2002.V022.04. ***Circoviridae*** **SG proposal** (now corrected in line with comment from EC)

1. Proposal: To recognise *Porcine circovirus 1* and 2 (PCV1, PCV2) as separate virus species in the *Circovirus* genus

2. Purpose: Porcine circovirus type 1 (PCV1) was isolated as a contaminant from porcine kidney cell line PK/15 in 1974. Porcine circovirus type 2 (PCV2) was isolated 1997 from pigs diseased with postweaning multisystemic wasting syndrome (PMWS).
The two viruses differ in the sequence of their genomic sequences, pathogenicity and antigenicity, while their other properties seem to be similar:

a) Genome sequence relatedness. PCV are the smallest viruses replicating autonomously in mammalian cells, the genome size of PCV1 is 1759 nt, of PCV2 1768 nt. The genomes of PCV1 and 2 are dominated by two open reading frames (*rep* and *cap*) transcribed divergently from the 111-bp origin of replication. The *rep* gene encodes the replication associated protein, the Cap protein is the major structural protein. Up to now, 46 isolates of PCV published in GenBank. After phylogenetic analyses, two separate clusters are found: The first cluster comprises seven sequences of PCV1, which show homology from 98.7 to 100%. The second cluster unites 39 sequences of PCV2, displaying an intra-group homology of 94.6 to 100% conserved nucleotides. If the PCV1 and PCV2 isolates are compared, a homology of 68.8 to 71.2 % is found. The degree of homology between PCV1 and 2 varies over the genome: While the origin of replication and the genes for the replication-associated protein, Rep, are highly conserved (80 and 82% homology), the *cap* gene encoding the structural protein shows more variance (62% homology between PCV1 and PCV2).

b) Natural host range. Antibodies to PCV1 and PCV2, and DNA specific to PCV1 and PCV2 have been detected in pigs. There is no substantiated evidence that these viruses do not replicate naturally in other species. Although antibodies reacting with porcine circovirus type 1(PCV) were found in sera of humans, mice and cattle, it was suggested that these were elicited by related circoviruses sharing antigenic epitopes with PCV (Tischer et al. 1995). No antibodies to porcine circovirus type 2 were detected in sera from cattle, sheep and humans. Experimental infection of lambs with this virus failed to produce lesions or seroconversion (Allan et al. 2000).

c) Cell and tissue tropism. Inoculation of leucocyte cells from pig sheep, cattle and a human with PCV1, demonstrated virus replication in cells derived from pigs and from cattle (Allan et al. 1994). PCV2 was found by PCR in almost all organs and tissues of one diseased animal (Mankertz et al. 2000).

d) Pathogenicity and cytopathogenicity. While PCV1 has been shown to be non-pathogenic in experimental infection of pigs (Tischer et al. 1986; Allan et al. 1995), the inoculation of pigs with PCV2 has led to reproduction of PMWS (Allan et al. 1999; Ellis et al. 1999). The role of PCV2 in other diseases than PMWS, as etiological agent of e.g. porcine nephropathy and dermatitis syndrome PNDS, is still a matter of debate.

e) Mode of transmission. A fecal/ oral route is supposed for transmission of PCV. PCV is also transmitted via the placenta (D. Tucker, pers. comm.). Experimentally, pigs are inoculated intranasally with PCV1 and 2.

f) Physicochemical properties of the virion. The capsids of PCV1 and PCV2 have the same icosahedral structure and and their diameters by EM are similar comparable, 14-16 nm (using PTA) and 16-18 nm (using UA).

g) Antigenic properties of viral proteins. First serological analysis revealed a seroprevalence of PCV up to 95% in different pig populations. This approach did not discriminate between PCV1 and PCV2 and has to be re-evaluated. A recent survey from Canada indicates that PCV2 appears to be the main PCV type circulating, and that serological evaluation using PCV1 underestimates the seroprevalence of PCV2 (Magar et al. 2000). PEPSCAN analysis performed on overlapping fragments of the genes encoding part of the rep gene and the entire cap gene led to the identification of five immunoreactive areas, one found on Rep and four on Cap. The ORF1-encoded Rep proteins in the two viruses were shown to be antigenically related, whereas the ORF2-encoded Cap proteins were recognized differentially by polyclonal anti-PCV2 antibodies (Mahe et al. 2000).

3. Revised organisation: The taxonomic implications for the family is that 2 different porcine circoviruses (PCV1 and PCV2) will be recognised as members of the genus. Porcine circovirus type 1 will be regarded as type species on the grounds that it was the first virus from this genus to be discovered and characterised and because the more is known about the molecular biology of this virus species than any of the other genus members.

4. Derivation of proposed name: The names *Porcine circovirus 1* (PCV1) and *Porcine circovirus 2* (PCV2) are currently used by those in the field and it is recommended that they should be adopted.

5. References:

Allan, G. M., Kennedy, S., McNeilly, F., Foster, J. C., Ellis, J. A., Krakowka, S. J., Meehan, B. M. und Adair, B. M. (1999). "Experimental reproduction of severe wasting disease by co-infection of pigs with porcine circovirus and porcine parvovirus." J Comp Pathol 121(1): 1-11.

Allan, G. M., McNeilly, F., Cassidy, J. P., Reilly, G. A., Adair, B., Ellis, W. A. und McNulty, M. S. (1995). "Pathogenesis of porcine circovirus; experimental infections of colostrum deprived piglets and examination of pig foetal material." Vet Microbiol 44(1): 49-64.

Allan, G. M., McNeilly, F., Foster, J. C. und Adair, B. M. (1994). “Infection of leucocyte cell cultures derived from different species with pig circovirus.” Vet Microbiol 41(3): 267-79.
Allan, G. M., McNeilly, F., McNair, I., Curran, M. D., Walker, I., Ellis, J., Konoby, C., Kennedy, S. und Meehan, B. (2000). “Absence of evidence for porcine circovirus type 2 in cattle and humans, and lack of seroconversion or lesions in experimentally infected sheep.” Arch Virol 145(4): 853-7.
Ellis, J., Krakowka, S., Lairmore, M., Haines, D., Bratanich, A., Clark, E., Allan, G., Konoby, C., Hassard, L., Meehan, B., Martin, K., Harding, J., Kennedy, S. und McNeilly, F. (1999). “Reproduction of lesions of postweaning multisystemic wasting syndrome in gnotobiotic piglets.” J Vet Diagn Invest 11(1): 3-14.
Hamel, A. L., Lin, L. L. und Nayar, G. P. (1998). “Nucleotide sequence of porcine circovirus associated with postweaning multisystemic wasting syndrome in pigs.” J Virol 72(6): 5262-7.
Magar, R., Muller, P. und Larochelle, R. (2000). “Retrospective serological survey of antibodies to porcine circovirus type 1 and type 2.” Can J Vet Res 64(3): 184-6.
Mahe, D., Blanchard, P., Truong, C., Arnauld, C., Le Cann, P., Cariolet, R., Madec, F., Albina, E. und Jestin, A. (2000). “Differential recognition of ORF2 protein from type 1 and type 2 porcine circoviruses and identification of immunorelevant epitopes.” J Gen Virol 81 Pt 7: 1815-24.
Mankertz, A., Domingo, M., Folch, J. M., LeCann, P., Jestin, A., Segales, J., Chmielewicz, B., Plana-Duran, J. und Soike, D. (2000). “Characterisation of PCV-2 isolates from Spain, Germany and France.” Virus Res 66(1): 65-77.
Tischer, I., Bode, L., Apodaca, J., Timm, H., Peters, D., Rasch, R., Pociuli, S. und Gerike, E. (1995). “Presence of antibodies reacting with porcine circovirus in sera of humans, mice, and cattle.” Arch Virol 140(8): 1427-39.
Tischer, I., Mields, W., Wolff, D., Vagt, M. und Griem, W. (1986). “Studies on epidemiology and pathogenicity of porcine circovirus.” Arch Virol 91(3-4): 271-6.

2002.V023.04.*Circoviridae* SG

1. Proposal: To classify *Pigeon circovirus* (PiCV) as a new member of the genus *Circovirus*

2. Purpose: Infections of pigeons with a circovirus-like virus were reported in the early 1990s. In the 7th ICTV Report, this virus, named Pigeon circovirus (PiCV), was recognised as an "unassigned" member of the family *Circoviridae* , on the basis of low-level DNA homology shared with beak and feather disease virus (BFDV), (Wood et al. 1994). There have now been 2 recent, independent reports describing the genomic sequence analysis of the *Pigeon circovirus* (Mankertz et al., 2000; Todd et al., 2001), and these provide the evidence to support this proposal.

These papers indicate that the genome of *Pigeon circovirus* shares a number of genomic features with BFDV and *Porcine circovirus 1* and 2 (PCV1, PCV2). These features include:

i) A potential stem loop and semi-conserved nonanucleotide motif, at which rolling circle replication (RCR) of the virus DNA is postulated to initiate,

ii) 2 major ORFs: the V1 ORF on the virus sense strand of the putative, circular double-stranded replicative form (RF), which is postulated to encode the replication associated (Rep) protein, and the C1 ORF on the complementary sense strand, which is postulated to encode the Capsid protein

iii) Existence of substantial levels of amino acid identity, when the Rep proteins of viruses of this genus are compared.

iv) Conserved amino acid motifs relating to RCR and dNTP-binding activity occur within the Rep proteins of viruses from this genus.

3. Revised organisation: The taxonomic organisation of the family remains the same except that *Pigeon circovirus* is classified as an additional member of the genus *Circovirus*, and not as an unassigned member of the family.

4. Derivation of proposed name: Although the name "columbid" circovirus was suggested in the paper by Mankertz et al. (2000) and was favoured by some members of the Study Group, on balance the name "*Pigeon circovirus*" was selected on the grounds that it is more commonly used by those working in the field and in previously published papers, and is the name used previously in the 7th ICTV Report (Todd et al., 2000). In addition, although it may very well turn out to be the case, we cannot be certain whether all avian species encompassed by the term "columbid" will be infected by the same virus species. Also, the choice of "*Pigeon circovirus*" as opposed to "columbid circovirus" is more consistent with the names chosen in the 2nd and 3rd new proposals concerning "*Goose circovirus*" and *Canary circovirus*". Therefore, we propose the name "*Pigeon circovirus*". The acronym selected "PiCV" is that used previously (7th ICTV Report) and allows distinction with PCV (*Porcine circovirus*).

5. References:

Mankertz, A., Hattermann, K., Ehlers, B., and Soike, D. (2000). Cloning and sequencing of columbid circovirus (CoCV), a new circovirus from pigeons. Arch. Virol. 145, 1-11.

Todd, D., Weston, J.H., Soike, D., Smyth, J.A. (2001). Genome sequence determinations and analyses of novel circoviruses from goose and pigeon. Virol. 286, 354-362.
Woods, L.W., Latimer, K.S., Niagro, F.D., Riddell, C., Crowley, A.M., Anderson, M.L., Daft, B.M., Moore, J.D., Campagnoli, R.P., Nordhausen, R.W. (1994). A retrospective study of circovirus infection in pigeons: nine cases (1986-1993). J. Vet. Diag. Invest. 6**,** 156-164.

2002.V024.04. *Circoviridae* SG

1. Proposal: To classify *Goose circovirus* (GoCV) as an additional member of the genus *Circovirus*

2. Purpose: A circovirus-like virus was detected in commercial geese in association with a runting syndrome (Soike et al., 1999). The genome of this virus has now been isolated, cloned and sequenced (Todd et al., 2001). Sequence analysis showed that its genome exhibits features, which are in common with porcine circoviruses types 1 and 2 (PCV1, PCV2), BFDV and *Pigeon circovirus*.
These features include:
i) A potential stem loop and semi-conserved nonanucleotide motif, at which rolling circle replication (RCR) of the virus DNA is postulated to initiate,
ii) 2 major ORFs: the V1 ORF on the virus sense strand of the putative, circular double-stranded replicative form (RF), which is postulated to encode the replication associated (Rep) protein, and the C1 ORF on the complementary sense strand, which is postulated to encode the Capsid protein
iii) Existence of substantial levels of amino acid identity when the Rep proteins of viruses of this genus are compared.
iv) Conserved amino acid motifs relating to RCR and dNTP-binding activity occur within the Rep proteins of viruses from this genus.

3. Revised organisation: The taxonomic organisation of the family remains the same except that *Goose circovirus* is classified as an additional member of the genus *Circovirus*.

4. Derivation of proposed name: The name, "*Goose circovirus*", and acronym, "GoCV" are consistent with that used above in relation to "*Pigeon circovirus*" taxonomic proposal, where the english name of the avian species has been selected. There are additional reasons for selecting "*Goose circovirus*" instead of the name "anatid circovirus" or "anserine circovirus", which use names derived from the Family (Anitidae) and Order (Anseriformes) respectively. Thus, at this stage we cannot be certain whether all avian species encompassed by the term "anatid" or "anserine"will be infected by the same virus species. Therefore, we propose the name "*Goose circovirus*". The acronym selected "GoCV", as opposed to "GCV" will permit easier distinction between goose circovirus and other, yet-to-be characterised circoviruses such as gull circovirus, for which the acronym "GuCV" might be proposed.

5. References
Todd, D., Weston, J.H., Soike, D., Smyth, J.A. (2001) Genome sequence determinations and analyses of novel circoviruses from goose and pigeon. Virol. 286, 354-362.
Soike, D., Kohler, B., Albrecht, K. (1999) A circovirus-like infection of geese related to a runting syndrome. Avian Path. 28, 199-202.

2002.V025.04. *Circoviridae* SG

1. Proposal: To classify *Canary circovirus* (CaCV) as an additional species of the genus *Circovirus*

2. Purpose: A circovirus-like virus has been detected in canaries in association with a disease known in the industry as "Black Spot" (Goldsmith et al., 1995). The occurrence of a circovirus in a diseased canary was confirmed by nucleotide sequence determination (Todd et al., 2001). The genome of this circovirus has now been isolated, cloned and sequenced (Phenix et al., 2001). Sequence analysis showed that its genome exhibits features, which are in common with porcine circoviruses types 1 and 2 (PCV1, PCV2), BFDV, *Pigeon circovirus* and *Goose circovirus*
These features include:
i) A potential stem loop and semi-conserved nonanucleotide motif, at which rolling circle replication (RCR) of the virus DNA is postulated to initiate,
ii) 2 major ORFs: the V1 ORF on the virus sense strand of the putative, circular double-stranded replicative form (RF), which is postulated to encode the replication associated (Rep) protein, and the C1 ORF on the complementary sense strand, which is postulated to encode the Capsid protein
iii) Existence of substantial levels of amino acid identity when the Rep proteins of viruses of this genus are compared.
iv) Conserved amino acid motifs relating to RCR and dNTP-binding activity occur within the Rep proteins of viruses from this genus.

3. Revised organisation: The taxonomic organisation of the family remains the same except that *Canary circovirus* is classified as an additional member of the genus *Circovirus*.

4. Derivation of proposed name: The name, "*Canary circovirus*", and acronym, "CaCV" are consistent with those used above in relation to taxonomic proposals for pigeon and goose circoviruses. There are additional reasons for selecting "*Canary circovirus*" instead of the names "fringillid circovirus" or , in which the family/ subfamily name is used . Thus, at this stage we cannot be certain whether all avian species encompassed by the term "fringillid" will be infected by the same virus species. Also, as outlined above, whereas mammalian viruses tend to be called by their family names eg equine herpesvirus, bovine adenovirus etc, this is not the case with avian viruses, for which the english names have tended to be adopted eg goose parvovirus, fowl adenovirus. Also, the term "canary" is more widely known in avian circles than the term "fringillid". Therefore, we propose the name "*Canary circovirus*". The acronym selected "CaCV", as opposed to "CCV" will avoid confusion with that adopted for "Channel Catfish virus (CCV)".

This choice of name and acronym is also consistent with those in the adjoining proposals (1 and 2), in which the names "*Pigeon circovirus*" and "*Goose circovirus*" are proposed.

5. References

Goldsmith, T.L. (1995) Documentation of passerine circoviral infection (Abstract) Proceedings of the Annual Conference of the American Association of Avian Veterinarians, Philadelphia (pp. 349-350).

Todd, D., Weston, J. H., Ball, N.W., Borghmans, B.J., Smyth, J.A., Gelmini, L. , Lavazza A. (2001) Nucleotide sequence - based identification of a novel circovirus of canaries. Avian Path. 30, 321-325.

Phenix, K.V., Weston, J.H., Ypelaar, I, Lavazza, A., Smyth, J.A., Todd, D., Wilcox, G.E., Raidal, S.R. (2001) Nucleotide sequence analysis of a novel circovirus of canaries and its relationship to other members of the genus *Circovirus* of the family *Circoviridae.* J. Gen. Virol. 82, 2805-2809.

Appendix 1

Pair-wise comparisons of amino acid identities of the Rep and Capsid proteins shared by existing and proposed new members of the genus *Circovirus*

				V1 ORF (Rep)		
	GoCV	**PiCV**	**CaCV**	**BFDV**	**PCV2**	**PCV1**
GoCV	-	44.7	45.4	46.4	43.2	44.1
PiCV	22.4	-	63.1	58.2	42.0	41.2
CaCV	23.6	40.1	-	60.3	40.4	42.3
BFDV	24.6	37.9	41.2	-	43.9	43.3
PCV2	28.2	27.2	28.3	26.8	-	86.0
PCV1	29.1	24.6	28.1	25.4	66.0	-

C1 ORF (Capsid)