Review Article

A review of the application of Next Generation Sequencing (NGS) in wild animal research

ABSTRACT

In era of sequencing revolution, scientists seek for knowledge about the ever-expanding field of technology, Next Generation Sequence (NGS) to be applied in their research due to its high reliability and rate of discovery. What is NGS? To obtain a detailed understanding about NGS, it is required to look back the history of sequencing and how the NGS stepped into life science. This review paper gives an overview about the wild animals' research or projects that have been studied under the umbrella of NGS, by using application such as whole genome sequencing and metagenomics.

Keywords: Next-generation sequencing (NGS); wild animals; whole genome sequence; metagenomics

INTRODUCTION

In 1953, the double helix structure of DNA or deoxyribonucleic acid was discovered [1]. Later, the first DNA sequencing was perceived after fifteen years elapse in 1968. In line with the development of chemical method [2], modern DNA sequencing began in 1977 and in the same year the first DNA sequence (phage ϕX174) was completed by Sanger and Coulson [3] which, demonstrated that sequences were capable to give profound insights into genetic organization. Sanger sequencing was a tool for deciphering complete genes and also entire genomes [4] until the Human Genome Project drafted in year 2001. Although, the first complete cellular genome sequences from bacteria appeared in 1995 [5,6,7], the drastic impact on Next Generation Sequence (NGS) began only after the completion of Human Genome Project in 2003.

NEXT GENERATION SEQUENCING

In era of sequencing revolution, NGS is the most demanding technology that getting greater popularity day by day. NGS has conquered almost every single field in applied and life science. NGS technology utilizes distinct sequencing biochemistry approaches and it is mainly accentuated by its ability to simultaneously perform millions of sequencing reactions. Among the most widely used applications of NGS are the whole genome de novo

sequencing, whole genome re-sequencing and also exome, targeted, whole transcriptome, metagenome and epigenome sequencing [8,9].

Although NGS has a wide range of biological outcomes, the cost per sample analyses often limit the use of this technique. Fortunately, the recent development in high-throughput sequencing techniques (Table 1) has reduced the burden. For example, sequencing cost has massively reduced from $5,292.39/Mb in 2001 to $0.06/Mb by April 2013 [10]. It is estimated that the sequencing costs will further reduce with precipitous dropping per-base cost with advancing techniques.

Basically, NGS sequencing has expended from second-generation to the next two levels, third-generation (3G) and fourth-generation (4G) (Table 1). These techniques allowed the genomics to move from platforms that required Polymerase Chain Reaction (PCR) amplification of the template in prior of sequencing to without a prior amplification step as in third-generation sequencing techniques, and to a more refined level of the fourth-generation. Even though, NGS techniques are quite diverse but conceptually they are similar. The preparation of library includes random shearing of DNA followed by ligation with common adaptors (Table 1).

NGS IN WILD ANIMAL RESEARCH

Whole genome de novo sequencing, re-sequencing and targeted sequencing

Wild animals are defined as undomesticated and free-ranging terrestrial vertebrates include reptiles, amphibians, birds, and mammals [11]. Since past few decades, researches on wild animals have been ascended. Numerous researchers and non-governmental organization (NGO's) investing millions of money in wild animals' projects with aim to protect and conserve them from extinct. A repository of wild animals' genome sequences is crucial for phylogeography [12,13], demographic history [14], multilocus population genomics [15,16], adaptation studies [17,18], and conservation efforts [19,20].

After the completion of the Human Genome Project, the first nonhuman primate to have its genome sequenced was chimpanzee (*Pan troglodytes verus*) from West Africa. The Chimpanzee Sequencing and Analysis Consortium (2005) reportedly utilized cloned primary blood lymphocyte DNA to generate sequence reads that were assembled via de novo assembly approach and also by aligning sequence reads with the human genome [21]. Their assembly covered 94% of the chimpanzee genome, with a consensus length of 2.7 gigabases (Gb). A genome-wide comparison of the draft chimpanzee genome with the human genome revealed 13,454 pairs of unambiguous human and chimpanzee orthologue genes, of which 29% the encoded proteins were discovered to be identical. The team also compiled a list of human, mouse, rat, and chimpanzee genes with unambiguous gene orthology. Comparisons of West African and Central African chimpanzee sequence reads were also performed to locate polymorphic positions within and between these individuals, which in turn show that the heterozygosity rate of the Central African chimpanzees to be two times the heterozygosity rate of the West African chimpanzees [21].

The next hominid nonhuman primate to be sequenced was the Sumatran orang utan (*Pongo abelii*). It is listed by the International Union for Conservation of Nature (IUCN, 2018) as critically endangered, because its habitat increasingly destroyed and fragmented by human encroachment. A female orang utan specimen housed in Gladys Porter Zoo, Brownsville, Texas was sequenced using the whole-genome shotgun sequencing approach, with an average of 5.5-fold coverage across the 3.08 Gb consensus assembly [22]. The orang utan

genome assembly was facilitated by referring to human gene models as well as orang utan complementary DNA (cDNA) [22]. Genomic-wide nucleotide identity comparisons and single nucleotide polymorphism (SNP) between the Sumatran and Bornean orang utan revealed that the Sumatran orang utanwas more diverse than their Bornean counterpart, despite having a smaller population size [23]. Further SNP analyses of the orang utan autosomal and mitochondrial genome was carried out whereby they observed that the majority of the orang utan genome underwent negative selection throughout their evolutionary history [24].

Among the old world monkeys, special attention is paid to the rhesus macaque (*Macacamulatta*) and the cynomolgus macaque (*Macacafascicularis*) due to their indispensable use as nonhuman primate model organisms. Their similarities to humans with regards to their biology, behaviour, physiology, and genetics make them choice selections for biomedical research, as well as drug response studies [25,26]. Extensive whole genome sequencing endeavours have been undertaken to sequence not only their respective genomes, but genomes of macaques originating from various geographical locations [25,26,27,28]. Another old world monkey, the proboscis monkey (*Nasalislarvatus*), though not a model organism, has had its genome sequenced and assembled by the Proboscis Monkey Functional Genome Consortium from The Department of Zoology, Universiti Malaysia Sarawak in 2014. The team utilized a combination of the 454 Sequencing and Illumina Hiseq sequencing platforms with 290-fold genome coverage across 2.67 Gb. Assembly of the proboscis monkey genome (GenBank assembly accession: GCA_000772465.1) was performed via a reference-guided assembly with the rhesus macaque genome as a reference.

The Amur tiger (*Pantheratigrisaltaica*) genome was sequenced using the Hiseq 2000 platform with a 83.5-fold coverage across the de novo assembled 2.4 Gb scaffolds[29]. An alignment of the Amur tiger genome sequence with domestic cat genome sequence showed that the tiger genome was 95.6% similar to that of the domestic cat genome. Given the similarity, further comparisons between the tiger and domestic cat genomes revealed 103 orthologous gene families shared uniquely between the tiger and the domestic cat. Concurrently with the Amur tiger genome assembly, also sequenced the genomes of four other big cats, including the Bengal tiger (*Pantheratigristigris*), the African lion (*Pantheraleo*), the white African lion (*Pantheraleokrugeri*), and snow leopard (*Pantherauncia*)[29]. Comparative genomic analysis between the big cat and domestic cat, revealed a high genomic synteny as well as similar repeat compositions in the genomes, indicating stable genome conservation and similar genome architecture among the big cats and domestic cats. Both the Amur tiger and Bengal tiger are listed as endangered by the IUCN, while the Malayan tiger (*Pantheratigrisjacksoni*) as critically endangered [29]. Presently, the Malayan tiger faces imminent extinction due to habitat fragmentation and commercial poaching [30], and has yet to have its genome sequenced. With there being an estimated 500 Malayan tigers left in the wild, an assessment of the Malayan tiger genome and their population genomics is critical for conservation efforts of wild and captive Malayan tigers [31].

Part of the Genome 10k Project, the endangered green sea turtle (*Cheloniamydas*) has also had its genome sequenced and described [32]. The turtle blood specimen was provided by the Genome 10k Project and was sequenced utilizing the Illumina Hiseq sequencing platform, with a 110-fold coverage over 2.2 Gb of de novo assembled scaffolds. Phylogenetics analysis of the green sea turtle using a set of 1,113 single-copy coding genes that are orthologous revealed that the turtles diverged from the archosaurians approximately 257 million years ago in between the Upper Permian to Triassic period, and are also suggested to be a sister group of crocodiles and birds. In another Genome 10k-related project, the Avian Genome Consortium [33,34] sequenced the genome of the rhinoceros hornbill (*Buceros rhinoceros silvestri*) together with the genomes of 47 other avian species.

The hornbill genome was sequenced using the Illumina Hiseq 2000 sequencing platform, with 35-fold coverage across 1.08 Gb. Assembly was carried out de novo, annotations of protein coding gene was based on chicken, zebra finch, and human gene sets. Comparative genomics analyses among the 48 avian genomes revealed that the avian genomes to be reduced in size due to reduced introns, fragmented microchromosomes, reduced repeat transposon activity, shorter protein coding genes, and large segmental deletions. The avian protein coding genes are on average 50% and 27% shorter than the mammalian and reptilian protein coding genes respectively. In addition, the avian genomes have a reduced number of genes, about 70% of the number of genes found in the human genome. Further phylogenomics analyses utilizing an alignment of around 41.8 million bp nucleotide data sets consisting mainly of orthologous exons from 8251 syntenic protein coding genes, introns from 2516 of these genes, and 3769 ultra conserved elements to infer evolutionary relationships between the 48 avian genomes revealed contradictions in avian phylogenies inferred from morphological characters, DNA-DNA hybridization, and mitochondrial genomes [33,34].

Metagenomics

Metagenomics application is popularly used in studies of assemblage of microorganisms in microbial ecology [35]. Plenty number of bioinformatics tools have been developed for metagenomics analysis. In general, bioinformatics tools are command-based programs, which run on Linux or Ubuntu Operating System but there are few programs developed in Window OS for user-friendly such as MEGAN4 and MG-RAST. Each of the metagenomics tools has their specific functions (Table 2). Numerous of metagenomics studies have been reported to study environmental samples [36] such as hair, feacal, soil and water samples. However, very limited metagenomics studies/research have been studied in wild animals.

Metagenomics analysis using a 454 GS Junior Instrument (Roche) enabled the detection of the presence of novel viruses or virus variants of theilovirus, phleboviruses, amdovirus, kobuvirus and picobirnaviruses in 10 different species of wild small carnivores including the American mink (*Neovison vison*), European mink (*Mustelalutreola*), European polecat (*Mustelaputorius*), European pine marten (*Martesmartes*), stone marten (*Martesfoina*), Eurasian otter (*Lutralutra*) and Eurasian badger (*Melesmeles*) from the family of Mustelidae; common genet (*Genettagenetta*) of the family of Viverridae; red fox (*Vulpesvulpes*) of the family of Canidae and European wild cat (*Felissilvestris*) of the family of Felidae) living in the northern part of Spain [37]. Metagenomics approach was used to understand the effective surveillance on wildlife-associate zoonoses in China, especially in bats [38]. The genomes of bats were sequenced using Solexa sequencing technology and nearly 1.2 trillion useful reads were generated. The raw reads were assembled into 4872 contigs whereby 36 viral families were annotated, which consist of 19 vertebrate virus families, 6 plant virus families, 4 insect virus families and 4 phages [38].

Bushpigs (*Potamochoeruslarvatus*) have been identified as the potential natural reservoirs for African swine fever virus, however is less known about what other viruses might be carried by bushpigs [39]. Moreover, there is a chance for interaction and sharing of pathogens with domestic relatives due to their habitat and movement at the boundary between the national parks and the farmland [40]. Thus a viral metagenomic study was carried out to determine whether bushpigs are carriers of known and/or unknown porcine viruses using sera samples [40]. The presence of PPV4 and novel TTSuV-1 and 2 variants were identified in the samples. The genetic relationships of these viruses and their distribution in both domestic pigs and in wildlife can be defined by further sequence analysis [40].

The red foxes (*Vulpesvulpes*) which distributed across Northern Hemisphere ranging from urban areas and farmlands to remote forests belongs to most widespread member of the order Carnivora, where these animals are known as carriers for number of pathogens that are harmful to humans, including *Echinococcusmultilocularis* and, in certain parts of the world, rabies virus [41]. Using metagenomic approach, the sequences obtained from fecal samples were detected with similarity to the sequences of Parvovirus and Hepevirus together with other viruses like picobirnavirus and astrovirus, however, the majority of the sequences had relatively low homology to known viruses [41].

Wild boars from an animal park in Hungary were subject to viral metagenomics analysis and complete genome sequencing [42]. The study identified Astrovirus sequence contigs in 50% (5/10) of fecal samples by metagenomic analysis. Based on the complete astrovirus genome sequence,this study showed wild boar may be a reservoir for astroviruses that infecting pigs and vice versa, and the PAstV-4 and WB lineages of astroviruses may have a single common origin because of their genetic similarities [42].

Metagenomic analysis of the viral flora in feaces of pine marten and European badger was carried out in the Netherlands[43]. In this project, researchers have used next-generation sequencing a 454 GS Junior instrument (Roche) technology to gain insight. Based on the metagenomics results, the total seven samples indicated the presence of bacteriophages from the order Caudovirales and family Microviridae. The result for pine marten, eukaryotic viruses with homology to kobuvirus from the Picornaviridae family, bocavirus from the Parvoviridae family, torque teno virus from the Anelloviridae family, and Sclerotiniasclerotiorumhypovirulence-associated DNA virus 1 (SSHADV-1) from the Geminiviridae-like family were identified[43]. Meanwhile, eukaryotic viruses with homology to Bombyxmoricypovirus from the Reoviridae family, columbid circovirus from the Circoviridae family, canine distemper virus from the Paramyxoviridae family, SSHADV-1 from the Geminiviridae-like family, and torque teno virus from the Anelloviridae family were detected in European badgers [43]. In addition, sequences with homology to viruses from the families Paramyxo- and Picornaviridae were also detected.

Zoonotic infections by rodents to human are very common due to their frequent contact[44]. A study was attempted to sequence for viral diversity in feces of 105 wild rodents (mouse, vole, and rat) collected in California and Virginiaand discovered a declining rate of sequences related to the mammalian viruses families *Circoviridae*, *Picobirnaviridae*, *Picornaviridae*, *Astroviridae*, *Parvoviridae, Papillomaviridae*, *Adenoviridae*, and *Coronaviridae*[44]. Several potentially new viral familiesrelated to the *Circoviridae*and *Picornaviridae*were characterized[44]. First murine astrovirus genome, papillomavirus genome, adenovirus and adenovirus-associated virus were also sequenced. This study also identified a large fraction of insect viruses namely the *Densoviridae*, *Iridoviridae*, *Polydnaviridae*, *Dicistroviriade*, *Bromoviridae*, and *Virgaviridae*and plant viruses such as*Nanoviridae*, *Geminiviridae*, *Phycodnaviridae*, *Secoviridae*, *Partitiviridae*, *Tymoviridae*, *Alphaflexiviridae*, and *Tombusviridae* families from which they rodents obtained through their diet [44].

With the advancement in metagenomics or NGS technologies, recent studies have demonstrated the existence of enormous virus diversity among wild animals including those uncharacterized viruses through conventional methods as per discussed above. As far as the animal conservation and welfare in concern, the expansion of knowledge of the virus diversity present in wild animals, as well as the potential transmission of these viruses to domestic animals or humans are essential.

CONCLUSION

In a world after the first human genome was successfully drafted [45], the labour and cost of sequencing a genome has reduced remarkably with the introduction of next-generation sequencing (NGS) platforms such as the Illumina's Hiseq, Roche's 454 pyrosequencing, ABI's SOLiD Platform, and various other up and coming platforms (Table 1). NGS is advantageous over Sanger sequencing in that a larger amount of data can be obtained in a much shorter period of time and at a fraction of the cost. These benefits enable genomes of non-model organisms to be sequenced. Asides from biomedical and pharmacological studies, phylogenomics and comparative genome studies will easily benefit from the large amount of data that are easily obtained from utilizing the NGS platforms, either from the genome proper or from whole mitochondrial genome. As of writing, there are at least 3000 eukaryote genomes at various levels of assemblies listed in NCBI. Wildlife animal are extinct day by day due illegal hunting, deforestation, defaunation and other factors. For future generation, the knowledge of NGS is very important in a way understanding the genome of an animal, genetic composition and diseases that could effect the organism or vice versa. Many researches should be studied in wildlife animal in order to preserve our nature and future.

Table 1: High-throughput sequencing methods

METHOD	ADVANTAGES	DISADVANTAGES	REMARK
Second-generation sequencing techniques			
454 sequencing	Generate long read lengths and relatively fast run times of the instrument	Poor interpretation of homopolymers leading to errors	First introduced NGS technique [46,47]

Illumina (Solexa) Genome Analyzer	Wide use analyser and short read length method a	Irregular incorporation of incorrect dNTPs by polymerases	Low multiplexing ability [48]
ABI SOLiD system	Reduction in error rates relative to Illumina NGS system	Have long run times and need for 2-20 µg DNA	Driven by DNA ligase than polymerase [49]
HiSeq 2000 (Illumina, CA, USA)	Requires less sample < 1 µg	75 (35-100) bp read lengths. More false positives	Addition of fluorescent-labeled nucleotides [50]
Polonator G.007	Decode the base by single-base probe nonamers	In coverage, positive selection rate adequate false- SNP	Ligation based sequencer [51]
Ion Torrent Sequencing	First platform to eliminate cost and complexity with 4-color optical detection used by other NGS platforms	High accuracy and short run time	Non-optical DNA sequencing [52]
SLAF-seq	De novo SNP discovery with reduced cost and high accuracy	Needs complex instrument	Double barcode system ensures simultaneous genotyping of large populations [53]
Third-generation sequencing techniques			
PacBio RS (Pacific Biosciences , CA, USA)	No amplification of template DNA required, real- time monitoring of nucleotide incorporation	High error rates and low reads	Generates long-read lengths 800-1000 bp [54]
HeliscopeT M Sequencer	Nonbiased DNA sequence	High NTP incorporation error rates	Single molecule sequencing [55]
Fourth-generation sequencing techniques			
Oxford Nanopore	Fastest sequencer whole- genome scan within 15 min	Not much data available, high cost perMb	Expanding technique [56]

293 **Table 2: Program and tools for Metagenomics application**

No	Software name	Operating system	Functions/application
1	MG-RAST (an automated analysis platform for metagenomes)	Windows	• Provides quantitative insights into microbial population information based on query sequences data [57]. • User-friendly.
2	IMG/M or known as “The	Linux/Ubuntu	• Command-based

	Integrated Microbial Genomes (IMG) system		
3	CAMERA	Windows	• This tool specifically developed to study microbial ecology and a centralized database for marine microbes [58]
4	CARMA	Windows	• Specifically developed for characterizing the taxonomic composition and genetic diversity of short-read metagenomes [59]
5	MOTHUR	Linux/Ubuntu	• Complete package to answer microbial ecology questions because composed of the development tools such as ARB, DOTUR, SONS, LIBSHUFF, UniFrac, Statistical package, phylogenetic tool. • This tool analyses 222,000 sequences less than 2 hours in personal computer compared to other existing tools where can analyses 102 to 104 sequences only. Besides, this software is very flexible and easy to maintain [60]

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