REVIEW ARTICLE

Avian astroviruses

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As poultry becomes more important in the world economy, it is increasingly important to fully understand the mechanisms of disease and poor production that affect the industry. To more accurately and reasonably treat these diseases, a more sophisticated understanding of interrelatedness is required. This review focuses on avian astroviruses (AAstVs), in particular the recent advances in our understanding of AAstV molecular biology, and also history, diagnosis, treatment and control. The known AastVs comprise duck astrovirus 1, turkey astrovirus 1 and 2, and avian nephritis virus of chickens. Nucleotide and amino acid identities between the avian and mammalian (human, ovine, bovine) astroviruses is very low (e.g. 20 to 25% and 12 to 15%, respectively) in open reading frame (ORF) 1a. There is also variation among the avian astroviruses, including between the two known types of turkey astrovirus. The ORF 1b sequence contains a number of conserved amino acid motifs; these could be the basis of degenerate oligonucleotide primers. A nomenclature for astroviruses is also proposed, based on: host species–astrovirus–type number/country/state/reference number/year of isolation. For example, turkey astrovirus 2/North Carolina/034/1999.

Introduction

Because of the growing importance of poultry in world economics, it has become imperative to establish rapid and accurate diagnostics in treating poultry diseases (Lowenthal et al., 1999). As an increasing number of ‘small round viruses’ (SRVs) are implicated in decreased production and increased mortality, it is crucial that they be characterized to completely understand distribution and design effective control mechanisms (Asplin, 1965b; Gough et al., 1984; Reynolds et al., 1987a,b; Johnson, 1990; Saif et al., 1990; Swayne et al., 1990; Guy & Barnes, 1991; Cavanagh, 1992; Qureshi et al., 1997, 2000; Imada et al., 2000; Koci et al., 2000b; Schultz-Cherry et al., 2000; Todd, 2000; Yu et al., 2000a,b; Cavanagh, 2001; Todd et al., 2001). SRVs typically fall into one of five viral families, Paroviridae, Circoviridae, Picornaviridae, Caliciviridae, and Astroviridae, each with characteristic morphologies visible by electron microscopy (Caul & Appleton, 1982). Viruses are not static biological entities, but rather a collection of genetically diverse quasi-species capable of adaptation (Schneider & Roossinck, 2001). Therefore, diagnosis and classification must involve a collection of characteristics and not rely completely on morphology (van Regenmortel et al., 2000). As new genera and subgroups emerge, it is possible that characteristic physical properties may change or become less prominent. For this reason it is necessary to use replication strategy and genome organization along with biochemical properties and particle structure to properly assign an isolate to a viral family (van Regenmortel et al., 2000). In this review, we will discuss the recent advances in our understanding of avian astroviruses (AAstVs).

Astroviruses are small round, non-enveloped viruses, typically 28 to 30 nm in diameter (Matsui & Greenberg, 2001). The name astrovirus comes from ‘astron’ (Greek for star) describing the characteristic five-pointed or six-pointed star-like surface projections detected by negative stained electron microscopy (EM) (Madeley & Cosgrove,
In poultry, astroviruses are more commonly recognized as a problem in turkeys, and can be accompanied by a moderate increase in mortality. In the US, TAstV-1 was first identified in the 1980s (TAstV-2) and shown to be widely distributed (Saif et al., 1985; Reynolds & Saif, 1986; Reynolds et al., 1987b). Reynolds et al. (1987b) demonstrated that astroviruses could be isolated from 78% of diseased turkey flocks, more than any other virus identified. Recently, we have isolated and characterized a TAstV associated with poult enteritis mortality syndrome (PEMS), which is genetically and immunologically distinct from previously described US isolates (Koci et al., 2000b). The PEMS-associated TAstV (TAstV-2) was originally isolated from the thymus of infected poults (Schultz-Cherry et al., 2000). Experimentally infected poults exhibit thymus and bursal atrophy, and virus can be isolated in other tissues, although replication is only routinely detected in the intestines (Behling-Kelly et al., 2001).

**Astrovirus Disease**

Astroviruses were first described by Madeley & Cosgrove (1975) as the cause of gastroenteritis in infants. Ironically, this was not the first case of astrovirus disease in humans. The first case was reported earlier that same year by Appleton & Higgins (1975), but this isolate did not exhibit the characteristic morphology and was identified as an astrovirus in a retrospective study (Appleton & Higgins, 1975; Matsui & Greenberg, 2001). The role of astroviruses in birds pre-dates that of Appleton & Higgins (1975). In 1965, a disease in ducklings was described (Asplin, 1965a,b) that was eventually identified in 1984 as an astrovirus (Gough et al., 1984, 1985). Presently, astroviruses have been reported to cause acute disease in the young of multiple species, including humans, cattle, sheep, cats, dogs, deer, chickens, turkeys, and ducks (Madeley & Cosgrove, 1975; Snodgrass & Gray, 1977; Woode & Bridger, 1978; Bridger, 1980; McNulty et al., 1980; Williams, 1980; Tzipori et al., 1981; Gough et al., 1984; Harbour et al., 1987). Astrovirus disease in most species causes gastroenteritis, which is usually mild and self-limiting; however, more severe diseases have been described in poultry (Matsui & Greenberg, 2001).

**Turkey astrovirus**

In poultry, astroviruses are more commonly recognized as a problem in turkeys, and can be accompanied by a moderate increase in mortality (McNulty et al., 1980; Reynolds et al., 1987b; Reynolds, 1991; Jordan & Pattison, 1996; Koci et al., 2000b; Yu et al., 2000a). Turkey astrovirus (TAstV) was first described by McNulty et al. (1980), and was associated with turkey poults in the UK suffering from diarrhea and increased mortality. In the US, TAstV-1 was first identified in the 1980s (TAstV-2) and shown to be widely distributed (Saif et al., 1985; Reynolds & Saif, 1986; Reynolds et al., 1987b). Reynolds et al. (1987b) demonstrated that astroviruses could be isolated from 78% of diseased turkey flocks, more than any other virus identified. Recently, we have isolated and characterized a TAstV associated with poult enteritis mortality syndrome (PEMS), which is genetically and immunologically distinct from previously described US isolates (Koci et al., 2000b). The PEMS-associated TAstV (TAstV-2) was originally isolated from the thymus of infected poults (Schultz-Cherry et al., 2000). Experimentally infected poults exhibit thymus and bursal atrophy, and virus can be isolated in other tissues, although replication is only routinely detected in the intestines (Behling-Kelly et al., 2001).

**Duck astrovirus**

Unlike other species, astroviruses in ducks have been associated with a fatal hepatitis, historically known as duck hepatitis virus type II (DHV type II) (Asplin, 1965b; Gough et al., 1984, 1985; Woolcock & Fabricant, 1991). This disease was first described in the UK by Asplin in 1965, associated with duck flocks vaccinated for DHV type I, which is believed to be a picornavirus (Asplin, 1965a; Woolcock & Fabricant, 1991). This new disease was not neutralized by anti-DHV type I sera (Asplin, 1965a), and vaccination resulted in little cross-protection between type I and type II (Asplin, 1965b). It was postulated that DHV type II represented the emergence of a new serotype (Asplin, 1965b). Several years later, Gough et al. (1984) described another outbreak of fatal hepatitis in ducklings in the UK. Examination of livers from affected ducklings revealed the presence of astrovirus-like particles (Gough et al., 1984). Vaccination of ducklings with DHV type II vaccine strains described by Asplin (1965b) protected against this new isolate (Gough et al., 1985). Therefore, DHV type II was declared an astrovirus and it was proposed that the name be changed to duck astrovirus (DAstV), while DHV type I and a later described type III isolated in the US are still classified as picornaviruses (Woolcock & Fabricant, 1991).

**Avian nephritis virus**

ANV was first isolated from rectal contents of normal broiler chicks (Yamaguchi et al., 1979). Experimental infections demonstrated that ANV primarily results in a subclinical disease (Imada et al., 1979, 1983; Maeda et al., 1979; Yamaguchi et al., 1979; Jordan & Pattison, 1996), although mild growth depression and mortality has been reported
with the G-4260 strain (Imada et al., 1979; Shirai et al., 1991a; Reece et al., 1992). ANV typically causes histological changes in the kidneys (Shirai et al., 1989, 1991b, 1992; Jordan & Pattison, 1996), although viral antigens can be detected in the liver, spleen, pancreas, kidney, jejunum, and rectum (Imada et al., 1979, 1983). Young chicks are the most susceptible, with resistance to disease developing after the first month of life (Imada et al., 1981). Antibodies against ANV have been found in chicken and turkey flocks throughout the UK and Japan, suggesting a broad distribution (Nicholas et al., 1988; Takase et al., 2000). ANV was initially classified as a picornavirus, based on EM (Maeda et al., 1979; Yamaguchi et al., 1979). However, this classification was changed following the complete sequencing of the viral genome (Imada et al., 2000). ANV was shown to have all the molecular properties and gene organization consistent with the Astroviridae family (Imada et al., 2000; Matsui & Greenberg, 2001).

Genome Organization and Molecular Biology

Astroviruses have a positive-sense, single-stranded (ss), RNA genome, 6.8 to 7.9 kb in length (Matsui & Greenberg, 2001). The complete sequence of five human astrovirus (HAstV) isolates (Jiang et al., 1993; Lewis et al., 1994; Willcocks et al., 1994) (GenBank accession numbers AF141381 and AF260508), two turkey isolates (Jonassen et al., 1998; Koci et al., 2000b), ANV (Imada et al., 2000), and a sheep astrovirus (OAstV) (Jonassen et al., 1998) are available in GenBank. The basic organization and replication strategy is conserved among all of the astroviruses sequenced. The astrovirus genome includes a 5’ untranslated region (UTR), followed by three open reading frames (ORFs), a 3’ UTR, and a poly-A tail (Figure 1). There is a retrovirus-like frameshift structure between ORF1a and ORF1b, and ORF2 is expressed from a subgenomic RNA (ORF1a and ORF1b, and ORF2 is expressed from a subgenomic RNA (Figure 1). The length of each of these features varies between

![Genome Organization and Molecular Biology Diagram](image-url)
species and serotypes. The specific details of the mammalian astroviruses (MAstVs) are thoroughly reviewed in the current edition of *Fields Virology* (Matsui & Greenberg, 2001); therefore, this review will focus on properties of the AAstVs.

Among the three AAstVs there is some variation in the overall lengths of the genomes and their respective internal components (Table 1 and Figure 1). In addition to variation in ORF lengths, there are also differences in the expression strategies for ORF2. Most MAstVs (except HAstV-8) have an overlap of approximately eight nucleotides between the stop codon of ORF1b and the start codon of ORF2, which is in the same reading frame as ORF1a. However, the AAstVs deviate from this somewhat in their genome structure. The start codon for ORF2 of ANV is 19 nucleotides downstream of the stop codon of ORF1b, although ORF2 is still in the same frame as ORF1a (Figure 1). The space between the ORF1b stop codon and the ORF2 start site for both TAstVs is 18 nucleotides (Figure 1), placing the TAstV ORF2 in the same frame as ORF1b (Figure 1). There are also some differences among the AAstVs toward the end of the genome. Sequence analysis of the last 19 nucleotides of ORF2 and the adjacent 3' UTR by Jonassen et al. (1998, 2001) described a conserved sequence and predicted secondary structure present in all astrovirus isolates sequenced, except for TAstV-2 (Figure 1). This conserved motif is also present in infectious bronchitis virus (a coronavirus) and equine rhinovirus type 2 (a picornavirus), which the authors suggested was evidence of recombination events between these viruses (Jonassen et al., 1998).

### Sequence Analysis and Translation Strategies

#### Non-structural proteins

Analysis of the polypeptides of ORF1a and ORF1b from HAstVs indicate that these ORFs probably encode non-structural proteins (Gibson et al., 1998). Examination of HAstV ORF1a has identified four potential transmembrane helical motifs, a serine protease, a putative bipartite nuclear localization signal (NLS), and a region referred to as the immune response element identified by antiserum produced against purified particles (Gibson et al., 1998; Willcocks et al., 1999). ORF1a is translated as one polyprotein, which is post-translationally cleaved into functional peptides by the serine protease (Matsui & Greenberg, 2001). The presence and function of these peptides in the AAstVs have only been characterized by sequence analysis (Figure 1), although many of these motifs have been identified (Imada et al., 2000; Koci et al., 2000b).

The overall ORF1a sequence similarities between the AAstVs and the MAstVs is quite low, ranging from 20 to 25% nucleotide identity (12 to 15% amino acids). However, it is the presence of astrovirus-like non-structural motifs that is most important. ORF1a is also the most conserved among the HAstVs, and has been used to define two distinct genogroups (Belliot et al., 1997). This is not the case for the AAstVs sequenced to date. There is a greater relatedness among the HAstVs, and to lesser extent OAstV, than among AAstVs (Figure 2). This suggests AAstV non-structural proteins are allowed greater flexibility in sequence variation than their mammalian counterparts. This may be related to differences in host range (Schneider & Roossinck, 2001). There is no evidence that the MAstVs cross species line (Matsui & Greenberg, 2001). However, based on surveillance studies of chicken and turkey farms, antibodies against ANV were isolated from both chickens and turkeys, suggesting that either support ANV replication (Nicholas et al., 1988; Cavanagh, 1992). Having greater genetic flexibility may increase the likelihood of replicating in whatever poultry species is available, so long as the overall functional motif is conserved (Schneider & Roossinck, 2001). This hypothesis has not been tested experimentally, and it should be pointed out that more isolates need to be sequenced to fully understand its significance.

The best-described protein encoded in ORF1a is the serine protease (Willcocks et al., 1994; Gibson et al., 1998). This viral protease is similar to chymotrypsin-like proteases of other positive-sense RNA viruses, although it differs in that a serine residue has been substituted for a cysteine in the

### Table 1. Comparison of the nucleotide lengths of the AAstV genome regions

| Avian astrovirus | 5' UTR | ORF 1a | ORF 1b | ORF 2 | 3' UTR | Total* |
|-----------------|-------|-------|-------|-------|-------|-------|
| ANV             | 14    | 3012  | 1527  | 2052  | 305   | 6927  |
| TAstV-2         | 21    | 3378  | 1584  | 2175  | 196   | 7325  |
| TAstV-1         | 11    | 3300  | 1539  | 2016  | 130   | 7003  |

*Excluding the poly-A tail.
third catalytic position (Gorbalenya et al., 1989; Matsui & Greenberg, 2001). Alignments of the three AAstV ORF1a predicted amino acid sequences allowed for identification of a putative serine protease. When compared with the MAstV serine protease sequence, the three predicted catalytic residues can be identified and are conserved (Figure 3). There is a one-residue shift of the second catalytic amino acid (aspartic acid) between the AAstVs and the MAstVs; the significance of this is unknown. However, the serine residues do align, as well as many of the residues predicted to be important in substrate binding (Figure 3).

Downstream of the serine protease, ORF1a is believed to encode a NLS. This putative NLS is 664 amino acids from the N-terminus of the ORF1a polyprotein of HAstV1 (Willcocks et al., 1999). The need or function of a NLS in an RNA virus is

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**Figure 2.** Phylogenetic analysis of astrovirus ORF1a. The predicted amino acid sequence of ORF1a from HAstV-1 (accession number NC_001943), HAstV-3 (accession number AF141381), HAstV-8 (accession number AF260508), OAstV (accession number NC_002469), ANV, TAstV-1, and TAstV-2 were aligned using DNASTAR (Madison, WI, USA). An unrooted heuristic search was completed using PHYLIP.

| Sequence       | TastV-2 | TastV-1 | ANV | HAstV-1 | OAstV |
|----------------|---------|---------|-----|---------|-------|
| Accession      | NC_001943 | AF141381 | AF260508 | NC_002469 |       |
| Amino acid     |         |         |     |         |       |
| Length         | 697     | 647     | 621 | 551     | 544   |

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**Figure 3.** Alignment of the putative astrovirus serine protease. The predicted amino acid sequence of the serine protease from ORF1a of TAstV-1, TAstV-2, ANV, HAstV-1, HAstV-2 and OAstV were analyzed using DNASTAR. Residues in bold are conserved in all five sequences. The suspected catalytic triad for each virus is underlined. Numbers in parentheses are the number of residues not shown. Numbers at the end of each row are amino acid positions from the N-terminus.
still unclear, but several investigators described limited nuclear staining for astrovirus antigen (Aroonprasert et al., 1989; Willcocks et al., 1999). A similar motif was identified for ANV, corresponding to amino acid positions 719 to 735 (Imada et al., 2000). Similar amino acid sequences can be found in both TAstVs, but none of the putative AAstV NLSs have been tested experimentally.

ORF1a most probably encodes for several other non-structural proteins that have not been identified. Sequence analysis of all the astroviruses have not identified the presence of a VPg or a helicase, both being proteins that conventional wisdom would suggest were essential (Willcocks et al., 1994; Gibson et al., 1998; Matsui & Greenberg, 2001).

Another distinct feature of the astrovirus genome is its translation machinery for ORF1b (Marczinke et al., 1994). Sequence analysis of ORF1b does not yield a clear picture of the overall translation strategy. The first start codon of ORF1b for the HAstVs is found more than 400 nucleotides inside the reading frame, in a suboptimal position according to Kozak’s rules (Matsui & Greenberg, 2001). The ORF1a/ORF1b overlap region contains a heptameric shift sequence (AAA AAC) and the potential for the formation of a downstream stem-loop and possible pseudoknot that would provide a ribosomal frameshift mechanism (Willcocks et al., 1994; Lewis & Matsui, 1995, 1996; Imada et al., 2000; Koci et al., 2000b). This mechanism is similar to that used by retroviruses and coronaviruses; however, unlike those viruses, the pseudoknot is not required for the astrovirus frameshift to occur (Lewis & Matsui, 1997). This heptameric sequence, and predicted secondary structure has been identified in all three AAstVs (Figure 4).

It is believed that this frameshift structure allows for the translation of ORF1a and ORF1b to occur as one polyprotein that is then cleaved into functional subunits. Analysis of ORF1b indicates that it encodes for an RNA-dependent RNA polymerase (Poch et al., 1989; Ishihama & Barbier, 1994; Lewis et al., 1994; Marczinke et al., 1994). This region of the astrovirus genome is the most conserved between the MAstVs and the AAstVs, as well as among the AAstVs (Figure 5).

Figure 4. Analysis of the heptameric shift sequence and predicted frameshift structures of the AAstVs. (a) The predicted frameshift sequences of ANV, TAstV-1, and TAstV-2 were analyzed using DNASTAR. The heptameric ‘slippery sequence’ is outlined by a black box. Nucleotides shown in bold are predicted to be part of the retrovirus-like frameshift structure. (b) The RNA secondary structure of ANV, TAstV-1, and TAstV-2 was predicted using RNAfold (Scientific & Educational Software).
Structural proteins

ORF2 is translated from a subgenomic message, and encodes the viral capsid protein (Monroe et al., 1993). The capsid protein is translated as one long precursor protein of approximately 73 kDa (TAstV-2), 80 kDa (TAstV-1), or 74 kDa (ANV), which is post-translationally cleaved to form mature virion subunits in a mechanism that is not understood (Bass & Qiu, 2000). Both nucleotide and amino acid analyses of all the astrovirus capsid genes (Figure 6) demonstrate that the MAstVs are more closely related than the AAstVs (Jonassen et al., 2001). Analysis of ORF2, by different groups, showed that the N-terminal end of the capsid gene is generally more conserved than the C-terminal end (Jonassen et al., 2001; Wang et al., 2001). This observation may be useful in the design of oligonucleotide primers for a diagnostic reverse transcriptase-polymerase chain reaction (RT-PCR) test.

Diagnosis

Until recently, the most common method to identify astrovirus infection in birds was EM (Reynolds, 1991). However, only 10% of particles may exhibit the five-pointed or six-pointed star-like morphology, making it difficult to accurately identify astroviruses using direct EM, especially when there are very few viral particles present (Caul & Appleton, 1982; Reynolds, 1991; Matsui & Greenberg, 2001). Because of this limitation, Reynolds (1991) suggested using immune EM (IEM) to encourage viral aggregation. This is a reasonable alternative, although it should be pointed out that the addition of purified antibody or convalescent sera to a virus sample can actually mask the characteristic physical features or fail to detect new serotypes (Matsui & Greenberg, 2001). IEM can be an effective diagnostic tool if the antibody and the antigen it recognizes are completely characterized. For example, Guy & Barnes (1991) described the isolation and partial characterization of a small enterovirus-like virus isolated from turkeys with enteritis. Using a monoclonal antibody developed against that virus (generous gift from James Guy, North Carolina State University), we determined that it recognized recombinant TAsTV-2 capsid protein by western blot analysis, enzyme-linked immunosorbent assay, and immunofluorescence in transfected cells (unpublished observation). This suggests that TAsTV-2 was associated with diseased turkey flocks as early as 1991.
Diagnosis of both ANV and DAstV includes growth in embryonated eggs, as well as various serological tests (Asplin, 1965b; Gough et al., 1985; Nicholas et al., 1988; Decaestecker & Meulemans, 1991; Woolcock & Fabricant, 1991; Jordan & Pattison, 1996; Takase et al., 2000). These tests can be very accurate and rapid, although they are strain specific and, similar to IEM, risk misdiagnosis of new serotypes. TAstV can also be isolated in embryonated eggs, although no tools to detect the presence of antibodies against TAstV-1 or TAstV-2 have been described (Reynolds, 1991; Koci et al., 2000b). Furthermore, ANV is the only AAstV shown to replicate in cell culture (Imada et al., 1981).

Accurate detection of new AAstV isolates genetically similar to those already in GenBank is best accomplished using RT-PCR primers specific for each virus. By designing primers with knowledge of genome organization and conservation, one can select sites that are conserved among similar serotypes and potential new serotypes. We have previously described a RT-PCR protocol for the detection of TAstV-2 in field samples (Koci et al., 2000a). These primers have been used by our laboratory and others to detect TAstV-2-positive flocks in several states across the US. The ultimate diagnostic goal is the design of primers, or a panel of primers, that could be used to detect any AAstV from a clinical sample.

Analysis of the AAstV sequences suggests that a few areas may be useful for primer design. One potential site for primer design is the conserved sequence and RNA structure described in the 3’ end of the genome (Jonassen et al., 1998). This area has been described in almost all astroviruses to date, although TAstV-2 does not have this sequence (Koci et al., 2000b; Jonassen et al., 2001). Because this motif was not present in TAstV-2, many were not willing to accept that it was an astrovirus until it had been completely sequenced (Koci et al., 2000b). In addition, this conserved site is part of a stem loop structure, which makes the design and selection of primers without hairpins difficult. Primers specific to regions of the capsid gene are functionally more reliable, but would not be useful pan-specific diagnostic tools because of the large amount of sequence divergence among the AAstV capsid genes (Figure 6). However, capsid-based primers may be important in detection of specific serotypes.

Analysis of the most conserved gene of the AAstVs (ORF1b) indicates that there are potential priming sites that should cross-react between any two of the three viruses. However, potential sites specific for all three are not apparent. These three sequences have only 50% nucleotide identity, and the likelihood that a fourth would match all three in exactly the same two sites is unknown. Variation in this most conserved region suggests that degenerate primers may be the only solution for pan-reactive AAstV primers. Based on predicted amino acid alignments of ORF1b, several regions of conserved motifs can be identified that could be potential degenerate priming sites (Figure 7). However, to determine the most reliable and economic diagnostic technique, more AAstV isolates need to be fully characterized.

To ensure proper diagnosis and classification of any new SRV isolated, molecular characterization will be required. The failure of previously described astrovirus specific primers to detect an isolate does not infer the isolate is not an astrovirus. Classification needs to include determination of genome composition, gene organization and sequence similarities (van Regenmortel et al., 2000). Overlap in properties such as diameter, surface projections, buoyant density, and capsid proteins among the
SRVs (presented in Table 2) demonstrates that molecular properties are the most reliable characteristics for classification. If an isolate is determined to contain a ssDNA genome (Table 2), it is either a parvovirus or circovirus (van Regenmortel et al., 2000). These two viruses are distinguished (Figure 8a,b) by the presence of a circular DNA genome in circoviruses and the larger linear DNA genome of parvovirus (Berns et al., 2000; Todd, 2000; Todd et al., 2000, 2001). Conversely, isolates with ssRNA genomes are most likely to be picornavirus, calicivirus, astrovirus, or the part of the genus 'Hepatitis E-like viruses' (van Regenmortel et al., 2000). All of these viruses have positive ssRNA genomes of similar size. The major differences among these viruses are in their replication strategies and order of their genes. In Picornaviridae (Figure 8c), which includes the enteroviruses, the genome is translated into one polyprotein that is then cleaved into the individual structural and non-structural proteins (King et al., 2000). The caliciviruses and astroviruses differ from picornaviruses in that their genomes have distinct ORFs, each translated separately.

Figure 7. Amino acid alignment of AAstV ORF1b. The amino acid sequences of ORF1b of TastV-1, TastV-2, and ANV were analyzed using DNASTAR. Positions that are conserved in all three sequences are shown in bold. Regions of ORF1b with six or more consecutive conserved residues, which could be potential degenerate priming sites, are underlined.
overlaps both the first and second ORFs that encodes a protein of unknown function (Berke & Matson, 2000; Green et al., 2000c). By defining these molecular characteristics of any new isolate, that virus can be definitively assigned to a viral family, or can be demonstrated to be unique, suggestive of a new viral family. This ultimately leads to a more complete understanding of both AAstVs as well as virology at large.

### Treatment and Control

Strict containment is the only known method of preventing and controlling infections with any of the known astroviruses. Infected flocks, especially those that exhibit severe loss in viability and production, need to be treated with the utmost concern for biosecurity, strictly adhering to the principles discussed in Diseases of Poultry (Zander & Mallinson, 1991). Astroviruses are extremely stable in the environment and resistant to inactivation by most routinely used disinfectants (Kurtz et al., 1980; Abad et al., 1997; Schultz-Cherry et al., 2001), similar to chicken anaemia virus or foot-and-mouth disease virus. Studies in our laboratory with TAstV-2 demonstrated that partially purified astrovirus remained infectious following treatment with a panel of commercial disinfectants, including 10% bleach. The only products completely effective at inactivation were 0.3% formaldehyde, 1.5% Virkon S, 0.1% β-propiolactone, and 90% methanol. TAstV-2 is also very heat stable, resisting inactivation following treatment at 60°C for 10 min, and resistant to low pH (Schultz-Cherry et al., 2001). These findings suggest that, once a poultry production facility has been infected with astrovirus, complete sanitation of all materials and restricted access to facilities by personnel is required to contain the outbreak to an affected farm. To eliminate astrovirus infections, contaminated farms should be thoroughly disinfected. All the litter and manure should be removed and disposed of in a manner that ensures runoff does not contaminate the driveways or entrances to poultry houses. The floors, walls, fans, feeders, watering systems and all equipment should then be adequately scrubbed and disinfected using compounds and procedures proven useful at eliminating highly stable SRVs. Additionally, service personnel and attending veterinarians should be mindful of which farms are affected and those that are not, and should schedule their visits to these properties to minimize the risk of transporting the virus to healthy flocks either on their person or on their vehicles (Zander & Mallinson, 1991).

The combination of age susceptibility and highly stable virions suggest that multiple age farms may

| Viral family | Diameter (nm) | Surface structure | Chloroform resistance | Stable at 60°C for 10min | Number and size of expected proteins | Bouyant density | Genome |
|--------------|---------------|-------------------|-----------------------|--------------------------|-------------------------------------|----------------|--------|
| Circovirus   | 12 to 26      | None              | Yes                   | Yes                      | One capsid protein in some, 50 to 36 kDa | 1.33 to 1.37   | Circular ssDNA, 1.7 to 2.3 kb |
| Parovirus    | 18 to 26      | None              | Yes                   | Yes                      | Two to four major capsid proteins: VP1, 96 to 80 kDa; VP2, 85 to 64 kDa; VP3, 75 to 60 kDa; VP4, 52 to 49 kDa | 1.39 to 1.42   | Linear ssDNA, 4 to 6 kb |
| Picornavirus | 28 to 30      | None              | Yes                   | Some strains             | Four capsids: VP1, VP2, VP3, 41 to 24 kDa; VP4, 13.5 to 5.5 kDa VPg, 2.4 kDa | 1.33 to 1.45   | Linear +ssRNA, 7 to 8 kb |
| Calicivirus  | 30 to 38      | Cup-shaped depressions (not seen in Norwalk virus) | yes                   | Some strains             | One major capsid protein, 71 to 59 kDa One minor protein in some viruses, 30 to 28 kDa VPg, 15 to 10 kDa | 1.33 to 1.40   | Linear +ssRNA, 7.4 to 7.7 kb |
| Astrovirus   | 28 to 30      | 5- or 6-pointed star (only seen in ~10% of virions) | Yes                   | Yes                      | At least two major proteins, maybe three, 39 to 29 kDa Possible smaller proteins, 36 to 13 kDa | 1.36 to 1.39   | Linear +ssRNA, 7.2 to 7.9 kb |
help prolong the period of poor production as older birds may recover and no longer exhibit clinical signs but still harbor virus. There is no experimental evidence that affected poultry develop a protective immune response. This may explain why new poults routinely develop enteritis soon after being placed in ‘cleaned’ houses on farms with multiple aged birds (Edens & Doerfler, 1999). These factors also suggest that there is little hope for development of an effective vaccine strategy. The most practical prevention method is to use strict biosecurity prophylactically. A nominal investment of time and energy spent on keeping each farm pathogen free will greatly reduce the likelihood of contracting an astrovirus infection, and likewise periods of prolonged poor production. This strategy is also advantageous for the control of most other poultry diseases, as procedures successful in the inactivation of astroviruses also inactivate other pathogens (Brunet, 1997).

**Nomenclature**

The family *Astroviridae* is tentatively divided into two genera representing mammalian and avian astroviruses. The species within these genera are defined based on the animal that they infect (Table 3). There have been two different serotypes

| Nomenclature | Abbreviation |
|--------------|--------------|
| Mammalian astrovirus |             |
| Bovine astrovirus | BAstV        |
| Bovine astrovirus 1 | BAstV-1     |
| Bovine astrovirus 2 | BAstV-2     |
| Feline astrovirus | FAstV        |
| Feline astrovirus 1 | FAstV-1     |
| Human astrovirus | HAstV        |
| Human astrovirus 1 | HAstV-1     |
| Human astrovirus 2 | HAstV-2     |
| Human astrovirus 3 | HAstV-3     |
| Human astrovirus 4 | HAstV-4     |
| Human astrovirus 5 | HAstV-5     |
| Human astrovirus 6 | HAstV-6     |
| Human astrovirus 7 | HAstV-7     |
| Human astrovirus 8 | HAstV-8     |
| Ovine astrovirus | OAstV        |
| Ovine astrovirus 1 | OAstV-1     |
| Porcine astrovirus | PAstV       |
| Porcine astrovirus 1 | PAstV-1    |
| Avian astrovirus |             |
| Duck astrovirus | DAstV       |
| Duck astrovirus 1 | DAstV-1     |
| Turkey astrovirus | TAstV       |
| Turkey astrovirus 1 | TAstV-1    |
| Turkey astrovirus 2 | TAstV-2    |
| Chicken astrovirus | CAstV       |
| Avian nephritis virus | ANV        |

### Table 3. Genera and species described in the family *Astroviridae*

| Astrovirus species       | Abbreviation |
|--------------------------|--------------|
| Mammalian astrovirus     |             |
| Bovine astrovirus        | BAstV        |
| Bovine astrovirus 1      | BAstV-1      |
| Bovine astrovirus 2      | BAstV-2      |
| Feline astrovirus        | FAstV        |
| Feline astrovirus 1      | FAstV-1      |
| Human astrovirus         | HAstV        |
| Human astrovirus 1       | HAstV-1      |
| Human astrovirus 2       | HAstV-2      |
| Human astrovirus 3       | HAstV-3      |
| Human astrovirus 4       | HAstV-4      |
| Human astrovirus 5       | HAstV-5      |
| Human astrovirus 6       | HAstV-6      |
| Human astrovirus 7       | HAstV-7      |
| Human astrovirus 8       | HAstV-8      |
| Ovine astrovirus         | OAstV        |
| Ovine astrovirus 1       | OAstV-1      |
| Porcine astrovirus       | PAstV        |
| Porcine astrovirus 1     | PAstV-1      |
| Avian astrovirus         |             |
| Duck astrovirus          | DAstV        |
| Duck astrovirus 1        | DAstV-1      |
| Turkey astrovirus        | TAstV        |
| Turkey astrovirus 1      | TAstV-1      |
| Turkey astrovirus 2      | TAstV-2      |
| Chicken astrovirus       | CAstV        |
| Avian nephritis virus    | ANV          |

**Figure 8.** Diagram of basic small round virus genome organization. (a) Circovirus, (b) parvovirus, (c) picornavirus, (d) calicivirus, (e) astrovirus, (f) hepatitis-like virus. Untranslated regions are shown as unshaded regions, non-structural proteins are indicated with diagonal lines, and structural proteins are shown with solid shading. Unknown reading frames are indicated by cross-hatching.
described for bovine astroviruses, eight serotypes for HAstV, and two serotypes for TAstV. Serotypes are defined by a 20-fold or greater difference in cross-reaction of neutralization titers, and are assigned numbers (e.g. TAstV-1, TAstV-2). The ICTV number designation in absence of neutralization data is based on the order by which they were characterized in sufficient detail to be considered distinct types. Currently, there is no established nomenclature scheme for new isolates within Astroviridae. We propose that nomenclature should follow a model similar to that used for influenza virus, species/serotype/strain identified/location of isolation/year. For example, the PEMS-associated TAstV should be listed as: turkey astrovirus 2/North Carolina/034/1999 (TAstV-2/NC/034/99).

Conclusions

Astroviruses infect and cause disease in several animal species, but their overall impact on animal health and economics is not fully understood in any system (Matsui & Greenberg, 2001). Very few astroviruses have been adapted to propagate in cell culture, and there is no established animal model for astrovirus disease. It most systems, astrovirus infection results primarily in mild-to-moderate gastroenteritis with no observed pathologic changes outside the intestines. Astrovirus infections in birds have been reported to affect several different organs. TAstV, historically, has been described to cause gastroenteritis, growth depression, and a slight increase in mortality (McNulty et al., 1980; Saif et al., 1985; Reynolds & Saif, 1986; Reynolds et al., 1987a,b; Thouvellen et al., 1995a,b). More recently, TAstV-2 has been associated with PEMS and isolated from non-intestinal tissues (Koci et al., 2000b; Schultz-Cherry et al., 2000). ANV was described to cause subclinical pathologic changes to the kidneys of infected chicks (Yamaguchi et al., 1979), while DAstV infection can cause a fatal hepatitis in ducklings (Asplin, 1965b; Gough et al., 1985). Each of these viruses can be cultured in embryonated eggs, which makes studying the AAvs the most promising model for unlocking some of the unknowns about Astroviridae (Asplin, 1965b; Yamaguchi et al., 1979; Imada et al., 1982, 2000; Woolcock & Fabricant, 1991; Jordan & Pattison, 1996; Koci et al., 2000b).

Genomic alignments of the three AAvs completely sequenced suggest there is far less conservation in nucleotide sequence than that detected among the MAvs. This may change as new AAvs are isolated and characterized. Until recently, there has not been an active, ongoing survey for poultry flocks for astroviruses. This is partly due to a lack of tools specific for the detection of astroviruses. It is possible that more diseases of poultry, currently attributed to picorna-

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**RÉSUMÉ**

**Astrovirus aviaires**

Du fait que les volailles prennent plus d’importance dans l’économie mondiale, il est de plus en plus important de bien comprendre les mécanismes de maladie et les pertes de production qui affectent l’industrie. Dans le but de traiter plus précisément et plus raisonnablement ces maladies, une compréhension plus sophistiquée des interactions est nécessaire. Cette synthèse comprend l’histoire, le diagnostic, le traitement et le contrôle des astrovirus aviaires (AAstVs), en s’appuyant sur les résultats des recherches récentes en biologie moléculaire des AAstVs. Les astrovirus sont connus pour entraîner des symptômes chez les canards (astrovirus-1 du canard : DastV-1), les dindes (astrovirus-1 et –2 de la dinde : TastV-1 et –2) et les poulets (virus de la néphrite aviaire : ANV). Historiquement, le diagnostic reposait sur la microscopie électronique et l’immunomicroscopie. Pour fournir une détection plus rapide et plus sensible des astrovirus, des tests de diagnostic basés sur la biologie moléculaire sont nécessaires pour apporter une image plus précise de tout l’impact des astrovirus en pathologie aviaire. Cette synthèse compare les trois AAstVs séquencés: ANV, TastV-1 et TastV-2 dans le but d’identifier les régions conservées et les motifs qui pourraient servir de cibles à des outils de diagnostic. De plus, une nomenclature pour les astrovirus est également proposée, basée sur l’hôte, le type d’astrovirus/le pays/la référence/année d’isolement.

**ZUSAMMENFASSUNG**

**Aviare Astroviren**

Da das Geflügel in der Weltwirtschaft an Bedeutung gewinnt, ist es zunehmend wichtig, die Mechanismen von Krankheiten und mangelhafter Produktion, die die Geflügelwirtschaft beeinträchtigen, voll und ganz zu verstehen. Um diese Krankheiten genauer und angemessener zu behandeln, wird ein komplexeres Verständnis der Zusammenhänge benötigt. Die vorliegende Übersicht behandelt die Geschichte, Diagnose, Behandlung und Bekämpfung der aviren Astroviren (AAsV) mit besonderer Betonung der jüngsten Fortschritte in unserem Verständnis der Astrovirus-Molekularbiologie. Astroviren sind als Krankheitsursache an Extremist- und DastV-1, TastV-1 und –2 und Hühnern (avian Nephritisvirus, ANV) nachgewiesen worden. Die Diagnose ist immer schon stark auf die Elektronenmikroskopie und Immunelektronenmikro-
Roskopie angewiesen gewesen. Um für einen schnelleren und empfindlicheren Astrovirusnachweis im Feld zu sorgen, werden diagnostische Tests auf molekularer Grundlage benötigt, um ein genaueres Bild der gesamten Auswirkungen der Astroviren bei den Geflügelkrankheiten zu liefern. In der vorliegenden Übersicht werden die drei vollständig sequenzierten aviären Astroviren ANV, TAstV-1 und TAstV-2 verglichen, um konservierte Regionen und Motive zu identifizieren, die Angriffspunkte für pan-reactive AAstV-Mittel sein könnten. Außerdem wird auch eine Nomenklatur für die Astroviren vorgeschlagen, basierend auf: Wirtsspezies-Astrovirus-Typnummer/Land/(Staat)/Referenznummer/Jahr der Isolierung.

**RESUMEN**

**Astrovirus aviares**

La avicultura es cada vez más importante en la economía mundial y, por ello, también es cada vez más importante entender los mecanismos de las enfermedades y de las bajas producciones que afectan a esta industria. Con la finalidad de tratar estas enfermedades de forma más precisa y razonable, es necesario una comprensión más profunda de sus interrelaciones. Esta revisión contiene la historia, diagnóstico, tratamiento y control de los astrovirus aviares (AAstVs), con énfasis en los avances recientes en nuestra comprensión de la biología molecular de los AAstV. Los astrovirus causan enfermedad en patos (astrovirus del pato-1, DAvstV-1), en el pavo (pavo astrovirus-1 y –2, TAstV-1 y –2) y pollos (virus de la nefritis aviar, ANV). Históricamente, el diagnóstico se ha basado en la microscopía electrónica y en la inmunoelectromicroscopía. Para poder detectar de forma más rápida y sensible los astrovirus en el campo se requieren técnicas diagnósticas basadas en la biología molecular. Estas técnicas a su vez permitirán conocer de forma más precisa el impacto que tienen los astrovirus en las enfermedades de las aves. Esta revisión compara los tres virus que han sido totalmente secuenciados AAstV's, ANV, TAstV-1 y TAstV-2 para identificar las regiones conservadas y las secuencias diana que podrían ser usadas en técnicas pan-reactivas de AAstV. Además, se propone una nomenclatura para los astrovirus, basada en: especie huésped-astrovirus-tipo-úmero/país/estado/número de referencia/año de aislamiento.