ORIGINAL ARTICLE

# A simplified method of calculating cPRA for kidney allocation application in Hong Kong: a retrospective study

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## SUMMARY

Calculated panel reactive antibody (cPRA) represents possibility of encountering an incompatible donor for organ transplant candidates and has gradually replaced traditional PRA as a measurement of sensitization level. We tested two cPRA calculation methods on a cohort of renal candidate ($n$ = 613). HLA typing of 563 Chinese deceased renal donors was used to estimate allele and haplotype frequencies of Hong Kong donor pool. The OPTN formula was adopted to generate cPRA (cPRA (freq)). We also incorporated a computer script to compare unacceptable antigens of patients against HLA phenotype of donors. The cPRA based on historical donor filtering was the percentage of filter out count over total number of donors (cPRA (filter)). Values of cPRA (freq) and cPRA (filter) showed almost perfect agreement with Lin's correlation coefficient equal to 1.000. SD of bias was 0.6 cPRA point. Limit of agreement was 0.9 to −1.5 points difference. Furthermore, the poor agreement between our in-house cPRA and values from other online calculators indicated the necessity to use local population data for accurate cPRA calculation. Built-in donor filtering method was more practicable for Hong Kong due to factors such as cost and flexibility. An on-going donor pool can reflect population allele frequencies and permits efficient periodic update of cPRA.

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**Key words**
calculated panel reactive antibody, organ allocation, renal transplantation, sensitization, unacceptable antigen, virtual cross-match

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## Introduction

Historically, the sensitization level of patients in organ allocation programme is assessed by a measurement termed panel reactive antibody (PRA). In 1969, Patel and Terasaki initiated the concept of PRA using a randomly selected donor lymphocytes panel to estimate the risk of graft failure [1]. PRA is calculated from the result of cross-match based on cytotoxicity method. By testing patient's serum against a panel of donor lymphocytes, PRA is the percentage of positive cross-match over total number of donor tested. A high PRA percentage




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indicates a low chance for a patient to encounter a suitable donor organ. PRA is important for organ allocation because highly sensitized patients often have a lower chance of encountering compatible donor. To compensate for the unfavourable situation of these patients, some countries started an acceptable HLA-mismatch programme for highly sensitized candidates [2]. In general, patients with PRA >80% are qualified to enter these programmes. Historically, the United Network for Organ Sharing (UNOS) in the United States gave those patients with a PRA equal to or over 80% an extra four points during allocation [3]. To measure PRA in an accurate and representative manner, several requirements must fulfil. The panel of donor lymphocytes should be large and diverse enough to address the genetic variation and ethnicity of organ donor pool from the population under consideration. The PRA testing method should produce consistent and comparable result across time and different transplant centres. Finally, the antibody quantitation should be high enough to produce a positive cytotoxicity cross-match result. Unfortunately, it is often not easy to achieve. Traditionally, the panel used for PRA consisted of not more than fifty donors. Given the great diversity of HLA allele in a population, each episode of PRA testing can only produce a partial reflection of the general donor pool. The PRA value will also fluctuate depending on the panel used at each time. It is often hard to compare result from different transplant centres given that their PRA may be produced by different methods. Cross-match by cytotoxicity method is less sensitive than solid phase technology. Only a low titre of HLA antibody may present in patient's serum which may not induce a positive cross-match before transplantation, but can post a threat to the organ after transplantation when the antibody titre increase significantly. Other non-HLA antibodies can produce positive cross-match but may not be clinical significant to transplantation.

To overcome various shortcomings of traditional PRA measurement and better utilize the more sensitive data produced by solid phase technology, the concept of calculated PRA (cPRA) was introduced. cPRA is defined as the percentage of donors expected to have HLA antigens that are unacceptable for a candidate. It is the probability for a patient to give a positive cross-match. UNOS Board of Directors implemented Policy 3.5.11.3 in December 2007, requiring the listing of unacceptable antigens and cPRA for each candidate. In October 2009, cPRA officially replaced traditional PRA as the assessment of patient sensitization [4]. In 2013, UNOS approved a new kidney allocation policy. The new sliding scale allows the addition of up to 202 allocation points based on patient's sensitization level, which is inversely correlated with the probability of encountering incompatible donors (i.e. cPRA) [5]. Comparing with traditional PRA, cPRA has the advantage of producing consistent and comparable assessment for sensitization level. Determination of cPRA value does not require additional laboratory procedures. Instead, the calculation only requires the data of unacceptable antigens identified from routine antibody monitoring of patients. cPRA also represent the effect of both HLA Class I and II antibody in one single value. Several online cPRA calculators are available for the enquiry of cPRA scores through the entry of unacceptable antigens, for example, the cPRA calculator by the US Organ Procurement and Transplantation Network (OPTN) [6], the Eurotransplant virtual PRA calculator [7], and the Canadian PRA calculator [8].

Currently, two types of cPRA calculation approach are available. The first approach involves collecting a sample of donor HLA phenotypes and directly observes the percentage of incompatible donors for each patient based on their unacceptable antigens. Eurotransplant virtual PRA calculator utilized such approach. Eurotransplant's cPRA calculation is based on HLA phenotype of 6 870 deceased renal donors within the Eurotransplant service area between the year 2010 and 2014. After the input of patient's unacceptable antigens, the calculator returns the frequency of donors that possess such unacceptable antigens.

On the other hand, OPTN in the United States employed a different approach. Its cPRA calculation requires two types of data. The first one is HLA gene frequencies. OPTN counts the single locus gene frequencies from 14 282 deceased kidney donors. The two, three, four and five locus haplotype frequencies were estimated from the observed HLA phenotype using the expectation maximization (EM) algorithm [9]. The second type of data is ethnic frequencies. The cPRA is first calculated by each ethnicity gene frequencies separately, followed by multiplying such cPRA by the proportion weight of that ethnicity within the whole donor pool. The final cPRA for a patient is the summation of all these multiplied values [10]. To our knowledge, there is neither study nor data regarding cPRA in Hong Kong. Therefore, we embark on employing different types of cPRA calculation methods on a renal transplant candidate cohort. By calculating the agreement between these methods, a practicable cPRA calculation protocol for Hong Kong patients can be selected and implemented with confidence.

## Materials and methods

### Data collection

HLA-A, -B and -DR typing of all Chinese deceased donors ($n$ = 563) registered under the Hospital Authority Organ Registry and Transplant System (ORTS) database from February 1996 to July 2015 was included in the current study. All HLA typings were performed at the Division of Transplantation and Immunogenetics, Queen Mary Hospital through serological microlymphocytotoxicity method before 5 December 2014, PCR sequence-specific oligonucleotide probe method (PCR-SSO) and/or PCR sequence-specific primer (PCR-SSP) method after that date. Around 95% of donors in this study were typed by serological method; molecular typing (SSO/SSP) was performed to further confirm any uncertain serological typing result. All the HLA typings were expressed as serological split group. Unacceptable antigens profiles of 1 894 on-list renal patients were extracted from the ORTS. Antibodies were detected by Lifecodes Class I and Class II ID kit, and Lifecodes Class I and Class II LSA kit (Immucor, Stamford, CT, USA).

### cPRA calculation by allele frequency

Calculated PRA by allele frequencies method (cPRA (freq)) was based on the formula used by OPTN online calculator [11,12]. Similar to our previous report [13], the three-loci (A, B, DRB1) haplotype frequencies were estimated from the observed phenotypes with Markov Chain Monte Carlo (MCMC) simulation algorithm by the PHASE computer program [14]. The simulation process involves recursively sampling haplotypes from all the theoretical haplotypes based on the observed phenotypes from a pool of unrelated individuals. Single- and two-locus haplotype frequencies were derived from these estimated three-locus haplotype frequencies by marginalizing on the corresponding locus. As only A, B and DRB1 loci were included in this study, the equation for cPRA calculation is:

$$\text{cPRA} = 1 - (1 - \text{S1} + \text{S2} - \text{S3})^2$$

S1, S2 and S3 represented the sum of all possible combination of one, two and three-loci haplotypes frequencies respectively, based on the unacceptable antigens of a specific patient. For example, if a patient had unacceptable antigens of A2, B46 and DR9, S1 was the sum of A2, B46 and DR9 allele frequencies. S2 was the sum of A2-B46, A2-DR9 and B46-DR9 haplotype frequencies. S3 represented the frequency of A2-B46-DR9 haplotype. We first generated all possible haplotype combinations for each patient according to the definition of S1, S2 and S3, then extracted the corresponding frequencies from the aforementioned marginalized haplotype frequencies using 563 Chinese deceased donors. S1, S2 and S3 of each patient were then feed into the OPTN equation to get the final cPRA. All calculation procedures were written in Python.

### cPRA calculation by donor filtering

The principle of donor filtering was to compare historical deceased donors HLA typing against current patients on the waiting list at the generation time point. A computer script was written to compare listed unacceptable antigens of patients against HLA typing of each historical donor according to the HLA-antigen filtering mapping table. Patients were filtered out once if they have at least one unacceptable antigen against a donor. cPRA (filter) was expressed as the percentage of filter out count over total number of donors, which represented the estimated possibility of a patient encountering an incompatible donor.

### Comparison with online cPRA calculators

To assess the validity of using online cPRA calculators for Hong Kong patients, unacceptable antigens data from 70 renal patients were randomly selected for the trial. Online calculators and the resulting cPRA scores were compared with in-house produced cPRA value. cPRA (freq) was compared with cPRA from the OPTN cPRA calculator (cPRA (OPTN)) because both methods utilized allele frequencies for cPRA estimation. Similarly, cPRA (filter) was compared with cPRA from the Eurotransplant virtual PRA calculator (cPRA (Euro)) as both methods express cPRA as a percentage of virtual crossmatch positive donor over total number of historical donor.

### Methods agreement analysis

Agreement between cPRA calculation methods was analysed by Bland–Altman plot. Concordance correlation was assessed by Lin's concordance coefficient (Rc) using SPSS Version 21.0 (IBM, Armonk, NY, USA). Lin's coefficient was a reproducibility index which assessed the correlation between two readings that fall on a 45-degree line going through the origin [15]. A Lin's



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coefficient over 0.99 indicates an almost perfect agreement between two methods, while a value of 0.95–0.99 means a substantial agreement.

## Results

For the period of 1996–2015, there were 563 Chinese deceased donors in Hong Kong. It consisted of 256 (45.5%) female and 307 (54.5%) male donor, with a median age of 49. Tables 1 and 2 showed the allele and estimated haplotype frequencies of HLA-A, -B and -DR loci from this Chinese deceased donor cohort, respectively. The allele frequencies were used in the calculation of patient cPRA (freq).

A total of 1 894 on-listed renal patients were reviewed, in which 1 281 (67.6%) of them did not have any enlisted unacceptable antigen, and thus, the cPRA was zero. cPRA of the remaining 613 renal patients with unacceptable antigen was calculated by both the allele frequency-based method (cPRA (freq)) and the donor filtering method (cPRA (filter)) based on the same cohort of 563 Chinese donors. Both methods were significantly correlated. Fig. 1 showed the correlation plot between these two types of cPRA scores. Lin's correlation coefficient for the 613 cPRA pairs was equal to 1.000, indicating an almost perfect agreement [16]. Fig. 2 showed the Bland–Altman plot for these two cPRA. The standard deviation of difference between the two scores was 0.6 cPRA point. The limit of agreement was between +0.9 to −1.5 cPRA points difference between cPRA (filter) and cPRA (freq). The insignificant difference between cPRA (filter) and cPRA (freq) suggested that the two methods were interchangeable.

Lin's coefficients were 0.824 and 0.829 for cPRA (freq) against cPRA from OPTN and cPRA (filter)

**Table 1.** Single locus serological equivalent antigen frequencies in Chinese deceased donors.

| HLA-A | Frequency (%) | HLA-B | Frequency (%) | HLA-DR | Frequency (%) |
|---|---|---|---|---|---|
| A2 | 30.25 | B46 | 16.37 | DR9 | 17.26 |
| A11 | 29.99 | B60 | 14.77 | DR12 | 17.17 |
| A24 | 15.48 | B75 | 10.59 | DR15 | 12.55 |
| A33 | 10.14 | B13 | 10.32 | DR4 | 12.46 |
| A11.2 | 4.18 | B58 | 8.01 | DR8 | 6.94 |
| A26 | 2.40 | B38 | 5.60 | DR14 | 6.85 |
| A30 | 1.95 | B51 | 5.34 | DR17 | 6.76 |
| A29 | 1.34 | B62 | 4.81 | DR16 | 5.25 |
| A31 | 1.33 | B54 | 3.11 | DR11 | 5.16 |
| A3 | 0.80 | B35 | 2.67 | DR7 | 4.71 |
| A1 | 0.44 | B27 | 2.40 | DR13 | 2.85 |
| A23 | 0.36 | B39 | 2.22 | DR10 | 1.78 |
| A68 | 0.27 | B55 | 2.13 | DR1 | 0.27 |
| A32 | 0.27 | B48 | 1.69 | | |
| A203 | 0.27 | B61 | 1.69 | | |
| A2403 | 0.27 | B7 | 1.51 | | |
| A74 | 0.18 | B44 | 1.42 | | |
| A34 | 0.09 | B18 | 0.98 | | |
| | | B76 | 0.71 | | |
| | | B52 | 0.71 | | |
| | | B56 | 0.71 | | |
| | | B71 | 0.53 | | |
| | | B45 | 0.45 | | |
| | | B8 | 0.44 | | |
| | | B37 | 0.36 | | |
| | | B72 | 0.18 | | |
| | | B50 | 0.09 | | |
| | | B57 | 0.09 | | |
| | | B81 | 0.09 | | |

A11.2 is the serological-defined split antigen of A11, encoded by A*11:02.

A203 is the serological-defined split antigen of A2, encoded by A*02:03.

A2403 is the serological-defined split antigen of A24, encoded by A*24:03, A*24:10, A*24:23 or A*24:33.

**Table 2.** Common HLA haplotype in Chinese deceased donors (Frequency > 0.01).

| A-B | Freq. (%) | B-DR | Freq. (%) | A-DR | Freq. (%) | A-B-DR | Freq. (%) |
|---|---|---|---|---|---|---|---|
| A2-B46 | 10.53 | B46-DR9 | 7.98 | A2-DR9 | 6.99 | A2-B46-DR9 | 4.93 |
| A11-B75 | 6.63 | B75-DR12 | 6.22 | A11-DR12 | 6.86 | A33-B58-DR17 | 4.41 |
| A11-B60 | 6.48 | B58-DR17 | 5.87 | A11-DR9 | 5.32 | A11-B75-DR12 | 3.62 |
| A33-B58 | 5.96 | B13-DR15 | 3.12 | A33-DR17 | 4.58 | A2-B38-DR16 | 2.26 |
| A2-B38 | 4.17 | B60-DR12 | 2.99 | A2-DR15 | 4.37 | A11-B60-DR9 | 1.74 |
| A11-B13 | 3.76 | B60-DR4 | 2.97 | A11-DR4 | 4.00 | A11-B60-DR8 | 1.64 |
| A24-B60 | 3.47 | B60-DR9 | 2.78 | A2-DR4 | 3.93 | A11-B75-DR15 | 1.59 |
| A2-B60 | 3.31 | B60-DR8 | 2.74 | A2-DR12 | 3.73 | A30-B13-DR7 | 1.48 |
| A11-B46 | 2.31 | B38-DR16 | 2.45 | A24-DR12 | 3.41 | A11-B60-DR12 | 1.29 |
| A2-B13 | 2.27 | B46-DR14 | 2.15 | A24-DR15 | 3.41 | A11-B46-DR9 | 1.29 |
| A24-B13 | 2.16 | B62-DR4 | 2.15 | A11-DR15 | 3.29 | A2-B46-DR14 | 1.29 |
| A11-B51 | 2.03 | B75-DR15 | 2.07 | A24-DR9 | 2.62 | A24-B13-DR15 | 1.29 |
| A11-B62 | 1.84 | B13-DR7 | 1.94 | A2-DR16 | 2.58 | A33-B44-DR7 | 1.16 |
| A30-B13 | 1.79 | B13-DR12 | 1.91 | A2-DR14 | 2.49 | A2-B46-DR4 | 1.14 |
| A2-B51 | 1.58 | B46-DR4 | 1.76 | A24-DR4 | 2.48 | A11-B60-DR4 | 1.10 |
| A24-B75 | 1.34 | B51-DR9 | 1.50 | A11-DR8 | 2.41 | A24-B75-DR12 | 1.08 |
| A2-B62 | 1.34 | B60-DR15 | 1.49 | A2-DR8 | 2.40 | | |
| A33-B44 | 1.24 | B54-DR4 | 1.38 | A11-DR11 | 2.02 | | |
| A2-B75 | 1.24 | B44-DR7 | 1.33 | A2-DR11 | 1.86 | | |
| A24-B54 | 1.14 | B46-DR8 | 1.33 | A11-DR14 | 1.84 | | |
| A11-B58 | 1.13 | B58-DR13 | 1.18 | A11-DR16 | 1.82 | | |
| A24-B35 | 1.12 | B13-DR16 | 1.14 | A11.2-DR12 | 1.61 | | |
| A33-B46 | 1.10 | B46-DR12 | 1.08 | A30-DR7 | 1.51 | | |
| A11.2-B27 | 1.07 | B7-DR10 | 1.07 | A33-DR7 | 1.33 | | |
| A24-B46 | 1.03 | B27-DR12 | 1.03 | A24-DR14 | 1.24 | | |
| A11-B54 | 1.02 | | | A11-DR13 | 1.07 | | |

A11.2 is the serological-defined split antigen of A11, encoded by A*11:02.

A203 is the serological-defined split antigen of A2, encoded by A*02:03.

A2403 is the serological-defined split antigen of A24, encoded by A*24:03, A*24:10, A*24:23 or A*24:33.

against cPRA from Eurotransplant respectively, which indicated a poor agreement in both situation (Fig. 3). Standard deviation of difference between cPRA (freq) and cPRA (OPTN) was 16.2 cPRA points, with the limit of agreement between +37.5 to −26.2 points. Standard deviation of difference between cPRA (filter) and cPRA (Euro) was 15.9 cPRA points, with the limit of agreement between +37.0 to −25.2 points (Fig. 4). This indicated that cPRA generated from foreign database cannot reflect the actual chance of encountering incompatible local donors, and as a result, foreign cPRA calculators cannot be employed for Hong Kong patients. Calculator based on local HLA typing data is thus imperative for transplant patient management.

## Discussion

The Organ Registry and Transplant System (ORTS) was first developed in 1995 by the Central Renal Committee of the Hospital Authority of Hong Kong. It contains centralized Renal Registry database, which provides HLA-matching function and patient scoring system for the purpose of deceased donor kidney allocation.

Hong Kong is a city with a population of 7.3 million [17]. The population consisted of 93.6% Chinese citizens [18]. Among all the renal donors registered under the ORTS database, over 95% of them are Chinese origin. On the other hand, the donor pool used by UNOS included only 333 (2.3%) Asian donors with unknown countries of origin. The dataset employed by Eurotransplant virtual PRA calculator included mostly renal donors from Austria, Belgium, Croatia, Germany, Hungary, Luxembourg, Netherlands and Slovenia. Donors from non-Eurotransplant service area only accounted for around 0.2% of total donors used [19]. Unfortunately, the factor race is not registered in Eurotransplant, and therefore, information about Asian or Chinese descent in the composition cannot be obtained [20]. The HLA allele frequencies in the UNOS and Eurotransplant donor pool were thus expected to be

significantly different from our local donor pool. The limit of agreement between local cPRA values and cPRA from foreign calculators was much wider than that between cPRA (filter) and cPRA (freq). Significant difference in cPRA score could be observed in patients with a cPRA between 10% and 80%. The result demonstrated that using the foreign calculators, cPRA values of a patient could be over- or underestimated by more than 20 points. Such discrepancy of cPRA will lead to misinterpretation of the sensitization level of a patient and directly affect candidate's priority on the transplant waiting list. This highlighted the necessity to use local donor data for accurate cPRA calculation.

Agreement analysis regarding our two cPRA calculation methods indicated that both the allele frequency-based and the donor filtering method produced highly correlated cPRA values. This implied that the two methods were interchangeable on cPRA estimation. However, cPRA estimation by donor filtering still shows several advantages over the allele frequency-based algorithm. Firstly cPRA (filter) is the simplest and most straight forward calculation method of cPRA. The calculation represents the definition of cPRA. It involves the collection of donor HLA phenotypes, followed by calculating the percentage of donors that is expected to be incompatible for a specific patient.

Secondly, calculation of cPRA (filter) required relatively low technical expertise. One can easily calculate cPRA for a patient without the need of any additional statistical analysis software or knowledge in programming language. Jang JY *et al.* had demonstrated the possibility of developing a cPRA calculator with only Microsoft Excel and HLA phenotypes information of 1 662 Korean donors [21]. In more automated system such as the ORTS system in Hong Kong, cPRA value of all on-list patients can be updated over a scheduled time interval.

Value of cPRA (freq) is estimated from re-constructed potential haplotypes based on assumption of Hardy–Weinberg equilibrium. The actual phenotype frequency within a population is often deviated from this expected frequency. From a recent study, such deviation from Hardy–Weinberg equilibrium has been observed in Hong Kong population [13]. Another potential source of error for cPRA (freq) comes from ethnic frequencies. In theory when the number of interracial marriage increase over time, the estimated haplotype frequencies calculated from self-reported ethnicity ratio may become inaccurate. Interracial marriage is not common in Hong Kong. The percentage of mixed ethnic minorities in Hong Kong population was 0.29% in year 2001 and 0.41% in year 2011, not a problem in Hong Kong [22]. As the historical donor filtering approach depends on actual HLA phenotype rather than assumption of Hardy–Weinberg

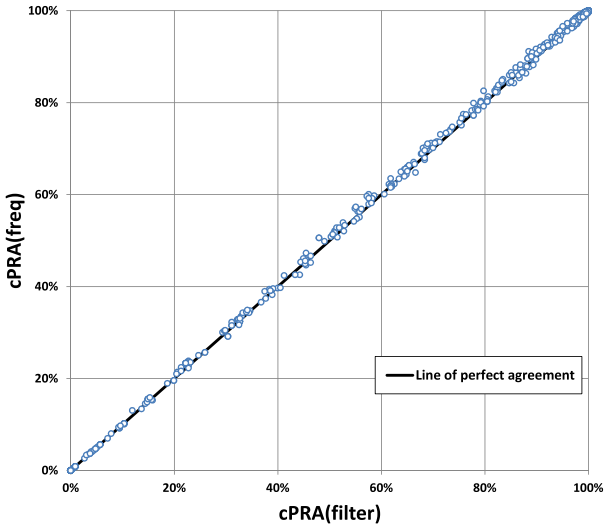


**Figure 1** Correlation plot of cPRA (filter) against cPRA (freq) values. Lin's correlation coefficient was equal to 1.000.

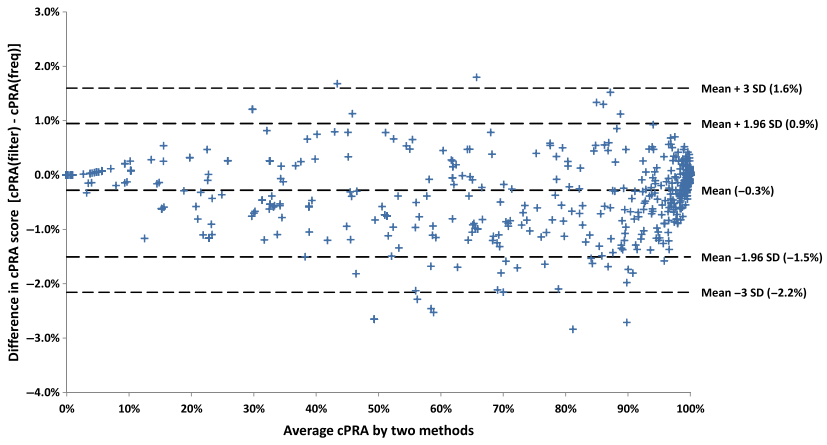


**Figure 2** Bland–Altman plot of cPRA (filter) against cPRA (freq) values. Standard deviation of difference between the two scores was 0.6%. Limit of agreement was between +0.9% to −1.5%.

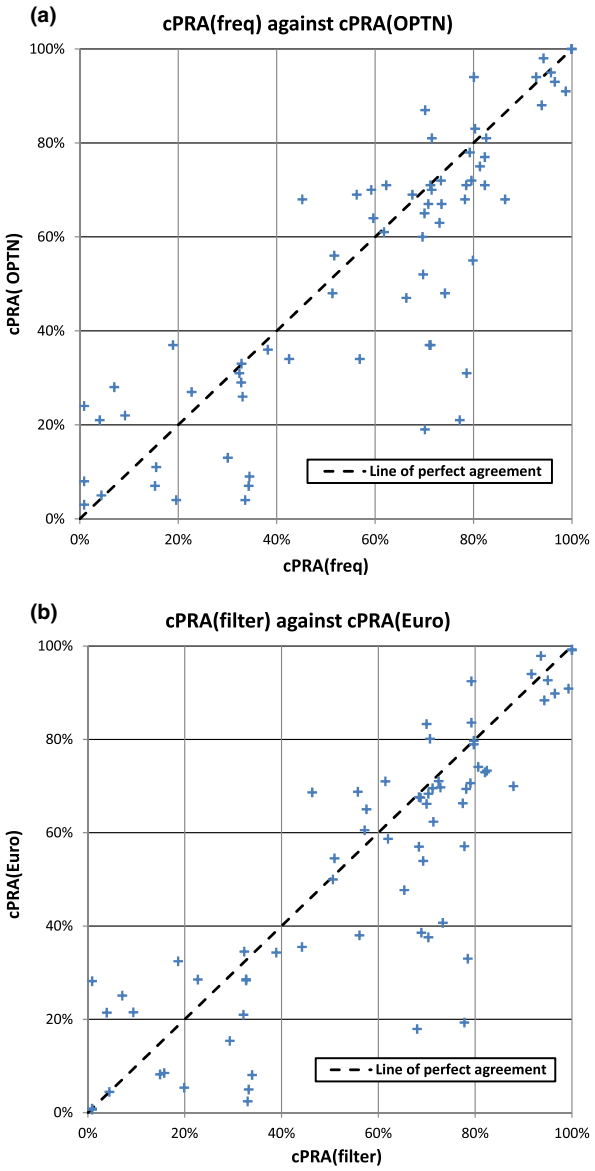


**Figure 3** Correlation plot of cPRA (freq) against cPRA (OPTN) (a) and cPRA (filter) against cPRA (Euro) (b). Lin's coefficients were 0.824 and 0.829 for cPRA (freq) against cPRA from OPTN and cPRA (filter) against cPRA from Eurotransplant, respectively.

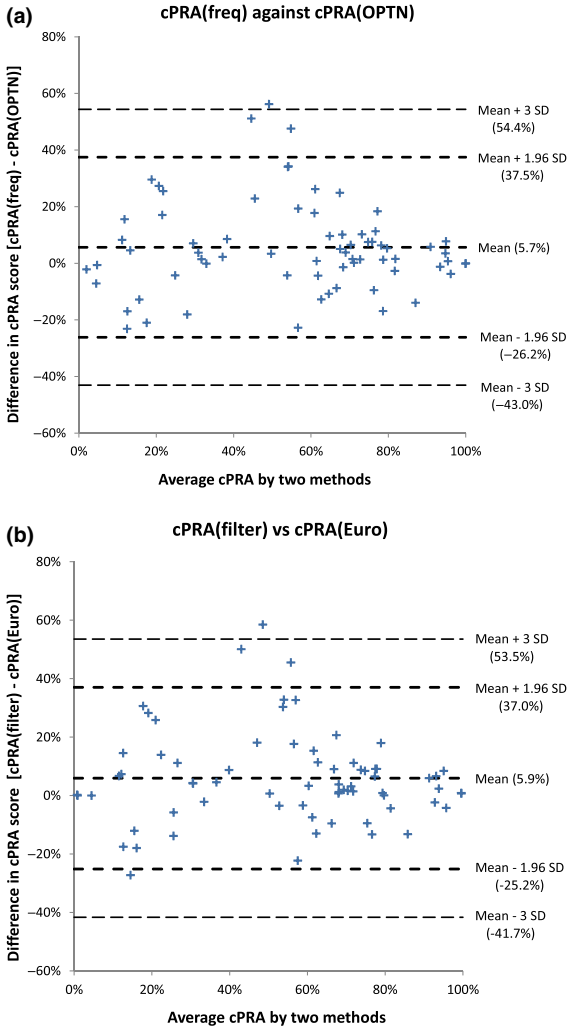


**Figure 4** Bland–Altman plot of cPRA (freq) against cPRA (OPTN) (a) (SD of difference = 16.2%, Limit of agreement = +37.5% to −26.2%) and cPRA (filter) against cPRA (Euro) (b) (SD of difference = 15.9%, Limit of agreement = +37.0% to −25.2%).

equilibrium nor ethnic frequencies, cPRA (filter) is free from these potential errors.

Another major advantage of cPRA (filter) method is the flexibility to expand donor sample size and locus under consideration in the future. New donor HLA information can be added to the donor dataset any time before cPRA calculation. For cPRA (freq), the allele and ethnic frequencies need to undergo major update periodically to ensure the cPRA being a faithful representation of current donor population. This may post both manpower and financial pressure on centres with a limited budget or technical expertise.

A potential limitation of cPRA (filter) is that some of the rarer HLA phenotypes may be omitted from the calculation when the donor sample size is not sufficiently large. In such case, cPRA (freq) can be superior over the historical donor filtering method as in theory, we can deduce expected HLA phenotype based on assumption of Hardy–Weinberg Equilibrium in the population. This could be the rationale that UNOS chooses cPRA (freq) over cPRA (filter). However, in practice, there is no evidence that knowledge of these rare HLA alleles contributes significantly to the final cPRA value.

This study has the following caveats. First, it involved a relatively small sample size of donor pool in Hong Kong. However, the studied sample could still represent Hong Kong Chinese population as the gene frequencies

obtained from the 563 deceased donors are quite comparable with those of the HKBMDR voluntary donor pool reported earlier from a larger database of 7 595 subjects [13]. Additionally, the sample size was also similar to the previous studies conducted in Korea and China [21,23].

Second, only HLA-A, B and DRB1 loci were included for the cPRA calculation in this study as these are the antigens for matching allocation and filtering and not all donors had the DQ typing at the time of work up. However, it is worth to note that Korea and China currently are also adopting a similar approach, that is only A, B and DRB1 are included for cPRA calculation [21,23].

Value of cPRA can be applied in organ allocation programme for highly sensitized patients for renal and other organs such as heart or lung recipients. Extra allocation points can be granted to the highly sensitized patients to counter-balance their current unfavourable situation. From our cPRA data analysis, it was found that approximately 17% of renal transplant candidates are highly sensitized with a cPRA higher than or equal to 80 in Hong Kong. However, highly sensitized patients only account for a small proportion of current organ allocation. In 2015, there were a total of 65 patients getting deceased donor kidney transplantation in Hong Kong, among which only five patients (7.7%) were highly sensitized, with three of them were allocated with a kidney only because of the zero mismatch priority.

We also noticed that among the 1 894 renal patients reviewed in the current study, anti-DQ antibodies were found in 14.63% of them. Additionally based on one of our preliminary studies, anti-DP antibodies could be found in 3.16% ($n$ = 285) of renal patients before transplantation. Information on anti-DQ and anti-DP antibodies can be incorporated into cPRA estimation when knowledge on DQ and DP phenotypes on the donors becomes more comprehensive.

In conclusion, it is essential to use data from local donor pool during calculation in order to provide an accurate estimation on patient's cPRA. Historical donor filtering method can be easily implemented with ease in Hong Kong because the corresponding database and HLA-matching function are ready in the current ORTS system. No extra infrastructure cost is required to calculate cPRA for all on-list renal candidates. cPRA (filter) incorporates both existing and new donors in the calculation instead of allele and haplotype frequencies captured at one specific time point. Such a real-time donor pool can reflect the population allele frequencies and also permits efficient periodic update of cPRA scores.

## Authorship

JSYK: designed study. JSYK, YPC, MWKW, LWMT and NKMY: collected data. JSYK, YPC, MG and NKMY: analysed data. JSYK, YPC, PI: wrote and edited the paper. JSYK, WY, PI, PKTL, CBL, KFC and JCKL: provided resources.

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## Conflicts of interest

The authors have declared no conflicts of interest.

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