Fuzzy Adaptive Particle Swarm Optimization for Confronting Two-Pair Primer Design

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***Abstract*—PCR-CTPP (Polymerase chain reaction with confronting two-pair primers) is a simple SNP genotyping method with time- and cost-effective. Many SNPs have been successfully genotyped by PCR-CTPP. However, the design of feasible PCR-CTPP primer sets is still challenging. In this study, we propose a FAPSO (fuzzy adaptive particle swarm optimization)-based method to design feasible PCR-CTPP primer sets. Two hundred and eighty-eight SNPs which exclude the deletion/insertion polymorphism (DIP) and multi-nucleotide polymorphism (MNP) in SLC6A4 gene were tested *in silicon* by the proposed method. The results shown the proposed method provides more feasible PCR-CTPP primers than a native PSO (particle swarm optimization)-based method. In conclusion, the FAPSO-based method is useful to assist the biologists and researchers to design feasible CTTP primer sets.**

***Index Terms*—PCR-CTPP, FAPSO, PSO, SNP**

I. Introduction

SNPs (Single Nucleotide Polymorphisms) are usually used in association studies of diseases and cancers due to its great quantity. Many high-throughput platforms of SNP genotyping such as real-time PCR (polymerase chain reaction) [1] and SNP array [2] have been introduced to validate SNPs or novel mutations by some laboratories, but the PCR-restriction fragment length polymorphism (RFLP) genotyping [3-5] is still favorite due to its inexpensive for the small-scale genotyping. However, the PCR-RFLP is usually long digestion time in 2-3 hours for restriction enzymes [6, 7].

Recently, a restriction enzyme-free SNP genotyping technique [8, 9] was developed named PCR with confronting two-pair primers (PCR-CTPP). PCR-CTPP genotyped many SNPs successfully, such as interleukin-1B (IL-1B) C-31T, interleukin-2 (IL-2) -330G, beta2-adrenergic receptor (beta2-AR) Gln27Glu, aldehyde dehydrogenase 2 (ALDH2) [10], pylori-induced gastric atrophy [11], severe coronary artery disease [12], and esophageal cancer risk [13]. PCR-CTPP is suitable and reliable for most cases of SNPs. However, the lack of an effective computation method for designing feasible PCR-CTPP primer sets.

In the past, we have introduced a genetic algorithm to design available PCR-CTPP primer sets [14, 15]. However, the computational results still need to be improved, especially the factor of T_m (melting temperature) difference. PCR-CTPP primers are only tolerant of a small difference in melting temperature between the four primers [16]. The fuzzy adaptive particle swarm optimization (FAPSO) [17] is therefore proposed to apply to the problem.

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II. Method

Particle swarm optimization (PSO) developed by Kennedy and Eberhart is a population-based stochastic optimization technique [17]. PSO simulates the social behavior of organisms, such as birds in a flock or fish in a school. In a PSO, each single candidate solution is described as "an individual bird of the flock", that is, a particle in the search space. Each particle finds the better solution using its own memory as well as knowledge gained by the swarm. Each particle has a fitness value evaluated by an optimized fitness function and a velocity directs the movement of the particles. During movement, each particle adjusts its position in terms of its own experience and the experience of a neighbouring particle, thus making the best position encounter. PSO has been successfully applied in many fields, such as function optimization, artificial neural network training, and fuzzy system control. A comprehensive survey of PSO algorithms and their applications can be found in Kennedy *et al.* [18]. However, a fixed inertia weight or linearly decreasing inertia weight used in PSO simplifies the complex non-linear search process [19, 20]. In order to balance the global and local search ability of PSO, a fuzzy system adapts the inertia weight of PSO dynamically had been implemented [21]. In this paper, we introduced the fuzzy adaptive PSO (FAPSO) for the design of PCR-CTPP primer sets. The problem definition and the proposed method of PCR-CTPP primer design is described below in detail.

A. Problem formulation

Let T_D be the DNA template sequence composed of nucleotide codes with an identified SNP. T_D is defined as:

$$T_D = \{B_i \mid i \text{ is the index of DNA sequence}, \\ 1 \le i \le \iota, \exists! B_i \in \text{IUPAC code of SNP}\} \quad (1)$$

where B_i is the regular nucleotide code ('A', 'T', 'C', or 'G') mixed with a single IUPAC code of SNP ('M', 'R', 'W', 'S', 'Y', 'K', 'V', 'H', 'D', 'B' or 'N') ($\exists!$ is the symbol for existence and uniqueness).

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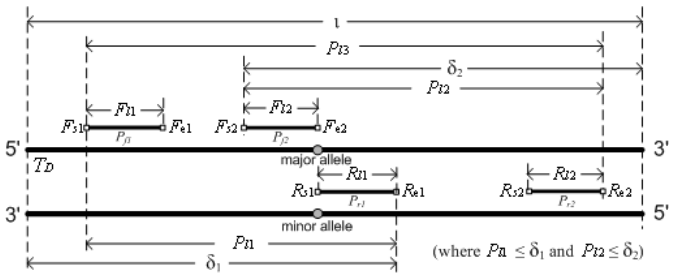

Fig. 1. Parameters of the DNA template and the PCR-CTPP primer set. Symbols indicate: *F*: Forward primer; *R*: Reverse primer; *s*: Start nucleotide position; *e*: End nucleotide position; *P*: Length of PCR product using a primer set (F/R); *l*: Length of primer or product; ι : Length of DNA template; δ_1: Length from the R_{s1} end to downstream of DNA template; δ_2: Length from F_{s2} to the downstream end of DNA template.

The PCR-CTPP primer design is to find two available short sequences in T_D based on a defined SNP site as illustrated (Fig. 1). The forward primer 1 (P_{f1}) is a short sense sequence in the upstream (5' end) of T_D far from a defined SNP site; the reverse primer 1 (P_{r1}) is a short antisense sequence which contains a nucleotide (the minor allele in the defined SNP site) located at its 3' end; the forward primer 2 (P_{f2}) is a short sense sequence which contains a nucleotide (the major allele in the defined SNP site) located at its 3' end, and the reverse primer 2 (P_{r2}) is the antisense sequence in the downstream of T_D far from a defined SNP site. These four primers are defined as follows:

$$P_{f1} = \{B_i \mid i \text{ is the index of } T_D,\ F_{s1} \le i \le F_{e1}\} \quad (2)$$

$$P_{r1} = \{\overline{B_i} \mid i \text{ is the index of } T_D, R_{s1} \le i \le R_{e1}\} \quad (3)$$

$$P_{f2} = \{B_i \mid i \text{ is the index of } T_D, F_{s2} \le i \le F_{e2}\} \quad (4)$$

$$P_{r2} = \{\overline{B_i} \mid i \text{ is the index of } T_D, R_{s2} \le i \le R_{e2}\} \quad (5)$$

where both P_{f1}/P_{r1} and P_{f2}/P_{r2} are two sets of primer pairs. F_{s1} *vs.* F_{e1} and R_{s1} *vs.* R_{e1} indicate the start index *vs.* the end index of P_{f1} and P_{r1} in T_D, respectively. F_{s2} *vs.* F_{e2} and R_{s2} *vs.* R_{e2} indicate the start index *vs.* the end index of P_{f2} and P_{r2} in T_D, respectively. $\overline{B_i}$ is the complementary nucleotide of B_i, which is described in formula (1).

The SNP site defined at the 3' end positions of P_{f2} and P_{r1} indicated by the symbols F_{e2} and R_{s1} in Fig. 1, respectively. A vector (v) with F_{l1}, P_{l1}, R_{l1}, F_{l2}, P_{l2} and R_{l2} is used to represent a PCR-CTPP primer set. This vector is defined as follows:

$$P_v = (F_{l1}, P_{l1}, R_{l1}, F_{l2}, P_{l2}, R_{l2}) \quad (6)$$

F_{l1}, P_{l1}, R_{l1}, F_{l2}, P_{l2} and R_{l2} represent the number of nucleotides of the forward primer 1, product length between P_{f1} and P_{r1}, reverse primer 1, forward primer 2, product length between P_{f2} and P_{r2} and reverse primer 2, respectively. Consequently, the forward and the reverse primers can be calculated from P_v. P_v is used to perform evolutionary computations as described in the following sections.

B. PCR-CTPP design method

The flowchart of the proposed method is shown as Fig. 2.

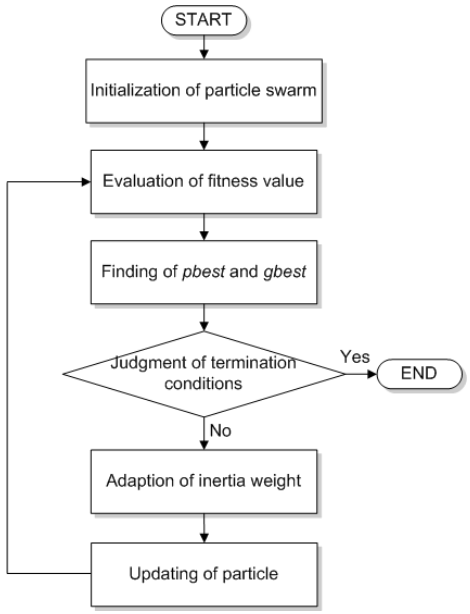

Fig. 2. Flowchart of the FAPSO-based CTPP primer design. At first, the velocities and positions of a specific number of particles are generated randomly. And then all fitness values of all particles are calculated by the fitness function. A judgment on termination conditions is carried out, and if the termination conditions are reached then the algorithm will be finished, else the algorithm proceeds with the following processes. Find out the *pbest* from each particle and find out *gbest* from all particles and then update velocities and positions for all particles according to the updating formulas. Repeat related steps shown as the figure until the best solution is found or the preset generation number is reached.

The proposed method consists of six processes: (1) initialization of particle swarm, (2) evaluation of fitness value, (3) finding of *pbest* and *gbest*, (4) judgment of termination conditions, (5) adaption of inertia weight, and (6) updating of particle, are described below.

(1) Initialization of particle swarm

To start the algorithm, particles $P_v = (F_{l1}, P_{l1}, R_{l1}, F_{l2}, P_{l2}, R_{l2})$ of particular number are randomly generated for an initial population without duplicates. F_{l1}, R_{l1}, F_{l2} and R_{l2} are randomly generated between the minimum and the maximum length of the primer length constraint. The minimum and maximum primer length constraints are set to between 16 bp and 28 bp, respectively. The PCR product lengths, P_{l1} and P_{l2} are randomly generated between 100 bp and δ_1, and between 100 bp and δ_2, respectively. (δ_1 and δ_2 are maximum tolerant PCR product length of P_{l1} and P_{l2} shown in Fig.1)

(2) *Evaluation of fitness value*

The fitness value in the fitness function is used to individually ascertain that a particle (i.e., solution) is either good or bad. We use formula (7) [14] to evaluate the fitness values of all particles in the population for related operations later.

$$\begin{aligned} Fitness(P_v) = {} & 3 \times (Len_{diff}(P_v) + GC_{proportion}(P_v) + GC_{clamp}(P_v)) \\ & + 10 \times (dimer(P_v) + hairpin(P_v) + specificity(P_v)) \\ & + 50 \times (Tm(P_v) + Tm_{diff}(P_v)) + 100 * Avg\_Tm_{diff}(P_v) \\ & + 60 * PCRlen_{ratio}(P_v) \end{aligned} \quad (7)$$

The weights (3, 10, 50, 60 and 100) of the fitness function are applied to estimate the importance of the primer

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constraints. These weights are set by the experiential conditions for PCR-CTPP. They also accept adjustment based on the experimental requirements. The respective function is described as follows:

Primer length

A feasible primer length for a PCR experiment is set between 16 nt and 28 nt. Since the random values of F_{l1}, R_{l1}, F_{l2} and R_{l2} have been limited by the constraint condition, the primer length estimation does not be considered to join to the fitness function. A length difference (Len_{diff}) less than or equal to 3 bp between the F_{l1}/R_{l1}, F_{l2}/R_{l2}, and F_{l1}/R_{l2} primer sets is considered optimal. The $Len_{diff}(P_v)$ function is used to judge the constraint.

GC content

In general primer design, the typical GC proportion constraint is set between 40% and 60%. However, the designed PCR-CTPP primers contain the target SNP limiting the range of the GC proportion. To relax this constraint, the constraint of GC proportion in a primer is adjusted to between 20% and 80%. The $GC_{proportion}(P_v)$ function is proposed to lead the GC proportion of PCR-CTPP primers corresponding this constraint.

GC Clamp

To meet the presence of 'G' or 'C' at the 3' terminal of a primer to ensure a tight localized hybridization bond, the $GC_{clamp}(P_v)$ function is proposed to meet the criterion.

Melting temperature

The melting temperature (T_m) for each PCR-CTPP primer must be considered carefully for PCR experiment. The T_m calculation formula for a primer is described as follows:

$$Tm_{BM}(P) = 81.5 + 16.6 * (\log_{10}[Na^+]) + 0.41 * (GC\%) - 675 / |P| \quad (8)$$

where P represents a primer and $|P|$ represents the length of primer P; Na^+ is the molar salt concentration. The suffix BM represents the formula which was proposed by Bolton and McCarthy [22].

The $Tm(P_v)$ function is proposed to confine a PCR-CTPP primer set ranging from 45°C to 62°C. Similar T_m between a primer pair is important when a PCR experiment is performed in a tube. The $Tm_{diff}(P_v)$ function is proposed to guide the difference of the melting temperatures to less than or equal to 1°C. In order to balance the T_m values among a PCR-CTPP primers, the $Avg\_Tm_{diff}(P_v)$ function is proposed to calculate the average T_m difference.

Dimer and hairpin

Primer dimers (annealing of two primers), such as cross-dimers (a forward primer and a reverse primer) and self-dimers (two forward primers or two reverse primers) must also be avoided. To check for the occurrence of primer dimers, the function $dimer(P_v)$ is proposed. In addition, the hairpin check is also implemented to avoid annealing to itself. To check for the presence of a hairpin structure in PCR-CTPP primers, the $hairpin(P_v)$ function is proposed.

Specificity

The function $specificity(P_v)$ is proposed to check for each PCR-CTPP primer if reappearance in the template DNA sequence to ensure its specificity. The PCR experiment may fail when a designed primer is not sequence-specific (i.e., it appears more than once in the DNA template).

PCR product length

The $PCRlen_{ratio}(P_v)$ function is proposed to calculate the appropriate PCR product length. Three ratios, i.e., ratio1, ratio2 and ratio3, are introduced to the function of $PCRlen_{ratio}(P_v)$ representing P_{l1}, P_{l2} and P_{l3}, respectively. The minimum PCR product length needs to be greater than 100 bp.

(3) Finding of pbest and gbest

One of the characteristics of PSO is that each particle has a memory of its own best experience. Each particle finds its personal best position and velocity (called *pbest*) and the global best position and velocity (called *gbest*) when moving. If the fitness of a particle P_v is better than the fitness of *pbest* in the previous generation, *pbest* will be updated to P_v in the current generation. If the fitness of a particle P_v is better than *gbest* in the previous generation and is the best one in the current generation, *gbest* will be updated to P_v. Each particle adjusts its direction based on *pbest* and *gbest* in the next generation.

(4) Judgment of termination conditions

The algorithm is terminated when *gbest* has achieved the best position, i.e., its fitness value is 0, or when a maximum number of generations have been reached.

(5) Adaption of inertia weight

In PSO, the inertia weight is used to balance the global and local search ability. A large inertia weight facilitates a global search while a small inertia weight facilitates a local search [21]. In order to adjust the search ability, the inertia weight is changed dynamically using a fuzzy system. In this paper, we used the fuzzy system proposed by Shi and Eberhart [21]. According to Shi and Eberhart, two variables are used as inputs for the fuzzy system. The first variable is the current best performance evaluation (*CBPE*) and the other is the current inertia weight. The *CBPE* is converted into a normalized format so that it can be applied to apply to the specific primer design problem. The normalized *CBPE* (*NCBPE*) is described by:

$$NCBPE = \frac{CBPE - CBPE_{\min}}{CBPE_{\max} - CBPE_{\min}} \quad (9)$$

where $CBPE_{\min}$ represents the real minimum and $CBPE_{\max}$ represents the real maximum.

(6) Updating of particle

In each generation, the particles will change their position and velocity. Equations (9) and (10) give the updating formulas for each particle.

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$$v_i^{next} = w \times v_i^{current} + c_1 \times r_1 \times (s_i^p - s_i^{current}) + c_2 \times r_2 \times (s^g - s_i^{current}) \quad (9)$$

$$s_i^{next} = s_i^{current} + v_i^{next} \quad (10)$$

In equations (9) and (10), v_i^{next} is the updated velocity of the ith particle; $v_i^{current}$ is the current velocity of the ith particle; c_1 and c_2 are the acceleration constants; w is the inertia weight; r_1 and r_2 are a number which is randomly generated within 0~1; s_i^p is the personal best position of the ith particle; s^g is the global best position of the particles; $s_i^{current}$ is the current position of the ith particle; s_i^{next} is the updated position of the ith particle. In order to prevent a particle from overshooting the limits of F_s, F_l, P_l and R_l during the update process, we randomly reset the particle according to the primer constraints.

III. Results and Discussion

A. Template sequence

A point mutation was identified and shown to be associated with psychosis [23], and bipolar [24] patients in the SLC6A4 gene. Here, two hundred and eighty-eight SNPs were used to estimate the efficiency of the proposed method exclude the deletion/insertion polymorphism (DIP) and multi-nucleotide polymorphism (MNP) in SLC6A4 gene. All SNPs were retrieved with 500 bp flanking length (at both sides of the target SNP) from SNP-Flankplus (http://bio.kuas.edu.tw/snp-flankplus/) [25] as available template sequences.

B. Parameter settings

Four main parameters are set for both the FAPSO- and PSO-based methods, i.e., the number of iterations (generations), the number of particles, the inertia weight w, and the acceleration constants c_1 and c_2. Their values were set to 50, 10, 0.8, 2 and 2, respectively.

C. The results for the PSO- and FAPSO- based PCR-CTPP primer design methods

We design the primer lengths are all randomly generated between 16 nt and 28 nt for the 288 SNPs. The results of the entire designed PCR-CTPP primers are shown in Table 1. For PSO, 82.87% designed primers satisfy the length difference criterion. Most of the primer length differences were between 0 and 5 bp (data not shown). For GC%, 96.61% primers satisfy the criterion; only 15 primers were less than 20%, 28 primers were more than 80% (data not shown). There are 57.73% primers satisfy the GC clamp criterion. Most of the designed primers also satisfy T_m (95.40%); more than half of the primer pairs are satisfied with the T_m difference criteria (58.80%). The criterion for the product length is satisfied in 57.06%. For the criteria for primer dimer and specificity, only few primers are problematic (3.85% and 1.91%, respectively). For hairpin, 13.37% primers are not satisfactory.

For FAPSO, 86.0% designed primers satisfy the length difference criterion. Most of the primer length differences were between 0 and 5 bp (data not shown). For GC%, 97.31% primers satisfy the criterion; only 12 primers were less than 20%, 23 primers were more than 80% (data not shown). There are 60.94% primers satisfy the GC clamp criterion. Most of the designed primers also satisfy the T_m (96.53%) and the T_m difference criteria (73.61%). The criterion for product length was satisfied in 57.06% of the designed primer pairs. For the criteria for primer dimer and specificity, only few primers were problematic (3.19% and 2.43%, respectively). For hairpin, 10.94% primers are not satisfactory.

TABLE I
Results of PCR-CTPP primer design

Constraints	PSO satisfactory rate (%)	FAPSO satisfactory rate (%)	Rate of improvement (%)
primer length difference	82.87	86.00	3.13
GC%	96.61	97.31	0.7
GC clamp	57.73	60.94	3.21
T_m	95.40	96.53	1.13
T_m difference	58.80	73.61	14.81
product length	57.06	57.06	0
dimer	96.15	96.81	0.66
hairpin	86.63	89.06	2.43
specificity	98.09	97.57	-0.52

The results of the designed PCR-CTPP primers showing the satisfactory rate (%) based on PSO-based and FAPSO-based methods for SNPs of the SLC6A4 gene.

D. Comparison of the results of FAPSO-based with PSO-based PCR-CTPP method

From Table 1, all satisfactory rates of the primer constraints using FAPSO-based method is better than PSO-based method eliminating the specificity criterion. The satisfied primer length difference of FAPSO-based method is higher 3.13% than PSO-based method. The satisfied GC% of FAPSO-based method is higher 0.7% than PSO-based method. The satisfied GC clamp of FAPSO-based method is higher 3.21% than PSO-based method. The satisfied T_m and T_m difference of FAPSO-based method is higher 1.13% and 14.81% than PSO-based method, respectively. The satisfied product length of FAPSO-based method is equal to PSO-based method. The satisfied dimer and hairpin of FAPSO-based method are higher 0.66% and 2.43% than PSO-based method, respectively. However, the satisfied specificity of FAPSO-based method is lower 0.52% than PSO-based method.

In PCR-CTPP, the T_m difference is the most important factor that affects experiments. From the above results, we observe the satisfactory rate of T_m difference is greatly improved by FAPSO-based method. Simultaneously, the other criteria are also improved eliminating the specificity. Although satisfactory rate of the specificity is lightly decreased, it still arrives 97.57%. In summary, the FAPSO-based PCR-CTPP primer design method is useful to facilitate SNPs genotyping.

IV. Conclusions

The FAPSO-based PCR-CTPP primer design method provides better melting temperature as well as better common

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primer constraints estimation than PSO-based method. Feasible PCR-CTTP primer sets are always obtained to assist SNP genotyping experiments. The experimental flexibility of the FAPSO-based designed PCR-CTPP primers in 288 polymorphisms has been confirmed by *in silicon* simulations. In the future, PCR-CTPP may replace PCR-RFLP due to its lower costs and shorter genotyping times [16]. To date, we have developed the PCR-CTPP primer design methods to facilitate PCR-CTPP for validating SNPs or novel mutations. In conclusion, the *in silicon* simulation results indicate that FAPSO applied to PCR-CTPP primer design sets outperform a native PSO method. FAPSO-based method is a useful tool to design feasible PCR-CTPP primers since its conformation of the most of the PCR-CTPP constraints and with a closer melting temperature among designed primers.

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