

# Chapter 2

## Materials and Methods

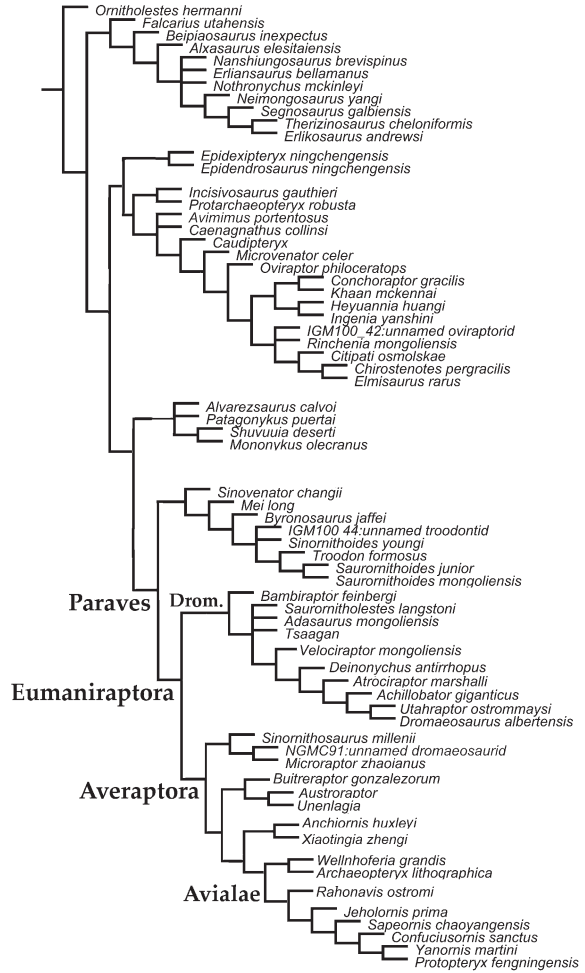
### Institutional Abbreviations

HMN	Museum für Naturkunde, Berlin, Germany;
IVPP V	The Institute of Vertebrate Paleontology and Paleoanthropology, Beijing, China;
MCF PVPH	Museo Carmen Funes, Plaza Huinul, Neuquén, Argentina;
MML	Museo Municipal de Lamarque, Lamarque, Río Negro, Argentina;
MPCA	Museo Provincial Carlos Ameghino, Cippolletti, Río Negro, Argentina;
UA	University of Antananarivo, Madagascar;
YPM	Yale Peabody Museum, Yale, USA.

In order to study sequences of appearance of synapomorphies in the theropod line to birds, we have polarized ingroup characters in the data matrix based on outgroup comparisons (i.e., *Allosaurus* and *Sinraptor*). Most characters are coded as binary (0, plesiomorphic; 1, apomorphic), with the exception of some multistate characters, for which 0 is plesiomorphic and 1,2, and/or 3 represents apomorphic states, considered as a progressive sequence. Question mark (?) indicates that the character state is unknown in available specimens. The script (-) indicates that due to the high apomorphic modifications of the taxon, the character state cannot be checked. These codifications are tabulated in a data matrix to show the distributions of character states.

With the aim to analyze the phylogenetic relationships of Dromaeosauridae with respect to other paravians we performed a phylogenetic analysis using the most recent version of the data matrix published by the TwiG, presented by Hu et al. (2009) and modified by Agnolín and Novas (2011). Definitions of characters 1 through 363 follow Hu et al. (2009); characters 364 through 366 have been modified from Novas et al. (2009). We added characters 369–412 from Xu et al. (2008) dataset. Character 367 is from Gianechini et al. (2009), character 368 has been added from Zheng et al. (2009), characters 413–415 have been added from Xu (2002), characters 416–426 were added from Xu et al. (2011a), and characters 427–429 are added from Osmólska et al. (2004). We have modified character 240 from Hu et al. (2009), in reducing the number of character states from 4 to 2. In this way, the present analysis contains one of the most comprehensive dataset employed up to now, consisting of 88 taxa scored

**Fig. 2.1** Phylogenetic analysis of derived coelurosaurian theropods. Present strict consensus tree depicts Microraptorina, Unenlagiidae, and (*Anchiornis* + *Xiaotingia*) as successive sister-groups of Avialae. *Abbreviations* Drom., Dromaeosauridae



for 429 characters (see Appendix 1, 2). Codifications by previous authors were analyzed in detail, and consequently, several characters from the combined data matrix of Xu et al. (2008), Hu et al. (2009) and Agnolín and Novas (2011), and Xu et al. (2011a) were re-scored (Appendix 2).

Phylogenetic analysis was performed using TNT 1.1 (Goloboff et al. 2008). All characters were equally weighted and treated as unordered. A heuristic search was performed with 10,000 replicates of the tree bisection and reconnection (TBR) branch-swapping algorithm. The maximum number of trees saved for each random addition sequence replicate was set to 100.

The phylogenetic analysis resulted in the recovery of 50 Most Parsimonious Trees (MPTs), which bring a Strict Consensus Tree of 1841 steps, with a consistency index of 0.27, and a retention index of 0.69 (Fig. 2.1).

As proposed by Makovicky et al. (2005), we consider *Neuquenraptor argentinus* Novas and Pol (2005) as junior synonym of *Unenlagia comahuensis* Novas and Puerta 1997 (contra Porfiri et al. 2011), and we follow Agnolín and Novas (2011) in the use of the original family name Unenlagiidae Bonaparte (1999) (instead of Unenlagiinae; sensu Makovicky et al. 2005), to emphasize the distinctiveness of this theropod group.

## References

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