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Miniaturization of multiplexed planar recombinant antibody arrays for serum protein profiling

Background: Antibody-based microarrays are a developing tool for high-throughput proteomics in health and disease. However, in order to enable global proteome profiling, novel miniaturized high-density antibody array formats must be developed. Results: In this proof-of-concept study, we have designed a miniaturized planar recombinant (single-chain Fragment variable) antibody array technology platform for multiplexed profiling of non-fractionated, directly labelled serum samples. The size of the individual spot features was reduced 225-times (78.5 μm²/spot) and the array density was increased 19-times (38,000 spots/cm²). These miniaturized, multiplexed arrays were produced, using a desktop nanofabrication system based on dip-pen nanolithography technology, and interfaced with a high-resolution fluorescent-based scanner. The reproducibility, sensitivity, specificity, and applicability of the set-up were demonstrated by profiling a set of well-characterized serum samples. Conclusion: The designed antibody array platform opens up new possibilities for large-scale, multiplex profiling of crude proteomes in a miniaturized fashion.
with proven high on-chip performances, for large-scale profiling represents a major issue [2]. Hence, additional efforts will be required to establish a viable miniaturized high-density antibody array technology platform.

Recently, a desktop tool designed for multiplexed deposition, simultaneously printing of up to 12 different proteins, with individual features in the 0.78 μm²/spot (Ø 1 μm) to 78.5 μm²/spot (Ø 10 μm) size range (size-dependent on tip-surface contact-time), based on dip-pen nanolithography (DPN) technology was presented [23]. It is noteworthy that sub-micron sized spot features (Ø 10 μm) would still be compatible with both high-density array layouts (< 510,000 spots/cm²) and fluorescence-based sensing of high-density arrays using conventional, high-resolution scanners. In fact, fluorescence is by far the most commonly used read-out system for conventional antibody microarrays [24] (for review see [2]). Interestingly, the viability of DPN-generated arrays visualized using fluorescence-based sensing was recently indicated for a 1-plex monoclonal antibody array [25].

In this discovery study, we have designed the first miniaturized planar recombinant antibody array technology platform, with significantly reduced spot features (78.5 μm²/spot) and increased array density (38,000 spots/cm²), for multiplexed assay of crude, directly labelled serum samples. To this end, we uniquely combined a probe source based on a renewable, large recombinant single-chain Fv (scFv) antibody library, microarray adapted by molecular design [2], with the next generation of a DPN®-based desktop tool, NanoArrayer 3000, interfaced with a high-resolution fluorescent-based scanner.

### Key terms:

- **Proteome**: All proteins present in a given sample at a given time-point.
- **Antibody microarray**: Miniaturized assay in which a set of antibodies are deposited one-by-one onto a solid support in an array pattern, and used to detect the corresponding antigens.
- **Dip-pen nanolithography**: Technology in which the tip of an atomic force microscope cantilever is used as a ‘pen’ to write (print) ink, for example, protein onto a surface.
- **Multiplexed assay**: One assay used to detect several (>1) analytes at the same time.
- **scFv antibody**: Fusion protein of the variable regions of the heavy (VH) and light chains of antibodies capable of specifically binding antigen.

### Experimental section

#### Antibodies

Twenty-eight human recombinant scFv antibody fragments, directed against eight human complement proteins (CPs), eight human cytokines, and one non-human serum protein (Supplementary Table 1S), were stringently selected from a large phage display library, as previously described [26].

#### Production & purification of scFv antibodies

All scFvs were produced in *Escherichia coli* and purified from expression supernatants using affinity chromatography on Ni²⁺-NTA agarose (Qiagen, Hilden, Germany) [27]. The degree of purity and integrity of the scFvs were evaluated using 10% SDS-PAGE (Invitrogen, Carlsbad, CA, USA). The protein concentrations were determined by measuring the absorbance at 280 nm (average concentration 0.72 mg/ml, range of 0.18–1.72 mg/ml). The specificity, affinity (1–10 nM range), and on-chip functionality of the phage-display derived scFvs were ensured by using: stringent selection protocols [26]; multiple clones (one to four) per target molecule; and/or a scFv library microarray adapted by molecular design [2,28]. The specificity of several scFv antibodies have previously been validated using well-characterized, standardized serum samples, and orthogonal methods, such as mass spectrometry, ELISA, Meso Scale Discovery assays, cytokine bead arrays and/or microarray spiking and blocking experiments (Supplementary Table 1S) [4,27–31] [Unpublished Data; Wingren et al.].

#### Serum samples & antigen

In total, six well-characterized (de-identified) human serum samples, including a large pool of normal human sera (NS), and five complement-deficient serum samples, that is, samples with known significantly altered levels of one or several CPs were obtained from the Institute of Laboratory Medicine, Section of Microbiology, Immunology and Glycobiology, Lund University (Sweden; Supplementary Table 2S). It is noteworthy that NS is used as a validated reference in the daily routine analysis of CPs in clinical samples. The levels of CPs in the complement-deficient sera were determined using electro immunoassay (rocket immunoelectrophoresis) and/or turbidometry (C3 and C4). The analytical range of these methods ranged from 1–6% up to 400% of the normal serum concentration of the protein (electro-immunoassay), and 0.05–20 g/l (C3) or 0.01–4 g/l (C4) (turbidimetry). Purified C1q were purchased from ElectraBox Diagnostica (Tyröso, Sweden). Cholera toxin subunit B (CT), originating from *Vibrio cholerae*, was purchased from Sigma (St. Louis, MO, USA).
Labeling of samples  
The serum samples (~90 mg/ml) were biotinylated using EZ-Link Sulfo-NHS-LC-Biotin (Pierce, Rock-
ford, IL, USA) according to previously optimized labeling protocol for serum proteome [27,31]. CT was spiked into the serum samples to a final concentration of 280 nM. The serum samples were labeled at a molar ratio of biotin: protein (15:1) assuming an average molecular weight of 50 kDa for the serum proteins [32]. Unreacted biotin was removed by extensive dialysis against PBS (pH 7.4) for 72 h using a Slide-A-Lyser (MWCO 3.5 kDa) (Pierce). The samples were aliquoted and stored at -20°C until further use.

C1q was labeled with Alexa-Fluor-647 at a molar ratio of 10:1 dye: protein, according to the recommenda-
tions of the manufacturers (Invitrogen). Briefly, NaHCO3 (pH 8.5) was mixed with 10 μl C1q (1 mg/ml) to a final concentration of 0.1 M. Alexa-Fluor-647 (Invitrogen) was added to the protein mixture to a final concentration of 0.02 mM. The sample was first incubated on ice for 5h, with careful mixing every 20 min, and then dialyzed against 40% (v/v) glycerol in PBS (pH 7.4) for 72h using a Slide-A-Lyser (MWCO 3.5 kDa) (Pierce). The samples were aliquoted and stored at -80°C until further use.

Production & handling of scFv arrays  
The scFv arrays were produced using a desktop nanofabrication system, NanoArrayer 3000, based on DPN technology (Nanolink Inc, Skokie, IL, USA). Prior to dispensing, the tips, DPN Probes Type M-ED Side M2 with 12 modified “A frame” cantilevers (DPN pen) (Nanolink Inc.), were plasma cleaned for 1 min at low RF-value, using a gas mixture of Oxygen/Argon (20%/80%) at 1.4 bar using a Plasma Cleaner (PDV-002) (Harrick Plasma, Ithaca, NY, USA). The antibodies (0.1 to 0.5 mg/ml) where diluted in printing buffer (Nanolink Inc.), and Alexa-Fluor-555 cadaverine disodium salt (Invitrogen) was added to a final concentration of 0.02 mM of Alexa-647 conjugated streptavidin (Invitrogen) diluted in PBS-MT for 1 h. Finally, the arrays were washed three times with PBS-T and one time with PBS and then incubated with 60 μl biotinylated serum samples or directly labeled C1q (0.046 ng/ml to 460 ng/ml) for 1 h. All serum samples were diluted 1:10 (resulting in a total serum dilution of 1:450, corresponding to approximately 0.2 mg/ml) in 1% (v/v) fa- free milk powder and 1% (v/v) Tween-20 in PBS (PBS-MT). Then the arrays were washed three times with PBS-T. Any subarrays incubated with biotinylated serum samples were incubated with 1 μg/ml Alexa-647 labelled BSA (Saveen Werner, BDH Chemicals (Poole, Great Britain) were printed in eight replicates per sub-array, including 81 sub-arrays on seven slides.

Analysis of scFv arrays  
The arrays were scanned using a high-resolution fluorescent scanner, InnoScan®900 (Innopsys, Carbonne, France) at three different scanning setting (Detection gain at 635nm: 15, 50 and 100%). The slides were loaded and scanned one by one. All arrays were scanned with 1 μm/pixel resolution (the resolution, a factor of two above the maximum resolution, was selected to best match the diameter of the spots) and the Mapix software (V.4.6.2) (Innopsys) was used to quantify the mean intensity of each spot using the fixed circle method, a standard approach for quantifying array spots. The method applies user defined parameters of the spot diameter (10 μm) and back-
ground diameter (spot diameter plus 1 pixel), in that. Background is measured locally outside each spot. The local background was then subtracted from the spot intensity and to compensate for possible local defects, the highest and the lowest signal intensities were auto-
matically excluded [2,4], and each data point repre-
sents the mean value of the remaining six replicates. For protein analytes displaying saturated signal, values from lower scanning settings were chosen. The LOD was defined as the analyte concentration correspond-
ing to a signal 2× SD above the negative control. The
dynamic range was defined as the signal intensity that lies between 2× SD above the negative control and below the maximum (saturated) signal.

**Results & discussion**

In this proof-of-concept study, we have designed and evaluated miniaturized planar recombinant antibody arrays for multiplexed profiling of crude serum samples. To this end, 27 human recombinant scFv antibodies, targeting 17 high- (μM to nM range) and low-abundant (pg/ml) serum analytes, were used as probes (Supporting Information Table 1S). Six well-characterized serum samples, with known expression levels of eight complement proteins, were used as model systems (Supporting Information Table 2S). It should be noted that the probes were selected from a phage display library, microarray adapted by molecular design, thus representing a large, renewable probe source with features (shape and homogeneity) found to be adequate as judged by visual inspection, as illustrated in Figure 1A. The spot diameter was evaluated for ten scFv antibodies printed in eight replicates per sub-arrays, including 108 sub-arrays on six slides, after the capture of biotinylated targets, thus incorporating printing efficiency of functional scFv antibodies into the measurements. The results showed that the spot diameter ranged between 8.3 and 10.2 μm, to some extent reflecting antibody concentration (data not shown), giving a CV of 10.9%. Furthermore, we also printed directly labelled BSA to study the printing efficiency per se. To this end, labelled BSA was printed in eight replicates per sub-array, including 81 sub-arrays on seven slides. The spot morphology (shape, homogeneity) was found to be adequate (visual inspection) with consistent spot signal intensities (CV of 12%). Hence, the performance of the printing process was found to be adequate.

In the printing process, two planar slides, known to perform well in conventional antibody microarrays [31,35], including black polymer Maxisorb slides and Nexterion slide E, were evaluated as support. The advantage of using a simple planar surface is that the need for more elaborate surface architectures, e.g. nanowires [13], that in turn also would determine (limit) the array layout per se, could be bypassed. While the Maxisorb slide was found to be too soft to be printed on, creating indentations and heterogeneous spots (Supplementary Figure 1S), adequate spot morphologies, low non-specific background binding, and dynamic signal intensities were observed for sub-microarrays on Nexterion slides (Figure 1A). Hence, Nexterion slide E was used as support throughout the remaining part of the study.

Next, the technical reproducibility of the entire setup was evaluated by repeatedly analyzing replicates of crude, biotinylated serum samples, and determining
the: spot-to-spot variation; array-to-array variability; and chip-to-chip variability. The data was reported in terms of CV value or coefficient of determination ($R^2$). First, the spot-to-spot reproducibility was assessed for all 27 scFv antibodies, deposited in eight replicates/array, by analyzing six serum samples on 83 representative arrays (layout A - 24 arrays on 2 slides, layout B - 48 arrays on 4 slides, and layout C - 11 arrays on 1 slide) (Supporting Information Table 3S). The results showed that a mean CV value of 12% (range 5 to 27%) (by omitting one antibody clone the range was reduced to 5 to 21%) was obtained. In comparison, the established and (more) optimized conventional antibody microarrays regularly display a spot-to-spot variability of <10% (recombinant antibody microarrays) [36] and <20% (polyclonal and monoclonal antibody micro-
arrays [37,38]. In the case of antibody nanoarrays, the reproducibility is a key critical topic (often < 30% [15]) that still remains to be fully demonstrated [7–17,25].

Second, the array-to-array variability, i.e. samples analysed on different sub-arrays, but on the same slide, was investigated for 18 scFv antibodies, deposited in eight replicates/array, by analyzing six serum samples on 72 representative sub-arrays (layout A – 24 arrays on 2 slides, and layout B – 48 arrays on 4 slides). The results showed that a median $R^2$-value of 0.96 (range 0.80–0.98) was obtained (Figure 1B). A representative correlation plot, illustrated for the data associated with array layout A, is also shown in Figure 1B. In comparison, conventional antibody microarrays regularly display $R^2$-values of > 0.9 (recombinant antibody microarrays) [4,36] and > 0.7 (polyclonal and monoclonal antibody microarrays) [38].

Third, the chip-to-chip variability, that is, a sample analyzed on different sub-arrays and different slides (and different days), was assessed for 18 scFv antibodies, deposited in eight replicates/array, by analyzing six serum samples on in total 72 representative sub-arrays (layout A – 24 arrays on 2 slides, and layout B – 48 arrays on four slides). Two representative correlation plots for data associated with array layout A and B are shown in Figure 1C. The data showed that median $R^2$-values of 0.93 (array layout A) and 0.83 (range 0.71–0.89) (array layout B) were obtained. As might be expected (Figure 1C &B), the $R^2$-values dropped somewhat when introducing additional assay variables, that is, when running the assay on different slides and days. In comparison, conventional antibody microarrays regularly display $R^2$-values > 0.8 [4,36,38]. Taken together, the miniaturized recombinant antibody array set-up was found to display an adequate reproducibility, and in the same range as that observed for conventional antibody microarrays [4,36–38], for review see [2].

The LOD was evaluated by analyzing serial dilutions of directly labeled sample in the format of pure antigen (C1q) and/or crude serum samples. In the latter case, a well-characterized, standardized normal serum sample (NS) was applied (Supplementary Tables 1S & 2S). LOD was defined as the analyte concentration corresponding to a signal that is 2× SD above the background signal (negative control). In the case of the complement protein (CP) C1q, LOD was found to be about 0.46 ng/ml targeting pure analyte (Figure 2A), while the LOD increased about 35 times (LOD ≤ 15 ng/ml) when addressing crude serum, NS, with known concentration of C1q (Figure 2B). Furthermore, targeting a set of additional seven CPs of a priori known concentrations in NS, the LOD was found to be 10–1200 ng/ml (Figure 2C). The fact that different antibody clones targeting the same antigen, but different epitopes, displayed different LODs is often observed [27,31], and might be explained by differences in: affinity; antibody concentration; and/or epitope masking upon biotinylation. Next, the LOD was determined for a set of nine low-abundant cytokines of estimated concentration in NS (Figure 2D & E, & Supplementary Table 1S). The results indicated that the LOD was in the range of 3–180 fg/ml. Hence, the results showed that both high- and low-abundant serum analytes could be detected in crude, directly labeled proteomes, indicating on adequate assay sensitivity well in line with what is required for affinity-proteomics-based efforts (for review see [1–3]).

The ambient analyte theory [18,19] explains the theoretical background to why the assay sensitivity should be more sensitive for miniaturized assays, such as antibody microarrays versus conventional antibody immunoassays. It also postulates that miniaturizing the spot diameter below 1 μm is less likely to provide any additional assay benefit (set-up dependent), and the assay sensitivity will in fact be impaired rather than improved if the spot size goes below a certain limit (set-up dependent) [19]. To investigate the impact of our miniaturizing on the LOD, we first compared the LOD for our miniaturized recombinant antibody arrays (spot size – 78.5 μm² and Ø 10 μm) with that of our previously developed conventional recombinant antibody microarrays (spot size – 18 × 10³ μm² and Ø ~150 μm) [27,31] (Figure 2C). These set-ups are as identical as possible (e.g., using the same recombinant antibody clones), essentially differing only in spot size and choice of solid support. The results showed that the LOD was two-to 500-times worse (reduced) by miniaturizing the spot area 225-times (78.5 vs. 18 × 10³ μm²) and spot diameter 15-times (Ø 10 vs. 150 μm). The LOD for other high-end conventional antibody microarray set-ups, for example, [24,39] (not as directly comparable due to more substantial differences in assay set-up, such as different antibodies (both format and clones), different sample labelling protocols etc) are also high (pM range over fg/ml range), enabling truly low-abundant analytes, such as cytokines, to be targeted. Hence, also compared with those platforms, the same trend of reduced LOD was indicated. The observation that the miniaturization did not lead to an improved assay sensitivity in general might be explained by that: different fluorescence-based scanners and accompanying softwares were used (InnoScan®900 (Innopsys, Carbone, France vs. Scan Array Express, PerkinElmer Life & Analytical Sciences, Wellesley, MA, USA); different solid supports were used; we compared the 1st generation of miniaturized arrays with a highly optimized conventional microarray set-up [27,31,36]; and/or we have reduced the spot size beyond the opti-
mal settings according to the ambient analyte theory (reflecting both spot size and antibody affinity) [19].

Furthermore, the sample titration experiments enabled us to estimate the dynamic range, and representative titration curves are shown in Figure 2A, B & D. The results indicated that the dynamic range of the assay, defined as the range of analyte concentrations that lies between 2× SD above the background (neg-
tive control) and below the maximal signal, was in the range of $\leq 10^3$. Hence, this feature of the miniaturized recombinant antibody array set-up was similar to, or only slight worse, than that observed for recombinant antibody nanoarrays [14], conventional recombinant antibody microarrays [4], and conventional polyclonal and monoclonal antibody microarrays [24,39–40] (for review see [2,41]).

Finally, to demonstrate proof-of-concept for the applicability of the set-up, we performed multiplexed protein expression profiling of eight CPs in six well-characterized serum samples, including NS and five CP deficient serum samples (denoted DS1 to DS5) (Figure 3 and Supplementary Table 2S). It is noteworthy that only approximately 0.13 $\mu$L of serum was consumed per array, illustrating the wealth of information that could be generated using miniaturized antibody, while consuming minute amounts of a clinical sample. In addition, the array assay took less than 3.5 h to run, further illustrating the applicability of the set-up.

**Figure 3.** Serum protein expression profiling of eight complement proteins in six well-characterized human serum samples, using miniaturized recombinant antibody arrays. (A) Representative array image of normal serum (NS) and a complement deficient serum (DS1), deficient complement proteins indicated with a red box. (B) Comparison of the known clinical protein expression levels of the complement proteins, determined using orthogonal methods, with the antibody array data. ScFv: Single-chain Fv.
Representative array images of NS and DS1 (C1q and properdin deficient) are shown in Figure 3A. The results showed that significantly lower signal intensities were, in particular, observed for both C1q and properdin. Next, we compared the array signal intensities with the known expression levels of the CPs determined using orthogonal methods. Representative results, illustrated by those obtained for C1q, C1-INH, C3, C4, C5, FB, and properdin, are displayed in Figure 3B. The results showed that the array data correlated well with the expected expression profile of the CPs. In more detail, the significantly reduced expression levels (<70%) of e.g., C1q (DS1), C3 (DS2 and DS3), C4 (DS4), C5 (DS3), and properdin (DS1) could readily be detected. Furthermore, medium to small (<50%) changes in the expression levels, including both down-regulated (e.g., C1q in DS4, and FB in DS1) and up-regulated (e.g., properdin in DS3 and C5 in DS2) levels, could also be monitored. Taken together, we have generated proof-of-concept for the first generation of a miniaturized recombinant scFv antibody array platform. The set-up was demonstrated to provide a rapid, sensitive, and reproducible profiling of non-fractionated, directly labeled proteomes in a highly specific manner, thus paving the way for large-scale, multiplex profiling of crude proteomes in a miniaturized fashion.

Future perspective
We believe that miniaturized (recombinant) antibody microarrays will be an essential tool for large-scale, multiplexed profiling of crude proteomes, such as serum, in both health and disease. It opens up new possibilities for biomarker discovery, and in the second wave, for miniaturized assay set-ups suitable for clinical settings, requiring minimal amounts of both reagents and samples, and potentially also for point-of-care applications.

Supplementary data
To view the supplementary data that accompany this paper please visit the journal website at: www.future-science.com/doi/suppl/10.4155/BIO.13.342

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Ethical conduct of research
The authors state that they have obtained appropriate institutional review board approval or have followed the principles outlined in the Declaration of Helsinki for all human or animal experimental investigations.

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References
Papers of special note have been highlighted as:
• of interest; •• of considerable interest
• Presenting miniaturized protein arrays.


