**Supplementary Information 5: Summary of results for each factor.**

**This document contains a summary of the results found for each factor and an extended discussion of the implications of these.**

*Species*

Differences between *species* are discussed in the main text.

*Specimen*

The use of *specimen* was largely to encapsulate inter-individual variation. The within-species datasets demonstrated this as a significant effect in 23 of 32 comparisons across the four DMTA variables. However this effect was not significant when these eight species were combined into a single dataset. This is likely due to the sheer number of comparisons involved with the 353 specimens being compared. Any inter-individual variation for such a large dataset would be swamped by greater variation between species. This also demonstrates how comparisons of interspecific factors across multi-species datasets can be misleading.

Inter-individual variation in *specimen* was thought to perhaps encapsulate other factors such as *wear* and *ecoregion*. However both those factors were utilised in final models developed by the GLMM process. This suggests that inter-individual variation is due to other factors, or combinations of factors, including some not considered here, such as year and season that the specimen was collected particularly given the well-known ‘last supper phenomenon’ regarding dental microwear formation, and natural variations in diet (Calandra and Merceron, 2016). This finding also supports the use of *specimen* as a random factor in the GLMM models, as it likely represents a number of factors that in concert do not fit an easily modelled distribution (Zuur et al., 2009). This approach may also provide some of the utility behind *specimen,* as it allows for natural inter-individual variation as a random factor, while controlled inter-individual variation is predictively modelled (e.g. for *ecoregion*).

*Microscope*

Subsampling indicated that separating data by microscope enabled taxa to be distinguished with lower sample sizes for *Asfc* but not *epLsar,* and showed little to no improvement in distinguishing taxa for *Sdr* or *Vvv.* The two taxa which could be compared for *microscope* showed significant differences between microscopes in six of eight comparisons, and all four across the entire dataset. Microscope featured in the final GLMM models for *Asfc, Sdr* and *Vvv.* The effects of this cannot be visualised as the factor has only two levels and modelling requires one of these to be the dummy variable (Zuur et al., 2009).

Microscope was included in this analysis as it is known to differ between instruments, however it was hoped that the filter of Arman et al. (Arman et al., 2016) would minimise any systematic differences. While this appears to be largely the case for *epLsar,* it seems that differences are still apparent in the three other SSFA variables considered here*.* Unless further improvements can be made to the (Arman et al., 2016) method, or an alternate fix is found, these differences can only be managed by incorporating such factors into analysis. Doing so however should not present any serious difficulty, as such systematic differences are likely to be largely uniform and so easier to model than other factors.

*Element*

Subsampling was unable to determine if separating samples by element assisted in differentiating between species, as species sampled across upper and lower molars showed good separation of taxa prior to controlling for element. Of the two species where element was considered in isolation neither showed any difference for any variable. There were differences seen across the entire dataset, but confounding effects are likely. Element featured only in the final GLMM model for complexity (*Asfc*).

That element was seen to differ at all was somewhat surprising as the biomechanics of occlusion should suggest similar forces being found on the opposing wear facets, however experimental studies have shown that human teeth with slight irregularities, and even some without, show marked asymmetry in forces between upper and lower teeth (Osborn, 1961). Indeed, a number of other factors; that the dentary is mobile while the maxilla static, that the movement of foods are effected by other factors (e.g. the tongue), and that upper and lower molars possess quite different morphologies, may all be aspects which could lead to differences in microwear based on *element*. Indeed, differences have been noted previously, with (Schulz et al., 2010) analysing upper and lower teeth separately due to differences found. It then may be likely that differences between upper and lower teeth reflect complexities in the occlusal cycle, particularly considering *element* featured alongside *tooth* and *facet* in the final complexity GLMM model.

*Tooth*

Subsampling revealed little or no improvement in differentiating between *M. robustus* and *W.bicolor* for any variable when controlling for tooth. In the within-species analyses, *tooth* differed only in five of the 32 comparisons undertaken. No significance for tooth was seen when considered across the whole dataset. Tooth features in the final GLMM models for *Asfc* and *Sdr*, and the modelled effect of *tooth* can be seen in figure S4.1. This shows little difference between molars 1-3, but that *Asfc* and *Sdr* are slightly elevated for M4. Results for MX and MY are of little relevance as these were a small number of specimens for which tooth position was unknown.



#### Figure S5.1: Effects of tooth on interspecific models of DMTA data. Mean and 95% confidence intervals of ecoregion effects of models produced by GLMM (see main text table 5). Area-scale fractal complexity (*Asfc*) left; developed interfacial area ratio (*Sdr*) right. All variables normalised prior to analysis (see SI1), ‘dP3’ tooth used as dummy variable .

*Tooth* was considered *a priori* to be likely to effect microwear as the position of each *tooth* in the dental arcade should alter the size of particles being chewed in different parts of the mouth (Lucas, 2004), or that the forces of occlusion may vary with increasing distance from the fulcrum of the temporomandibular joint (Bakke, 2006). Inter-tooth differences in other herbivores have been rarely investigated in DMTA, though have been noted in canids along a number of parameters (Ungar et al., 2010) as well as *Equus grevyi* (Grevy’s Zebra) in Textural fill volume, an SSFA variable, and *Sal,* an STA variable, but not in *Asfc,* *epLsar*, or *Vvv* which were tested for (Schulz et al., 2010).

That there was little effect of tooth position may be in part due to molar progression. Molar progression is the anterior movement of teeth throughout an animal’s life and is best exemplified in macropodids (Lentle et al., 1999). This means that later in life posterior molars become effectively anterior molars, which may equalise any inter-tooth effects. With most differences focused between M4 and other teeth may be as this posterior-most molar rarely reaches an anterior position. One possibility to consider for future studies would be only considering microwear on molars 1-3.

*Facet*

Subsampling revealed that when controlling for *facet*, differences between *M. robustus* and *W. bicolor* were more evident for *Asfc, Sdr* and *Vvv,* but not *epLsar.* As mentioned in the main text, *facet* was the only factor aside from the necessary *species* and *specimen* that featured in each of the models favoured by the GLMM process. The effect of *facet* on the GLMM models is illustrated in figure S4.2. This demonstrates clear inter-facet differences for each of the four variables. It should be noted that that among the most variable facets were those with the lowest sample sizes (e.g., facet 2 *n*=23; facet 7 *n*=34) and the least variable were those with extensive sampling (facet 6 *n*=423; facet 9 *n=*235).

Overall, facet was one of the most consistently significant variables found, echoing well known concerns of inter-facet variation (Gordon, 1984, Krueger et al., 2008, Haupt et al., 2013). Ensuring consistent documentation of facets scanned then should be a priority for ongoing research. In addition, understanding differences between facets will help understand both DMTA differences and the functional morphology underlying it.



#### Figure S5.2: Effects of tooth on interspecific models of DMTA data. Mean and 95% confidence intervals of ecoregion effects of models produced by GLMM (see main text table 5). Left to right: Area-scale fractal complexity (*Asfc*); exact-proportion Length-scale anisotropy of relief (epLsar); developed interfacial area ratio (*Sdr*), and void volume of the valleys at a material ratio of 80% (*Vvv*). All variables normalised prior to analysis (see SI1), Facet 1 used as dummy variable.

Initial analyses also considered a number of reclassifications of facets as a more simplistic breakdown of inter-facet differences. This is due to skewed sample sizes because of larger facets having a higher likelihood of preserving dental microwear. Additionally, the bilophodont condition of macropodoids resulted in the repetition of functionally homologous facets between lophs. Facets were thus reclassified in three ways based on the upper molar to establish a more simplistic classification that would be better delineate inter-facet differences. *Facet side* reclassified facets based on position relative to the buccal or lingual margin of the tooth midline. *Facet face* specifies whether the facet exists on the anterior or posterior loph face. *Facet side + face* combines these anterior-posterior and buccal-lingual positional information into a single factor.

The reclassifications of *facet* (*facet side, facet face,* and *facet side + face*)were less able to discriminate the taxa than when controlling for *facet.* Comparable results were seen however for *facet side + face* in *Asfc.* For the within-species analyses, significant differences were apparent for all taxa except *T. thetis* for most variables. More significant differences were found for *Facet* (15), and *Facet side + face* (17), than *Facet side* (7), or *Facet face* (13). When considered across species, differences were only rarely evident, demonstrating that variation may be hard to detect when considered in multi-species datasets.

The reclassifications were considered as a simpler categorisation of their functional significance. That they were less successful than the original classifications suggests that despite similarities in apparent function at equivocal parts of each loph, there are still functional differences between each facet which alter microwear.

*Wear*

The subsampling analysis showed considerable improvement in differentiation between *M. robustus* and *W. bicolor* when the data were separated by *wear* stage for *Asfc,* and *Sdr,* but not *epLsar* or *Vvv.*

In isolation, differences between *wear* stages was significant only for 8 of 32 comparisons. The GLMM process featured *wear* in the final model for *epLsar*. The effect of *wear* in this final GLMM model for anisotropy is demonstrated in figure S4.3. While clearly overlapping, this demonstrates decreasing modelled anisotropy for more worn teeth. One explanation for this may be that as teeth wear the orientation of occlusal surfaces becomes decreased (McArthur and Sanson, 1988), so the movement of foods down a facet is lessened, leading to lower anisotropy values. Another possibility is that *wear* correlates with age (Death and Coulson, 2016), and demonstrates change in diet as an animal ages.



#### Figure S5.3: Effects of wear on interspecific models of anisotropy data. Mean and 95% confidence intervals of ecoregion effects of exact-proportion Length-scale anisotropy of relief (*epLsar*) models produced by GLMM (see main text table 5). Data normalised prior to analysis (see SI1), Wear stage 1 used as dummy variable.

*Taphonomy*

As there are no taxa which feature in both the modern and palaeontological datasets here, *taphonomy* cannot be considered by subsampling or the within-species analyses. *Taphonomy* was however significant in three of four comparisons across the whole dataset. It should be noted however that lumping the data in this way can be misleading. Note for instance that when lumped, the single species comparisons for *Asfc* found no significant differences for *facet* despite significant differences being noted in *Asfc* for facet in a number of species in isolation as well as the final GLMM model. *Taphonomy* did not feature in any final GLMM models, suggesting that taphonomic factors are not of major concern in this dataset.

*Ecoregion*

The subsampling analysis showed some differences between variables when controlling for a single *ecoregion* (tropical grasslands). For example, differences between *M. robustus* and *W. bicolor* for complexity were much greater when controlled for *ecoregion*, while those for *Vvv* were possibly less evident than for the whole dataset. However, *ecoregion* was included in the final models for *Asfc*, *Sdr* and *Vvv.* These seemingly contradictory results for *Vvv* make an important point. It may be that rather than acting universally improving differentiation between species, some levels of factors may in fact indicate circumstances that do not distinguish taxa. For instance it may be that in tropical grasslands taxa cannot be differentiated, but that in temperate forests they can.

The modelled effects of *ecoregion* also indicate the effects of each ecoregion on DMTA data (Figure S4.4). These show similar effects for each variable, with temperate grasslands having a broad range encapsulating the majority of all other data. Tropical grasslands and forests had lower variation, but similar central ranges, while temperate forests and deserts had low and high values respectively. Referring to known characteristics of complexity (*Asfc*), this accords with our understanding. High complexity values for deserts would be consistent with consumption of harder desert grasses (e.g. spinifex) and shrubs in contrast to more succulent vegetation in temperate forests. The implications of central tendencies for temperate grasslands and both tropical ecoregions are unclear.



#### Figure S5.4: Effects of ecoregion on Interspecific models of DMTA data. Mean and 95% confidence intervals of ecoregion effects of models produced by GLMM (see main text table 5) Plots left to right: Area-scale fractal complexity (*Asfc*); developed interfacial area ratio (*Sdr*), and void volume of the valleys at a material ratio of 80% (*Vvv*). All variables normalised prior to analysis (see SI1), ‘N/A’ ecoregion used as dummy variable .

Why DMTA data differ between ecoregions is largely due to environmental factors. *Ecoregions* were originally designed as a conservation tool to categorise ecosystems which share similar species compositions (Olson et al., 2001). While this overall is unlikely to directly affect microwear, the distributions of these taxa likely reflect underlying parameters such as rainfall and temperature (Olson et al., 2001). In addition, the inclusion of plant communities in ecoregion classification (Olson et al., 2001) is likely to have a more direct impact on microwear differences. This leads us then to consider what it is about different ecoregions that causes differences to be present. A few possibilities for such could be the plant communities themselves, however it is unclear which factors of the plants present (e.g. toughness of tissues, presence of phytoliths, C3/C4 pathway) differentiate microwear. Alternatively it may be the relative abundance of particular plants or even the presence of other herbivores through niche partitioning which effects the microwear of a species across *ecoregions*. Another possibility which may be reflected in microwear is gross aridity, particularly considering the ongoing discussion on the effect of airborne dust on microwear (e.g. (Lucas et al., 2013, Ryan, 1979, Ungar et al., 1995). Ultimately, determining which of these factors are relevant to DMTA may be undertaken by considering data where such factors can be controlled, such in vitro studies, or specimens where gut contents are available for direct comparison.

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