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# Pathogenomics and Molecular Advances in Pathogen Identification

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## Abstract

Today exists a spread spectrum of tools to be used in pathogen identification. Traditional staining and microscopic methods as well as modern molecular methods are presented in this chapter. Pathogen identification is only the beginning to obtain information related to pathogenicity of the microorganism in the near future. Once the pathogen is identified, genome-sequencing methods will provide a significant amount of information that can be elucidated only through bioinformatics methods. In this point, pathogenomics is a powerful tool to identify potential virulence factors, pathogenicity islands, and many other genes that could be used as therapeutic targets or in vaccine development. In this chapter, we present an update of the molecular advances used to identify pathogens and to obtain information of their diversity. We also review the most recent studies on pathogenomics with a special attention on pathogens of veterinary importance.

**Keywords:** pathogenomics, pathogen identification, phylogeny, genome sequencing, infectious diseases

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## 1. Introduction

Infectious diseases not only represent one of the biggest threats to public health but also to animal health and welfare. A significant number of pathogenic microorganisms can be transmitted by vectors; among these, vector-borne pathogens are considered important since they can spread easily pathogens to previously pathogen-free livestock areas [1].

Nowadays, we can identify cultured or non-cultured organisms with molecular techniques and even reconstruct a phylogeny to propose a new species or reclassify reported microorganisms.

Molecular identification methods offer some advantages as being more sensitive and quicker than traditional culture methods at relatively low cost. Many microorganisms are difficult to culture or noncultured which difficult their study *in vitro*, this is overcome by using genome sequencing as an alternative [2].

Currently, the high-throughput next generation sequencing (HT-NGS) technologies have provided a huge amount of information in genomics researches [3]. Genome sequencing and new omics studies, such as pathogenomics, reveal a new landscape of study of microorganisms and reveal unexpected aspects of pathogen biology. These studies have brought a re-evaluation of definitions of pathogens and virulence factors [4].

In order to understand the complex interaction established between host-pathogen, several genomes of farm animals are sequenced (<http://www.ensembl.org/info/about/species.html>): cat (*Felis catus*), chicken (*Gallus gallus*), cow (*Bos taurus*), dog (*Canis lupus familiaris*), horse (*Equus caballus*), pig (*Sus scrofa*), sheep (*Ovis aries*), turkey (*Meleagris gallopavo*), and duck (*Anas platyrhynchos*).

However, a scarce number of reports are focused on studying pathogenomics of microorganisms affecting farm animals, a field with a high potential to provide new insights to understand pathogen-host interaction from an omic point of view. The new omics techniques applied in veterinary studies provide a new landscape for research in order to elucidate the mechanisms that pathogens employ to develop infection, and then try to develop new mechanisms of control and treatment.

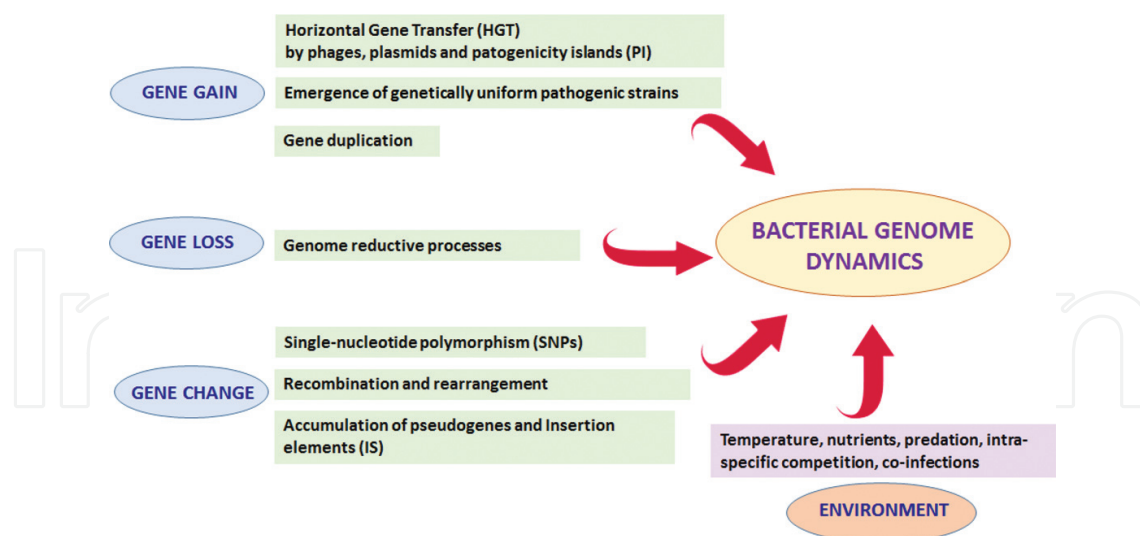
## 2. Pathogenomics

Molecular identification methods afford for culturable and non-culturable pathogens' identification; however, the entire genome information remains unknown. High-throughput sequencing technologies have opened the possibility to get access to valuable information contained in the genome [5].

Pathogenomics is a discipline that seeks to mark out virulence factors and their contributions to overall pathogenesis by comparing gene repertoires of pathogenic and non-pathogenic strains/species [4].

Today, sequencing and comparing genomes of several strains of a single pathogen is a relatively short time process [6]. One of the crucial genomic analyses is driven to understand microorganisms' pathogenicity and virulence through intensive and refined bioinformatics tools.

Over the years, the genomics information has changed the concept of a static microbial genome and has demonstrated that bacterial genomes are in a dynamic process. The bacterial genome dynamics is driven basically by three forces: gene gain, gene loss, and gene change, and these three forces comprise of several factors affecting bacterial genome dynamics, such as gene duplication, single-nucleotide polymorphism (SNPs), horizontal gene transfer (HGT), recombination and rearrangements, among others (**Figure 1**) [4, 6].



**Figure 1.** Gene gain, gene loss, gene change, and the environment are the main factors influencing on bacterial genome dynamics.

The smallest variation in bacterial genomes is the SNPs, which have been detected more recently by whole-genome sequencing. Sondgeroth et al. [7] used SNPs of five genes to monitor potential changes in the *B. bovis* population composition before and after passage through the tick vector. A substantial polymorphism among *E. hepatica* isolates was observed by Cwiklinski et al. [8], and they found that 48% of genes exhibited at least one non-synonymous SNP, and these genes were associated with biological processes as axonogenesis and chemotaxis.

## 2.1. Pathogenomics studies

In order to address what makes bacteria pathogenic is important to know the functional differences between pathogenic and non-pathogenic strains or species. Nowadays, the number of sequenced genomes increases constantly and this has made feasible comparative analyses between pathogenic and non-pathogenic bacterial genomes.

A significant variation in size and content of genomes between different genera and species, and even in strains of the same species has been reported [6].

Pathogenicity is an ability of an organism to cause disease and microorganisms possess several factors that enable them to increase their virulence or degree of pathogenicity.

Toxicity and invasiveness are the two properties of pathogens to cause disease; the first one refers to degree to which a substance causes harm and the latter is the ability to penetrate into the host and then spread [9]. Host and pathogens have co-evolved over millions of years and in this relationship, pathogens have modified their virulence to adapt to the host immune system.

Due to gain or loss of genes pathogens adapting to the changing environments, in this sense, genomic studies are indispensable to identify differences between genomes to provide invaluable insights into virulence and pathogenesis [10].

### 2.1.1. Mobile genetic elements (MGE)

The term MGE encompasses specialized genetic elements that play a role in genomic instability including plasmids, bacteriophages, transposons, genomic islands (GI), inteins, introns, retroelements and integrons, and many other specialized genetic elements such as insertion sequence elements (IS), miniature inverted-repeat transposable elements [MITEs], repetitive extragenic palindromic [REP] sequences, and bacterial interspread mosaic element [BIMEs] [11]. Among bacterial strains exist a particular interest due to the presence of virulence factors that may be introduced to a new host genome. As MGE are involved in genomic rearrangements and virulence acquisition they are considered important elements in bacterial genome evolution [12].

MGE encode proteins that are involved in cell surface structures (capsular polysaccharides, O-antigen, S-layer, flagella, pilli, and porins) and toxins [10]. Type II and type III toxin-antitoxin systems (TASs) belong to the class of bacterial MGEs that are spread by horizontal gene transfer and they appear to behave like selfish elements contributing to the stable maintenance and dissemination of plasmids and genomic islands in bacterial populations [13]. Here, we will focus on explaining some of the features of IS, GIs, and PAIs.

#### 2.1.1.1. Insertion sequences (IS)

IS elements represents an important component of most bacterial genomes; they usually have a size of ranging from 0.7 to 3.5 kB, including a transposase gene encoding the enzyme that catalyzes IS movement. ISs are the smallest and simplest autonomous mobile genetic elements that contribute massively to HGT and have an important role in genome organization and evolution. Many ISs are delimited by short terminal inverted repeat (IR) and are flanked by direct repeat (DR). More than 3500 ISs from bacteria and archaea have been described. These DNA segments are capable of transposing within and between prokaryotic genomes causing insertional mutations and chromosomal rearrangements.

They cause gene inactivation and have strong polar effects or activation or alteration of the expression of adjacent genes [14–17].

Although IS elements are genomics parasites that harm their host by increasing the rate of deleterious mutations, they generate beneficial mutations trough their transposition and recombination. Indeed, IS elements are considered important elements for the adaptive evolution of their host [15, 18].

#### 2.1.1.2. Genomic islands (GEIs)

There exists several ways how bacterial genomes can evolve, including mutations, rearrangements or HGT, contributing to diversification, and adaptation of microorganisms to environmental niches. GEIs are large DNA sequences specifically present in the genomes of certain bacteria strains but not in the genomes of closely related variants. These are non-self-mobilizing integrative and excisive elements that encode diverse functional characteristics; usually, they are integrated in bacterial chromosome but also can be found in plasmids or phages [11]. Recent information on GEIs suggests that these elements have become strongly selective for adaptive



and auxiliary functions (pathogenicity, symbiosis, aromatic compound metabolism, mercury resistance, and siderophore synthesis) [19–21].

### 2.1.1.3. Pathogenicity islands (PAIs)

PAIs are a group of GEIs that carry one or more virulence-associated genes and mobility genes and occupy chromosome regions as large as 10 kb to more than 100 kb; “pathogenicity islets” are smaller fragments of DNA ranging from 1 to 10 kb. PAIs are part of a flexible gene pool that contain mobility genes so that they can be integrated into the host genome including genes encoding to integrases, transposases, phage genes, and origins of replication [22]. **Table 1** shows the main features of PAIs.

Virulence factors (VFs) are encoded by genes found in pathogenic microorganisms. Pathogenic bacteria possess various VFs that allow them colonize a variety of niches, cause infection, and survive in the hosts [23]. In order to combat infectious diseases, it is absolutely necessary to discover virulence factors of pathogenic microbes to identify targets for novel drugs and design of new vaccines [24].

A special interest has emerged on VFs study, mainly due to the constant and persistent antimicrobial resistance observed in pathogenic microorganisms, because they have modified

| <b>Genomic Islands</b>   | <b>Ref.</b> |
|--|-------------|
| Large segments of DNA, 10-200 kb   | [22]        |
| GC content different from the rest of the chromosome   | [23]        |
| Often inserted at tRNA genes   | [23]        |
| Usually flanked by 16-20 bp perfect or almost perfect Direct Repeats (DR)  | [23]        |
| Contain genes encoding integrases or factors related to plasmid conjugation or phages involved in GEI transfer                         | [23]        |
| Often carry Insertion Elements or transposons to mobilize genetic material   | [24]        |
| Offer a selective advantage for hos bacteria and often described as pathogenicity, symbiosis, metabolic, fitness or resistance islands | [23]        |
| <b>Pathogenicity Islands</b>   |             |
| Clusters of contiguous genes present in some related strains or species, but absent in non-pathogenic bacteria.                        | [4]         |
| They confer on the host bacterium a complex and distinctive virulence phenotype by the presence of virulence factors.                  | [4]         |
| Presence of mobility genes (integrases, transposases)  | [5]         |
| High percentage of hypothetic proteins   | [5]         |
| Different genomic sequence signature   | [5]         |

**Table 1.** Characteristics of genomic and pathogenicity islands.

their virulence mechanisms to adapt to host defense system [9]. Today, complete genome sequences of different microbial species either pathogenic or non-pathogenic enable comparative studies to identify specific VFs in species through bioinformatics analyses.

As in other bacteria of clinical importance, some MGE have been identified in farm animals' pathogens. The intraerythrocytic parasite of cattle *B. bovis* has mechanisms to protect their cytoadhesion from the host adaptive immune response, and this function is mainly accomplished through antigenic variation of a virulence factor called VESA1 protein (Variant Erythrocyte Surface Antigen-1) [25]. VESA1 is a size-polymorphic, heterodimeric protein that comprises of two subunits of 105–115 and 120–135 kDa in mass approximately, depending on the isolate and clonal line [26]. Genomic and transcriptomic analyses reveal that sMORF could have a significant role for a rapid antigenic variation. However, experimental evidence is necessary [27].

In *F. hepatica*, some proteins are virulence-associated factors. These proteins are cathepsin L cysteine peptidase (FhCL) and have functions in parasite virulence including tissue invasion and suppression of host immune responses. Among the functions are degradation of red blood cells, a vital process when the parasite is located in the bile duct and needs to digest a large quantity of host cells to support the enormous production of progeny (30–50,000 eggs/day/worm) [28]. Through phylogenetic analyses, Robinson et al. [28] classified cathepsin L gene family into three clades (Clades 1, 2, and 5) expressed by tissue-migrating adult worms and two clades (Clades 3 and 4) expressed by early infective juvenile stage. Each of these cathepsins is expressed in different larvae stages. Collagenolytic activities have been reported in FhCL2 and FhCL3, suggesting that this activity is essential to the parasite in order to degrade the connective tissue matrix of the organs that break through during migration [29].

In Gram-negative pathogens, type IV Secretion System (T4SS) has a conserved structured and function that is crucial for virulence and intracellular survival. The importance of this system in *Anaplasmataceae* is its possibility as functional virulence factors due to its retention and protein conservation among rickettsial species [30]. Recently, the high complexity of the Rickettsia T4SS was revealed. Gillespie et al. [31] focus on the components of the Rickettsiales vir homolog (rvh), a collection of VirB and VirD protein-encoding genes. They found that these genes are comprised of unprecedented gene family expansion. Three families of gene duplication are contained in rvh genes: rvhb9, rvhb8, and rvhb4, and some genes are equivalent in other T4SS. This study shows the need to characterize Rickettsia rvh components.

Some molecules have been investigated because of their physiological importance in microorganisms. Aminopeptidases have been used as therapeutic and prophylactic targets in many parasitic infections and other diseases [32]. In *B. bovis*, a member of the methionine aminopeptidase (MAP) family was characterized and expressed in *E. coli*. The results showed that the construction aminopeptidase (MAP)-glutathione-S-transferase (GST) was antigenic by inducing high levels of cytokines and immunoglobulin IgG titers in the host, and importantly, inhibitors of MAP inhibit the growth of *Babesia* parasites both *in vitro* and *in vivo* [32]. Methionine aminopeptidases have an important role in N-terminal methionine excision from the polypeptide in ribosome during protein synthesis; their physiological importance relies on the lethality of its absence in bacteria and yeast [33, 34]. MAPs in malaria play an important role in parasite biology due to their role in parasite hemoglobin during peptide catabolism [35].

| Database  | Website   | Information   | Ref. |
|---|---|---|------|
| VFDB<br>Virulence Factor<br>Database  | <a href="http://www.mgc.ac.cn/VFs/">http://www.mgc.ac.cn/VFs/</a>   | Curating information about virulence factors of bacterial pathogens   | [33] |
| PAIDB v2.0<br>Pathogenicity<br>Islands Database                                     | <a href="http://www.paidb.re.kr">http://www.paidb.re.kr</a>   | Pathogenicity islands (PAIs), candidate PAIs and resistance islands (REIs) in prokaryotic genomes.                        | [35] |
| PHIDIAS-<br>Pathogen-Host<br>Interaction Data<br>Integration and<br>Analysis System | <a href="http://www.phidias.us/victors/intro.php">http://www.phidias.us/victors/intro.php</a>                                   | Comprises genes experimentally observed to be necessary for virulence, including bacteria, viruses, parasites, and fungi. | [39] |
| MvirDB  | <a href="http://mvirdb.llnl.gov/">http://mvirdb.llnl.gov/</a>   | Microbial database of protein toxins, virulence factors, and antibiotic resistance genes                                  | [34] |
| PIPS Pathogenicity<br>Island Prediction<br>Software                                 | <a href="http://www.bioinformatics.org/groups/?group_id=1063">http://www.bioinformatics.org/groups/?group_id=1063</a>           | Prediction of pathogenicity islands in an integrative manner.   | [40] |
| PredictBias   | <a href="http://www.bioinformatics.org/sachbinfo/predictbias.html">http://www.bioinformatics.org/sachbinfo/predictbias.html</a> | Identification of genomic and pathogenicity   | [41] |
| MP3 Software  | <a href="http://metagenomics.iiserb.ac.in/mp3/index.php">http://metagenomics.iiserb.ac.in/mp3/index.php</a>                     | Prediction of pathogenic proteins in genomic and metagenomic data   | [42] |
| ProtVirB  | <a href="http://bioinfo.icgeb.res.in/protvirdb">http://bioinfo.icgeb.res.in/protvirdb</a>                                       | Database of protozoan virulent proteins   | [43] |
| GIPSy<br>Genomic Island<br>Prediction<br>Software                                   | <a href="http://www.bioinformatics.org/groups/?group_id=1180">http://www.bioinformatics.org/groups/?group_id=1180</a>           | Prediction of GEIs including PAIs, REIs, and Symbiotic Islands (SIs)  | [40] |
| Island Viewer 3   | <a href="http://www.pathogenomics.sfu.ca/islandviewer/">http://www.pathogenomics.sfu.ca/islandviewer/</a>                       | Web-base resource for the prediction and analysis of GIs in bacterial and archaeal genomes                                | [44] |
| OASIS<br>Optimized<br>Annotation<br>System for<br>Insertion<br>Sequences            | <a href="https://github.com/dgrtwo/OASIS">https://github.com/dgrtwo/OASIS</a>   | Program that uses a library of IS to identify IS in bacteria  | [45] |
| ISfinder  | <a href="http://www-is.biotoul.fr/">http://www-is.biotoul.fr/</a>   | Database for bacterial IS   | [46] |
| ISsaga  | <a href="http://issaga.biotoul.fr/ISSaga/issaga_index.php">http://issaga.biotoul.fr/ISSaga/issaga_index.php</a>                 | Web application. Computational tools and methods for high quality IS annotation   | [17] |
| ISQuest Software  | <a href="https://omictools.com/isquest-tool">https://omictools.com/isquest-tool</a>   | Identifies bacterial IS elements in raw read data or contigs  | [47] |

**Table 2.** Selection of online resources for analysis and search of virulence factors, toxins, GEIs, and PAIs in microorganisms [39–47].



## 2.2. Bioinformatics tools in pathogenomics

As mentioned before, despite the recent advances of modern medicine based on genomic data, still infectious diseases are considered as one of the biggest threats to public and animal health [36]. Comparative genomic analysis of pathogenic and non-pathogenic bacteria can reveal horizontally transferred genes between bacteria, thus conferring new properties. PAIs have some detectable properties, like genomic signatures and mobility genes helping in integration into the host genome, as genomic signatures helps to identify pathogens, functional signatures provide information about what a pathogen is capable of [5, 37].

Recently, an updated database has been reported, the Virulence Factor Database or VFDB (<http://www.mgc.ac.cn/VFs/>) that provide the latest information about virulence factors of various bacterial pathogens, especially those obtained by next generation sequencing technologies (NGS) [36]. The Pathogenicity Islands Database, PAIDB (<http://www.paidb.re.kr>), is a database that contains comprehensive information on all reported PAIs and candidate PAIs in prokaryotic genomes; additionally, information of Resistance Islands (REIs) is considered.

The importance of PAIs, a subset of GIs, is that genomes of pathogenic bacteria mediate the horizontal transfer of genes encoding a significant number of virulence factors [38].

PAIDB also contains information of antimicrobial resistance islands, REIs. This, another, class of GIs is linked to pathogenesis by conferring resistance to multiple antibiotics and thus facilitating the emergence of multidrug-resistance pathogens. PAIDB contain 223 types of PAIs and 1331 GenBank accessions of complete or partial PAI and 88 types of REIs from 108 accessions [38]. Several database and software are available for *in silico* analysis of PAIs, VFs, and IS (Table 2).

## 3. Methods used to identify pathogens

### 3.1. Staining and microscopic methods

Many methods are available to identify bacteria, and microscopy has an important role in microorganism identification. Especially, when an urgent diagnosis is required, fast microscopic methods are the first option. Many bacterial pathogens are identified by staining methods, and among these, differential stains are common in microbiology and provide some information about the species and many times can be compared to automated species differentiation methods [48].

Gram-stain is an old differential technique, but very popular to distinguish between Gram-positive and Gram-negative bacteria. This method is based on the different cell wall structures and components of both bacteria types. The bacterial cell wall of Gram-positives is stained by crystal violet and iodine, which form an insoluble blue dye complex while Gram-negatives are counterstained by fuchsin or safranin. This staining is also applied to some fungi, such as *Candida* spp., *Nocardia* spp., or *Actinomyces* spp. When cells walls are damaged or even cells are dead, false Gram-negatives may result [48, 49].

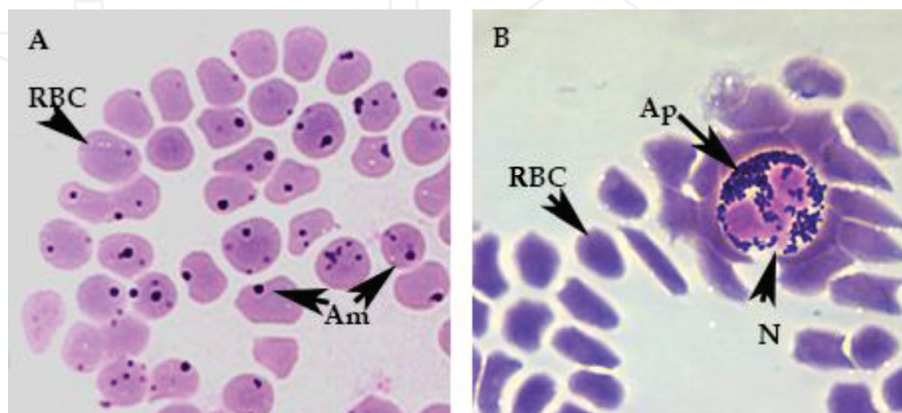
Another common technique is Giemsa staining, which was primarily developed for the visualization and histopathological diagnosis of *Plasmodium* spp. at the end of nineteenth century. Now, this staining method is used to identify many other parasites including *Babesia bovis*, *B. bigemina*; *Leishmania* spp., *Trypanosoma* spp.; *Toxoplasma gondii*, and others, and bacteria as *Anaplasma marginale*, *A. phagocytophilum*, and fungi (**Figure 2**).

The Giemsa's solution is a composition of methylene blue and oxidation products of methylene blue (Azure A and B) that stain primary proteins and nucleic acids [48].

Even natural herbal dyes as curcuma, alizarin, and henna have been used to stain *Fasciola hepatica* without the carcinogenic effect of traditional synthetic dyes [50, 51]. Fluorescent dyes such SYBR Green 1, YOYO-1, and ethidium homodimer-2 could be detected using fluorescent microscopy in combination with Giemsa staining, this method has been proposed to improve microscopic diagnosis of *Plasmodium falciparum* [52]. According to these results, the combinations of fluorescent and non-fluorescent dyes could be applied to enhance other microorganisms' identification.

Oocysts parasites identification is an issue that has been resolved through microscopic observation. In avian coccidiosis, most of the oocysts have a very similar morphological appearance with size differences that allow distinguish them. Castañón et al. [53] reported an approach based on image recognition by algorithms to identify *Eimeria* spp. oocysts; the authors extracted morphological information by using computer vision techniques in order to perform an automatic species differentiation of oocysts. The parameters considered in the identification process were: (1) multiscale curvature, (2) geometry, and, (3) texture to construct a 13-dimensional feature vector for each oocyst image. With this powerful tool, molecular diagnosis based on PCR using the ribosomal ITS1 or multiplex PCR can be complemented with the use of the *Eimeria* Image Database [53].

With the recent development of fluorescent techniques and imaging tools, farm animals' pathogen identification has become a more efficient and reliable process.



**Figure 2.** Visualization of (A) Giemsa staining of *A. marginale* (Am) inside bovine red blood cells (RBC), (B) Giemsa staining of *A. phagocytophilum* (Ap) inside a human neutrophil (N). (Anaplasmosis Unit, CENID-PAVET, INIFAP, Human blood was obtained with patient's consent).

### 3.2. Genotypic methods

Conventionally, cultural and biochemical techniques are the primary methodology for identifying most pathogens; however, Koch's postulates are critical for fulfilling most of the times [2, 54]. The culture-based testing usually yield results in several days or even up to weeks after sampling without success guaranteed, because of the unsuitable culturing conditions and the special requirements for the bacterial species [55].

Besides, pathogen identification can be a hard task when these cannot be cultured. With the development of molecular techniques and sequencing technologies, many non-cultured microorganisms, as *Mycoplasma haemobos* and *M. wenyonii* have been identified and many microorganisms already known have been reorganized phylogenetically [56].

#### 3.2.1. Polymerase chain reaction (PCR)

Molecular methods based on nucleic acid amplification have circumvented the culturing problem with some benefits. In the molecular detection by PCR, the pathogen is first detected by PCR product amplification and then identified by sequencing, resulting in more rapid diagnoses [55]. Several pathogens of veterinary importance have been detected successfully by PCR, including *A. marginale*, *B. bovis*, *Mycobacteria* spp., *F. hepatica*, and *F. gigantica*, *Theileria* spp., among others [57–61]. Ribosomal RNA (rRNA) genes have emerged as the most prominent target in microbial detection mainly due to fact that the region represents a versatile mix of highly conserved and moderately to highly variable segments [62]. In bacteria, the rRNA genes are firstly transcribed from the ribosomal operon as 30S rRNA and then cleaved into 16S, 23S, and 5S rRNA by RNase III. The ribosomal operon size, nucleotide sequences, and secondary structures of 16S, 23S, and 5D rRNA are well conserved within bacterial species [63]. Since rRNA genes are evolving more slowly than protein encoding genes they have a particular importance for identification and phylogenetic analysis of distant related species [64].

##### 3.2.1.1. Molecular markers

During the last two decades, the 16S rRNA sequences have been widely used for the identification and classification of bacteria, the main uses of 16S sequences are: identification and classification of isolated pure cultures and estimation of bacterial diversity in environmental samples without culturing through metagenomic approaches [65].

The rRNA operon in bacteria comprises 16S, 23S, and 5S, spaced by intergenic spacer regions (ITS, also called internal transcribed spacer) which have been used also to detect and differentiate pathogens [62]. Amplified PCRs products based on ITS sequences have distinguished 55 bacterial species, including 18 *Clostridium* and 15 *Mycoplasma* [66]. More recently, rRNA ITS, specifically 16S–23S, has been used in *Vibrio* identification [67], *Mycoplasma* from cattle [68], *Brucella* [69, 70], and *Mycobacteria* [71, 72].

Similarly to 16S rRNA, 18 s rRNA is a sequence commonly used for eukaryotic identification, such as parasites. Actually, there exists several molecular markers used to identify *B. bovis* and *B. bigemina* using 18S rRNA, cytochrome b gene, antigenic protein encoding genes msa-1 and msa-2, EF-1a, beta-tubulin, among others [73].

Alternatively, other genes less commonly used that can help in bacterial identification are chaperonin-60 (*cpn60*) [74], chaperonine GroEl [75], recombination and repair protein (*recN*), and DNA polymerase III subunits  $\gamma$ ,  $\tau$  (*dnaX*) [76], the  $\beta$ -subunit of RNA polymerase (*rpoB*) [76], and esterase (*est*) [77]. Among all genes used to identify bacteria, still 16S rRNA is the most used when the bacterial pathogen is non culturable, this is mostly because there exists a significant number of 16S rRNA sequences available in databases that can be used to compare and then identify [Ribosomal Database Project (<http://rdp.cme.msu.edu>) and Greengenes (<http://greengenes.lbl.gov>)]. These databases are not always complete because 16S rRNA sequences are constantly reported and many are still missing, besides, many times the species can only be identified at genus level and analyses with other genes are necessary [78].

Amplification of 16S sequence have allowed identification and phylogenetic reconstruction of several *Anaplasma* species in China, including *A. marginale* y *A. ovis* [79]; a comparison between *A. marginale* and *A. centrale* 16S rRNA revealed that both sequences have 98.08% identity, even with this level of identity *A. centrale* was identified by PCR primers based on 16S rRNA [80]. Bovine hemoplasmas "*Candidatus Mycoplasma haemobos*" and *Mycoplasma wenyonii* has also been detected by 16S rRNA PCR and RT-PCR in Brazil and Switzerland [81–83]. Detection of rickettsia *A. marginale*, causal agent of bovine anaplasmosis, using genomic DNA as template for PCR is an alternative diagnostic tool. Singh et al. [84] used a semi-nested PCR assay for the detection of *A. marginale* in carrier cattle in India. The PCR was optimized to identify the major surface protein 5 (Msp5) based on primers previously reported [85]. The nested PCR (nPCR) employing *msp5* primer sequences were able to detect as few as 30 infected erythrocytes per ml of the blood and then detect low levels of rickettsiaemia in cattle [85].

Noaman and Shayan [86] employed 16S ribosomal RNA (rRNA, GenBank M60313) gene of *A. marginale* on DNA isolated from blood samples of cattle. The nucleotide sequence of 16S rRNA is highly conserved in *Anaplasma* spp., and is use to amplify fragments of the gene in all known *Anaplasma* species.

*B. bigemina*, one of the several *Babesia* species known to cause bovine babesiosis has also been detected by PCR, besides, the amplified product is parasite and species specific [87]. From sensitivity studies, the authors showed that the 278-bp fragment amplified by PCR and visualized in reactions could contain as little as 10 pg. of parasite template DNA.

### 3.3. Multiplex PCR

A variant of the PCR is the multiplex PCR (mPCR) that detects more than one species at a time in a very effective way using a mixture of locus-specific primers in a single reaction [88]. mPCR offers an important advantage over single-species PCR because co-infections can be detected, for instance, detection of swine, avian and equine viruses [89–91], bacteria in fish [92], cattle bacteria and parasites, including *Mycobacterium bovis*, *T. annulata*, *F. hepatica*, and *B. bovis* [93–97], and nematodes [98] have been reported.

Multiplex PCR for detecting multiple pathogens has not been widely used in animal health diagnostic laboratories because this assay is difficult to optimize and validate [2].



### 3.4. PCR-restriction fragment length polymorphism (PCR-RFLP)

PCR-RFLP is an approach based on the fact that the genomes of closely related pathogen have variations in sequence, thus, a different length can be obtained from enzymatic digestion of a PCR fragment [99]. Due to that digested DNA represents a unique pattern, and this method offers a much greater sensitivity for the identification of pathogens, especially when culture is difficult. Using PCR-RFLP, *Theileria annulata* was identified in ticks (Ixodidae), showing that parasite has a preference for *Hyalomma anatolicum anatolicum* which suggest that its major role in transmission of parasite [100]. Identification of parasites as *Fasciola* species also employs PCR-RFLP analysis. The region between 18S and 28S (which includes ITS1, 5.8S, ITS2) of ribosomal RNA was amplified by PCR and then digested with restriction endonucleases, in this analysis, 90 *Fasciola* samples from different geographical regions were identified as *F. hepatica* or *F. gigantica* [58].

### 3.5. DNA microarrays

DNA microarrays are a viable platform for detection of pathogenic organisms. This detection has a cost lower than multiplex PCR and technologies like high-throughput sequencing [101]. A microarray is a miniaturized device that contains short single-stranded DNA oligonucleotides (25- to 70-mers) probes attached to a solid substrate. These probes would be complementary to segments of one or more target organism genome. El-Ashker et al. [59] identified *Babesia*, *Theileria*, and *Anaplasma* species in cattle using DNA microarray. This novel DNA microarray system was compared with microscopy and PCR assay for the diagnosis of bovine piroplasmosis and anaplasmosis. All samples positive by PCR for *Babesia/Theileria* spp. also were positive in the microarray analysis, which supports this technique as a valuable improvement in veterinary diagnoses. Another microarray developed for *Mycoplasma* spp. consist of probes for 55 different cattle pathogenic bacteria including *M. mycoides* subs. *Mycoides* [102]. To date, no microarray has been developed for diagnosis of bovine tick-borne diseases.

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