to form an
 aggregate or flocculate. However, DNA-free beads which have the
 COOH groups exposed, remain negatively charged thus
 electrostatically repel each other and readily dispersing into solution.

52 Besides the mechanism of aggregation, bridging flocculation is also
 53 distinct in many ways from many recently described aggregation

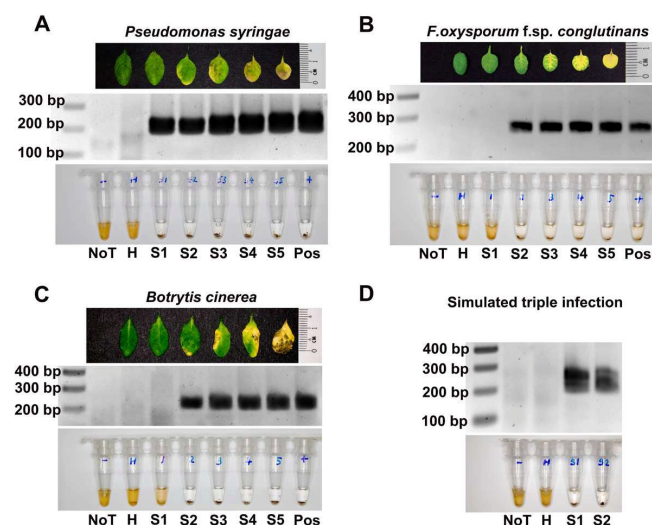


Fig 2. Performance at detecting three plant pathogens in *Arabidopsis thaliana*. (A) *Pseudomonas syringae*, (B) *F. oxysporum* f.sp. *conglutinans*, (C) *Botrytis cinerea*, (D) simulated triple infection. Top row: photographs of leaves at various times after infection, S1 to S5. H: healthy sample. Pos: positive control. NoT: no template control. Middle row: gel electrophoresis images of corresponding RPA reactions performed on the same leaf. Bottom row: photographs of the flocculation assay corresponding to the RPA reactions. Each figure is representative of at least 3

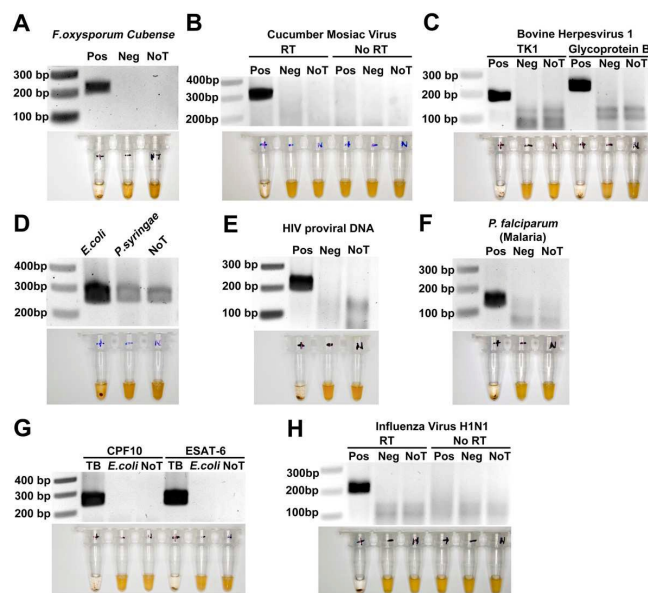


Fig 3. Detecting multiple disease pathogens from across various host kingdoms. (A) *F. oxysporum cubense* Race 1 in banana stems. (B) *Cucurbit mosaic virus* in *Nicotiana benthamiana* leaves. (C) *Bovine Herpesvirus 1* in bovine cells using two pathogen target genes, tyrosine kinase 1 (*TK1*) and Glycoprotein B. (D) *E. coli* in water using *P. syringae* as an unrelated control. (E) *HIV* proviral DNA in Jurkat cells. (F) *P. falciparum* blood cultures. (G) *Mycobacteria Tuberculosis* in cultures using two pathogen target genes, CFP10 and ESAT-6. *E. coli* was used as an unrelated control. (H) Influenza virus H1N1 in culture media. Top row: gel electrophoresis images of RPA reactions performed. Bottom row: photographs of the flocculation assay corresponding to the RPA reactions. Pos: positive sample. Neg: negative sample. NoT: no template control. RT: reverse transcriptase. Each figure is representative of at least 3 experimental replicates.

1 assays for biomolecule detection using gold nanoparticles via
 2 various strategies including antibody, DNA probe modified- and
 3 electrostatic-mediated aggregation.²¹⁻²⁴ For instance, unlike gold
 4 nanoparticle methods, the larger size and variety of colloidal
 5 particles/material which can be manipulated by a bridging
 6 flocculation process (e.g., the 1 μm sized particles used here) allows
 7 for better naked eye contrast and therefore does not require the use
 8 of spectrometry equipment to verify flocculation hence making the
 9 bridging flocculation assay ideal for resource-poor applications. 39

10 To enable a meaningful application, we married the robust
 11 isothermal recombinase polymerase amplification (RPA)²⁵, as a
 12 proof of concept, with our flocculation assay to detect some
 13 examples of agriculturally important pathogens. The RPA was used
 14 to facilitate the generation of large amounts of long DNA polymers
 15 (amplicons) that could trigger a flocculate only if the pathogen was
 16 present. To this end, we first analysed the model plant *Arabidopsis*
 17 *thaliana* infected with different pathogens at various degrees of
 18 infection severity. This was achieved by collecting leaf samples at
 19 various time points post infection (S1-S5, see ESI for details)²⁶. This
 20 approach also served both as a typical traditional visual diagnosis
 21 method, and to emulate situations when a farmer would want to
 22 diagnosis performed. 52

23 To enable a sampling procedure with minimal equipment, we used
 24 modified SPRI approach to extract total DNA from leaf cuttings
 25 (see ESI for detailed method description). This was then followed
 26 by the isothermal RPA amplification of pathogen-specific sequences
 27 at 37°C for 15 minutes. With this approach we could detect the
 28 bacterial pathogen *Pseudomonas syringae* very early in the infection
 29 process, even before disease symptoms manifested (Fig 2A). To
 30 verify that a flocculation was indeed a result of successful RPA
 31 amplification, an aliquot of the RPA reactions was also visualized
 32 via gel electrophoresis. As expected, flocculation occurred only
 33 when there was a successful RPA amplification, therefore
 34 confirming that the flocculation assay could be used as a viable
 35 approach to evaluate successful amplification which in turn, indicates
 36 presence of the offending pathogen. Compared with current methods

in the literature for detecting *Pseudomonas syringae* in plants, our
 approach is the fastest with comparable, if not better, sensitivity as
 other previously described methods (ESI Table S2).

In addition, the presence of two other important and devastating
 pathogenic fungi, *Fusarium oxysporum* f. sp. *conglutinans* and
Botrytis cinerea were also detected very early in the infection
 process when symptoms were just visible to the human eye (Fig 2B
 & Fig 2C). In contrast, an additional validation by qPCR could only
 detect *Fusarium* infection at a later time point using the same amount
 of starting material and primers (ESI Fig S3). While we could not
 reproducibly detect the earliest (S1) time point for *F. oxysporum* and
B. cinerea (Fig 2B and C), we do not view it as a major limitation
 since plants at these early disease stage were virtually symptomless,
 hence would have gone unnoticed by the farmer. In actual farming
 situations, disease diagnostic assays are only performed when
 potential disease symptoms appear.

To demonstrate a triplex detection assay, leaves from three plants
 inoculated with different pathogens were pooled together at their
 respective times post infection to simulate a triple infection. We
 could reliably detect the presence of pathogens in plants with early
 signs of infection (Fig 2D, ESI Fig S4). These results demonstrate
 both the feasibility and sensitivity of the assay in early detection of
 plant infections i.e. when phenotypic symptoms were just beginning
 to manifest. While the assay performed well on the *Arabidopsis*
thaliana plant model system, we wondered if the assay could be
 applicable to commercial crops and non-leaf tissues with different
 composition and putative assay inhibitors. To this end, we tested the
 approach on Lady Finger banana stem cuttings from diseased field
 plant samples to detect *F. oxysporum* f. sp. *cubense* Race 1. We were
 able to distinguish healthy from diseased sample, thus supporting the

1 potential for a viable on-site field test for agricultural applications
 2 (Fig 3A). Current practices for crop pathogen identification are done
 3 via ELISA or PCR-based methods performed off-site at central
 4 facilities.^{2, 4-10} While useful, the time delay (days) to obtaining
 5 results is not ideal as timely interventions are crucial for preventing
 6 catastrophic crop losses.² In contrast, our approach has the potential
 7 for on-site applications because it uses an isothermal amplification
 8 method coupled with a simple naked eye evaluation method that can
 9 be performed with minimal equipment in under 90 minutes.
 10 Recently, RPA has been performed using only body heat.²⁷ The
 11 coupled to a low resource DNA mediated bridging flocculation
 12 evaluation assay such as the one described herein could further
 13 advance low cost on-site molecular diagnostics.

14 As a large number of important pathogens use RNA as their genetic
 15 material we turned our attention to RNA-based pathogens. By
 16 adding MMLV reverse transcriptase (RT) to the RPA mix we
 17 performed RT-RPA^{28, 29} on *Nicotiana benthamiana* plants infected
 18 with cucumber mosaic virus, a RNA virus that affects a multitude of
 19 commercial vegetable crops. As was the case with DNA-based
 20 pathogens, only samples with viral infection but not healthy plants
 21 tested positive (Fig 3B). Finally we extended the approach to the
 22 detection of a wider variety of targets. These included bovine herpes
 23 virus 1 in bovine cells (Fig 3C), *E.coli* in water (Fig 3D); and
 24 human diseases such as proviral HIV (Fig 3E), malaria (Fig 3F),
 25 *Mycobacteria tuberculosis* (Fig 3G) and influenza virus H1N1
 26 (Fig 3F), all of which we could successfully discriminate between
 27 infected and uninfected samples using the flocculation assay
 28 to visualize positive amplifications.

30 Conclusions

31 In conclusion, we have described a novel bridging flocculation assay
 32 for naked eye qualitative evaluation of amplified DNA. The
 33 combination of RPA with the flocculation assay then forms the basis
 34 of a simple strategy for on-site nucleic acid diagnostics with minimal
 35 equipment that may find wide applications. This strategy was first
 36 applied successfully to detect economically important plant
 37 pathogens and then extended to detect a suite of pathogens of a
 38 variety of sources. While promising, a current limitation of this
 39 method is need for multiple wash steps which can be resolved by
 40 future improvements to the method. However, considering the wide
 41 range of pathogens and samples demonstrated here, we believe
 42 this assay has the potential for on-site, low resource applications.

44 Notes and references

45 ^aCentre for Personalized Nanomedicine, Australian Institute
 46 Bioengineering and Nanotechnology, The University of Queensland,
 47 QLD 4072, Australia.
 48 ^b Plant Genetic Engineering Laboratory, School of Agriculture and Food
 49 Sciences, The University of Queensland, QLD 4072, Australia.
 50 ^c School of Chemistry and Molecular Biosciences, The University of
 51 Queensland, QLD 4072, Australia.
 52 † Authors contributed equally.
 53 Emails: m.trau@uq.edu.au, j.botella@uq.edu.au

55 Electronic Supplementary Information (ESI) available: See
 56 DOI: 10.1039/c000000x/

58 Acknowledgments

We thank David Harrich and Dongsheng Li for providing the HIV
 samples, Timothy Mahony for the Bovine HPV-1 samples, Nick West for
 the MTB samples, Christopher Peatey for the malaria samples, Elizabeth
 Aitken and Juliane Henderson for the *F. oxysporum cubense* Race 1
 samples, Paul Young and Daniel Watterson for the influenza H1N1
 samples.

1. P. Yager, T. Edwards, E. Fu, K. Helton, K. Nelson, M. R. Tam and B. H. Weigl, *Nature*, 2006, **442**, 412-418.
2. G. N. Agrios, *Plant pathology*, 5th edn., Elsevier Academic Press, Amsterdam ; Boston, 2005.
3. J. G. Horsfall and E. B. Cowling, *Plant disease : an advanced treatise*, Academic Press, New York, 1977.
4. J. D. Janse and B. Kokoskova, *Methods in molecular biology*, 2009, **508**, 89-99.
5. J. A. Price, J. Smith, A. Simmons, J. Fellers and C. M. Rush, *Journal of virological methods*, 2010, **165**, 198-201.
6. J. Dai, H. Peng, W. Chen, J. Cheng and Y. Wu, *Journal of applied microbiology*, 2013, **114**, 502-508.
7. B. Kokoskova and J. D. Janse, *Methods in molecular biology*, 2009, **508**, 75-87.
8. Z. H. Wang, S. G. Fang, Z. Y. Zhang, C. G. Han, D. W. Li and J. L. Yu, *Journal of virological methods*, 2006, **134**, 61-65.
9. D. K. G. Heiny, D.G., *Physiological and Molecular Plant Pathology*, 1989, **35**, 439 - 451.
10. S. F. Wright and J. B. Morton, *Applied and environmental microbiology*, 1989, **55**, 761-763.
11. R. A. Ruehrwein and D. W. Ward, *Soil Science*, 1952, **73**, 485-492.
12. V. K. La Mer, *Discussions of the Faraday Society*, 1966, **42**, 248-254.
13. T. W. Healy and V. K. La Mer, *Journal of Colloid Science*, 1964, **19**, 323-332.
14. R. H. Smellie Jr and V. K. La Mer, *Journal of Colloid Science*, 1958, **13**, 589-599.
15. P. J. Flory, *J Chem Phys*, 1941, **9**, 660-661.
16. P. I. Flory, *J Chem Phys*, 1942, **10**, 51-61.
17. M. L. Huggins, *J Chem Phys*, 1941, **9**, 440-440.
18. M. M. Deangelis, D. G. Wang and T. L. Hawkins, *Nucleic Acids Res*, 1995, **23**, 4742-4743.
19. R. J. Hunter, *Foundations of colloid science*, 2nd edn., Oxford University Press, Oxford ; New York, 2001.
20. D. Napper, *Academic*, New York.
21. F. Xia, X. L. Zuo, R. Q. Yang, Y. Xiao, D. Kang, A. Vallee-Belisle, X. Gong, J. D. Yuen, B. B. Y. Hsu, A. J. Heeger and K. W. Plaxco, *P Natl Acad Sci USA*, 2010, **107**, 10837-10841.
22. X. W. Xu, J. Wang, F. Yang, K. Jiao and X. R. Yang, *Small*, 2009, **5**, 2669-2672.
23. H. X. Li and L. Rothberg, *P Natl Acad Sci USA*, 2004, **101**, 14036-14039.
24. C. A. Mirkin, R. L. Letsinger, R. C. Mucic and J. J. Storhoff, *Nature*, 1996, **382**, 607-609.
25. O. Piepenburg, C. H. Williams, D. L. Stemple and N. A. Armes, *Plos Biol*, 2006, **4**, 1115-1121.
26. T. Miedaner, G. R. Gang and H. H. Geiger, *Plant Dis*, 1996, **80**, 500-504.
27. Z. A. Crannell, B. Rohrman and R. Richards-Kortum, *PLoS one*, 2014, **9**, e112146.
28. M. Euler, Y. Wang, O. Nentwich, O. Piepenburg, F. T. Hufert and M. Weidmann, *J Clin Virol*, 2012, **54**, 308-312.
29. M. Euler, Y. Wang, D. Heidenreich, P. Patel, O. Strohmeier, S. Hakenberg, M. Niedrig, F. T. Hufert and M. Weidmann, *J Clin Microbiol*, 2013, **51**, 1110-1117.